

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LLVVPWTQRFFDSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFQKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG |
| 1595 | 7092 | A | 1718 | 41 | 597 | APSPRRPWVISQRRTKATITSLWKG \VNVE\DAGGETLGRLLVVPWT\ QRFFD\SFGNLSSASAIHGQPPKVQ GTWSKKVLTFLGEMP*KHL\DDLK GHLLPKPEVNLHC\DKPAMWDP\EN FKAPGEMLLVTRFWAIPFSAKEFHP WRLAGLPQKDG*LGVGQCPCSFQ IPLKPLGP*IQ\SFQG |
| 1596 | 7093 | A | 1719 | 3 | 573 | HSLFGTSEVINKLLVPDAHGSFHRG GPRLLSTSLWGKGECGKMLEEKPL GRLLVVPWTQRFF\SFGNLVLLP SCPSMGQPPKVKAHGKRRC*LSLG RCQ*STLDDL\KGTFCPSLKRNLHC* QACNVGS*RTSKLLGENVAG*PVFG QHFHRAKNFTPEGCKASWQKQKM AEDGDWSWPVPLFLPDYH |
| 1597 | 7094 | A | 1720 | 676 | 1283 | QRKILYTHNTTENKWEIINF*SF IFLFFLRSTLVAQAGVQ\WDLGS LQPLPPRFKQFSLGLPSSWDYR/RC VPAHPANFCIF**RWGFTMLARLLS NS*PQGDPPASASQ\SAGITGVSA/H APVRASFFLSLTVSGVQWRDLGSLQ PLPSGFKGFSLSLPSSWDYGCPPPS PANFCIFSRHGFSPCWSGWSQTPDL K |
| 1598 | 7095 | A | 1721 | 41 | 669 | APSSRRPWVISQRRTKATITSLWKG \VNVE\DAGGRKPLGKAPWLSTPWT \QRFFDSFGNLSSASA/LSMGKPPKS KAHGK\KVL\TSLGDA\TKHL\DDLK G\TFAQA*SATCTVDKLHV\DPGGT FKLLGENVAG*PVFGQHFHRAKNFT PGGCRASWQKQKMAEDGDWS\GQ CP\VLQIPLKLNCP*MQSFSRIRLLFL QAITNNKSISAKRSP |
| 1599 | 7096 | A | 1722 | 2 | 307 | TPYLVGVVAGAAQALQFESHAGH LGPQLFNKFALPYIRDVAKQVKARL REAGLAPVPMIIFAKDGHFALEELA QAGYEVV/GDDFGPHRYIANLGHG LYPDM |
| 1600 | 7097 | A | 1723 | 20 | 473 | AVEFEANGLGPQGFPKNDIFL*A AWGEETDYTPVWCMRQAGRYLPE FRETRAQDFFSTCRSPEACCELTL QPLRRFPLDAAIIFSDILVVPQWTLM TYMVEGGGSSTMAQAKRWLYQRP QASHQLLRILTDALVPYLVGVV GAQAL |
| 1601 | 7098 | A | 1724 | 3 | 1170 | CKHSLGHTCYSPRGSSYRQLTMEA NGLGPQGFPKNDITFLRAAWGEE TDYTPVWCMRQAGRYLPEFRETRA AQDFFSTCRSPEACCELTLQALGME VTMVPKGPSFPEPLREEQDLERLR DPEVVASELGYVFQAITLTRQRLAG |

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| | | | | | | RVPLIGFAGAPWTLMTYMVEGGGS STMAQAKRWLYQRPQASHQLLRIL TDALVPYLVGQVVAQAALQLFES HAGHLGPQLFNKFALPYIRDVAKQ VKARLAREAGLAPVPSIIFAKDGHF ALEELAQAGYEVVGLD\WTVAPKK AREC\LGKTVTLQGNLDPCALYASE EEIGQLVKQNL\DTFGPHRYIANLG HGLYPDMDPEHVGAFVDAGHKHS RLV*QNMWGPLWMLGINTHVWFD KTECIPLSRTPNPDDWLFSGP |
| 1602 | 7099 | B | 1725 | 92 | 846 | IIFAMDGHFALEELAQAGYEVVGLD WTVAPKKARECVGKTVTLQGNLDP CALYASEEEIGQLVKHMLDDFGPH RYIANLGHGLYPDMDPQHVGAFVD AVHKHLRLV* |
| 1603 | 7100 | A | 1726 | 1 | 804 | |
| 1604 | 7101 | A | 1727 | 178 | 1093 | TFLLPACLLAALLPLRHHVRGRAW VQGSILNEGVG*ALKDLINEACWG Y*APAGVNLQSMGHRPTVSL\VQLT LRV*GASTPYRC\DRNLGHGR*NLT SMSKILKMAAGNED\ISLTLRAEDN AGYLGR*YFEGTKPGRKFSYEMK LMDLDVEQLGIPEQEYSCVVKMPS GEYA\RICRESQPILGDAVVISCA\K DGSENFASGELGNET\IKLSQTSNV DKEEEA\VPKMNPEVQPNFCH*GY LNFFTK\ATPLSSTVDTPVCSADGTP LVGRSIKIAGYGDHLKYLLGLPKDP RIEEGSLGHS |
| 1605 | 7102 | A | 1728 | 58 | 483 | AARDRLHLRRTTEQHVPEVEVQVK RRRTASLSNQCQLYPRRSQQQVVP VVDFAELRQAFLAETPRGTVA AIAATASIAGAPTQYPPGRGT RRQTTPPPGIM\APPPGMRPPIG/PPPI GFPLARGTPI SMPPSGN |
| 1606 | 7103 | A | 1729 | 292 | 531 | FQAKTSLPLGFQKHQVLTVDIGFGG TAIMTVGKSSKMLQSLFPLQW/CFV KLCRVFVSFLPHFALIIANNKCIEQ KKKKK |
| 1607 | 7104 | B | 1730 | 326 | 419 | XRLTCKRSLARSIASLNAPQTDASGI SGGPDA* |
| 1608 | 7105 | A | 1731 | 774 | 1763 | GNPRSYLLSIAFPLGLQKAFKVFNC GTLDFGWNSNHDLFGKS\SKLLQHI DYRMRCILQDGRIFIGTFKAFDKH MNLILCDCDEFKIK\PKNAKQPRA VEE/ESRVLGLVLLRG\ENLVSMTE G\PPPKDT\GIARVPLAGAAEGPG\V GRAAGRGVPAG\VPISPGPLAGLAG PCSRGSLGGP/SPQQVMTSTGKEAL* AAAAVA\ATASIAGAPNTVPTQGT GTPAPTSGRATQP\PGIMAPPP\GM RPPMGP\PMGLRPARGTP\GMPAPG \MRPPPPG\IRGPPPP\GMRPHKTL SILFDPSQSLFPLQCVLVKLCRVSAELF CSLIIAIRC |
| 1609 | 7106 | A | 1732 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFFDSFGNLSSASAIM |

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| | | | | | | GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVLAIHFGKEFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG |
| 1610 | 7107 | A | 1733 | 1 | 591 | NFALEAKNSARAISLVPDAHGVIS QRRTKATITSLWGK\VNVE\DAGGE TLGRLLVVYPWTQRFFDQLLANLS SASAHGQPPKVQGHMAKKVLTFL GEMPIKHLDDLKGHLLPKPEVNCT VDKPAMWDPENFKAPGEMLLVT/L FWAIPFSGKEFTP*RLQASWAERWV TWS\GQCPCSFQIPLKPLGP*IQ\SFQ G |
| 1611 | 7108 | A | 1734 | 1 | 477 | RRPSWLVAAVLRNANMQIFVKTLT GONHHPLRYETQ*HPLKNVQKPKIS KNKGGYPHPD\QQRDLNLPQKQLE GWPALLSDYKHPRKESHAPWCLR LR\GGIIEPFSPGPLPKYYLRQR*SC RQVLCFAFNPPCLSTGRKK\KCGSH QTTLRPQEGRFK |
| 1612 | 7109 | C | 1735 | 9 | 254 | MEFHSCCPGWSAMARSQTAATAS QVQSDSPASASRVAGINRHALTHPA NFVFLVETRFLHVRQAGLELPPQPP KLLGLQV* |
| 1613 | 7110 | A | 1736 | 5 | 290 | FNLTHIESRPSRLKK/DEYE/FFTHLD KRSLPALTNIILRHDIGATVHEL RDKKKDTPVPWFPRTIQELDRFANQI LSYGAELDADHPVSPWPVG |
| 1614 | 7111 | A | 1737 | 68 | 312 | |
| 1615 | 7112 | A | 1738 | 317 | 916 | TSSPPSSLCFLSFSDICHELLGHVPLF SDRSFAQFSQEIGLASLGAPDEYIEK LATIYWFTVEFGLCKQGDSIKAYGA GLLSSFGELQYCLSEKPKLLPLELEK TGIONYTVTEFQPLYVAESINDAK EKVGNSAATIPRPFVRYDPYTQRIE GLDNTQQAHDLG*FHLTVEIGILCS ALQKNKVKAMDRMVVCQAVE |
| 1616 | 7113 | A | 1739 | 389 | 1881 | NLQPHVLFANLPVPEALKSQRPHSR GASMSTAVLENPGLGRKLSDFGQAE TSY\EDNCNQKWVPISLDPPHLKER KLGALGPKYCALFAENDVNLT\HIE S\RPSRLK\KDEYGFPPFGIKRSLPA LTNIILRHDIGATVHELSDKKKD TVPWFPRTIQ\ELDRFANQILSYGSG NWD\DHGPFKDPVYRARRKQFAD IAYNYRHGQPIPRVEYMEEEKKTW GTVFKTLKSLYKTHACYEYNHIFPL LEKYCASHEDNIPQL\EDVSQFL\QT CTGFRLRPVAGLLSSRDFLGDLAFR VFHCTQYIRHGSKPMYTPEDICHE LLGHVPLFSDRSFAQFSQEIGLASLG APDESIEKLAPIYWFTVEFGLCKQG DSIKAYGAGLLSSFGFQYCLSEK KLLPL/ESLEKTAIQNYTVTEFQPLY YLAE\SFNDAQGEI*GTFAATIPRPF SVRHDPHTPQRIGGSWDNTQQLKI LADSI*Q*IGIPFAVALQNIK |

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| 1617 | 7114 | A | 1740 | 1 | 191 | MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWQLST/FQQMWISKQEY DESGPSIVHRKCF |
| 1618 | 7115 | A | 1741 | 1 | 360 | SGACPAFLVDRNLRHHETTFNLIMK CDVDIRKDLYANTVLSGGTTMYPG IADRMQKEITAL/APPSTLRFRIAPP/ ERRKYSVWIGG\SILASLSTFQQMC LGKQEYDESGPSIVQRKCF |
| 1619 | 7116 | A | 1742 | 13 | 1277 | INPPLSRRCLSHSVLPPLRRRVSL PVAMEEEIAALVIDNGSGMCKAGF AGDDAPRAVFPSIVGRPRHQGMV GHGPRTDSYVGDEA/QRSKRGITL KYPIDHGIIVTNWDDMEKIWHHTFY NELRVAPEKHPVL\LTEAPLNPKAN REKMTQ/ILCFETFNTPGHVPWPIQA VLSL*SLWAQPIGIVMDSG\DGVT TV\PILRGATTLLHAI\NLRGLPLARD LTDYLMKILTERGYSFTTHGPGSKT FRNIKGEACATSPLDFEQEMGTAA SSSSLEKSYELPDGQVITIGNERFRC PEALFQPSFLGMESCGIHETTFNSIM KCDVDIRKDLYANTVLSGGTTMDP GVADKIAEGRSTALAAPAP*KIRVIA PP\ERK\YSVWIGGSILASLSTFPARF WISKQEYDESGPSIVHRKCF |
| 1620 | 7117 | A | 1745 | 644 | 844 | ELSPTTFMPFSEGAEHL\YLPQGPG* GSESPGGCPA/PPYSPYSAPPATPEP IEKSQPNPIRHRFP |
| 1621 | 7118 | A | 1746 | 2 | 271 | |
| 1622 | 7119 | A | 1747 | 83 | 420 | DSSNPSCQSPTQLSKANTLGWHV CELALPDQSSGTSASRGGLE*THLL VA*ALEPIVL*SGAGLPGKL\GPVRP LG*AAVGPGAESLLPSVRSGSSLPQ RREGLSPDGPLP |
| 1623 | 7120 | A | 1748 | 154 | 1030 | SDISQAQLSCTGPPAIPGIPGTPG PDGQPG\TPGIKGEKGLPG\LAGDHG EF\GEKGDGP\GIPG\N\PGKKFGPKGP MGPKGGPGAPGTPGP\KGDSGDYK ATQKIAFSATRTINVP/LLRRSQTNRF RPRCITNMNTN\YE\PRSGKFTLQGC PGLY*FNLSTPVSRLNLCVNLMRG RERAQKV\VTFCGLMAYNTFQ\VT GGHGSSAEE/GPQKEGGGKRPFF LQATDKN\SLTGAWEGANSVFSGL AFFQIWEGLTCGLASHTPAPPARN AHYTPNNNHMTKPNHNNDW |
| 1624 | 7121 | A | 1749 | 3 | 607 | FCPRGQEFGEKNKLLSPRRPWVISQ RRTKAT\TSLWGK\VKCGKNAGKE ETPGKGS\LVV\HPWTPRG\SFQELW QTCPSALCPSMGNPQSQGTMAKKV LTSLGRCP*STLD\DLKGHLLPKPEV NLHLLTSLHVG*RTFKLP\GEMLLV T/LFWAIPFSAKEFHPLKVAGFPQK DG*LGVGQCPCSFQIPLKPLGP*IQS FQG |
| 1625 | 7122 | A | 1750 | 2 | 585 | AAAAPAGGNPEQRLDYERAAALGG PDGRAWGGRSPLPPAP*AQGAPGP RWPPPRAGSPAPSPAGCGGGKGGG |

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| | | | | | | LVTPGRGGPRAAGREL/RAVRCPCP VRPRPPSKPALGGSLPQPEAAAPG PSIR/PVLPQTGSPWRRPKSLRPVL GTRVGRTPPLPPP/PDPAGPPPLPLPG P\HPSRPPPTGPWRPARADGRV |
| 1626 | 7123 | A | 1751 | 25 | 1295 | KLCATKDLSYLAAAASPTAFAYLG GLFSPKLPVTMAHRFPALTPEQKK ELSEIAQSIVANGKGILAADESVGT MGNRLQRIKV\ENTEENRRQFR\EIL FLLWDSSIQPGGIGGC*FLFPRR/YPL TQKGTARGKLFPGNIPSREKGDWS VGNQV*DQGRFLFCREPNKGNNH FKGLDGLF\ERFVQYKKDGVDFGK WRAVLRADS\CPSSLAIHENANAL ARYASICQQNGLVPIVEPQVIPDGD HDLEHCQYVTEKVLA\AVYKALND HHVYLEGTLLKPNMVTAGHACTK KYTPEQVGYGSP*QALHRTGPAAV PG\ICFLSGGMSEEDATLNLNAYQTF A/TSTKSPWKLSFSYG\RGLQAQCTG LPWGGKAANKGGNPR\TAFMKRAH GLTCQAAQRDSMFTRVLLGAASHP SRL\HKPCLYPT |
| 1627 | 7124 | A | 1752 | 1 | 186 | IFSRDGA\HRVTQDGLDLLTS*SARL SLPKCSDYSREPPRPAQT\PILIRFHIH NSKHEKTME |
| 1628 | 7125 | A | 1754 | 74 | 595 | RGGQGLLSTSLWGK\VNVE\ DAGGE TPGKGSLLVYPMPGPQRFDSFGNL SSASAIHGQTPKVK\AHGKKGADFP WDDAIKHL\DDLKGHLLPKPEVNLH C*QACNVGSLRTFKLPGENVAGLT VFGNPIFGKRISPLKVAGFPQKDG* LGVGQCPCSFQ\PLKPLGP*IQ\SFQ G |
| 1629 | 7126 | A | 1755 | 21 | 457 | NPRVRGALTMELSES\QKGFQMLA DPRSFDSNAFTLLLRAAFQSL\DAQ ADEAVL\DNKNSLEILLGSIGRSLPHI TDVSWRLEYQIKTNQLHRMYRPAY LVTL\SVQNTD\SPSYPEISSSCSMEQL QDLGGK\LDASKSLGKSTQL |
| 1630 | 7127 | A | 1756 | 1 | 455 | |
| 1631 | 7128 | A | 1757 | 3 | 468 | |
| 1632 | 7129 | A | 1758 | 50 | 895 | THASDGALTMELSES\QKGFQMLA DPRSFDSNAFTLLLRAAFQSL\DAQ AD\EA\LDHP\DLKHIDPVVLKHC\ HAAA\ATYILEAGKHRA\DKSTL\ST YL\EDCKILTEKRIELFFAREYQ\NNK VNSLE\LLGKY*GRSLPSYNRVFSW ALWIIQVKDQSTFHRMYRPA\YLG DLKVVQNTGIPPSIYPREL\VFSCQPW NQL\QDL\VGETLKDASKKPWKRA T SVVTLGKVNRSPSSRRKTQKPLP FSWNHRLCRA\GCPFSVEKNFSLNL YPFIHFGHFKNV |
| 1633 | 7130 | A | 1759 | 470 | 737 | RKSFFLAQTVLKWCCEKMSSPGKK LFPGEIWGVKGNKNKLWPLPDPSIR HRFERVPSHKRPLPGWVRWLTPIPS TLGGQSAVDHLRSGVRDQPGQHGE |

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| | | | | | | TPSVLKI*KLGRGGRQL*SQLFGRL RQENCLNTGG\RGCEPRSHCTPA WATE*NSWDYSCLPPRPANFYIFST DGVSPCWPGWSRTPDLK |
| 1634 | 7131 | A | 1760 | 1 | 297 | |
| 1635 | 7132 | A | 1761 | 1 | 162 | |
| 1636 | 7133 | A | 1762 | 54 | 504 | YTAIMSIMS YNGGAVMAMKGKNC VAIAADRRFGIQAQMVTTFQKIFP MGDRLYIGLAGLATDVQTVARLK FRLNLYELKEGRQIKPYTLMSMVA NLLYEK/RDPDHLFETISQAMLN AVDRDAVSGMGVIVHIEKDKITRTL KARMD |
| 1637 | 7134 | A | 1763 | 51 | 748 | YTAIMSIMS YNGGAVMAMKGKNC VAIAADRRFGIQAARLLTTFQKIFP MGDRLYIGLGPASPLDVQTS/VAQR LQVSGNLNLY*V*REG\RQIQTFITLM EAWLANLFVMRKRFGPLLTLRPVH LPGLGPERPFKALSIC/SL*DLIRVGP MGDLNDFCGSSGNLAPNQMLRECV ESLWGGPTWVPDSTVLKTIFPRPW NAVGPGWQCSGMGSSLFHIEKDKI TTRTLKARMD |
| 1638 | 7135 | A | 1764 | 433 | 851 | KPQPFILCSKYNQMILLHLRAPGHA DASTQKQQLWL*NLLTSLGQRLFN FFETESHVST*L/QCSGMISAYCNIC LPDSSNPPTSASRVAGTAKRQHHTQ LIFCIF/VVQTGFCHVGPGLGFTEAR AIHPPWV\PKVLGLQV |
| 1639 | 7136 | A | 1765 | 213 | 617 | KRFLV*KVASVLKGLHAAVVSDD GSTLLLKWANDNAPEHAF/RGPGFL \STFALATDQKGQTWDFSKNKSNC LLTPYQGGFNFSFYLVWGEFS*A QAGSAQLQGLICSA*EKGTWFPLF* RN*GQVVEVSLI |
| 1640 | 7137 | A | 1766 | 2 | 140 | |
| 1641 | 7138 | A | 1767 | 157 | 371 | |
| 1642 | 7139 | A | 1768 | 3 | 135 | |
| 1643 | 7140 | A | 1769 | 1 | 1431 | MHKAGLLGLCARAWNSVRMASSG MTRRDPLANKVALVTASTDGIGFAI ARRLAQDGAHVVSRRKQQNVQDQ AVATLQGEGLSVTGTVCHVGKAED RERLVATAVKLHGGIDILVSNAAVN PFFGSIMDVTEEVWDKTLINVKAP ALMTKAVVPEMEKRGGSVIVSSI AAFSPSPGFSPYNVSKTALLGLNNT LAIELAPRNIRVNC/LAPGLIKTSFSR MLGEPEDCAGIVSFLCEDASYITG ETVVNLSVMFTGGGVCRAASWKE GGTGTPTPTPRESRQREPGETSSTD TQENKVWNGLPANPQRPAAEGPVRR KTNKQKGIASTSAKDSNIRTGKDIH TKTPSIGHQHQRPKVDKTTKMERN QSKKAETSRNQNVSSLPKEYKSSPA REQNW MENKFDDLTDVSFRRSVIT NYTQLKEHVLTHCKEAKNLDKML NEWLTRMKNLEKSLNDLMELITTV |

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| | | | | | | QELHEGYTSFNS |
| 1644 | 7141 | A | 1770 | 53 | 582 | RKETVSVSPQQSRHLIGVRSPKGLS EVALAGLIHAQGAATSVHCARAGK SVRLASSGMTRRDPLTNKVALVTA STD*ALHRLSLDLTTTQARQGLFSR SAVALAQIAGATSQGPT/CQ*GKTQT SQAPFLYWLPVDYQAAKPYGGIDIL SSKAVVNPLFEA*RVSPPEARDLTL DIIG |
| 1645 | 7142 | A | 1771 | 44 | 1059 | AMHKTGLLGLCARAWNSVRMASS GMTRRDPLANKVALVTASTDGIGF AIARRLAQDGAHVVVSSRKQQNVD QAVATL\QGEGLSVTGTVCHVGKA EDRGAAWWPPAVKLHGGIDILVSN AAVNPFFGSIMDVTEEVD\WDKTLDI NVKGPKP*MTKAVVPEMEKRGGGS \VVIGLSIAAPSPSPGFSLYNVSKPAL LGLAQTLPIEL\APRNIRVNCLAPG LIKTSF\SRML\WMDKEKEESMKEIT LRIKKV*ASPEDCAGUVSFLCEDAS LHSLGKTVVVGSGTPVPASEGTGK TAQRPKVGLLSFLVLFPAIQPNWPF PTSCSTLLFHPHSNQFLPL |
| 1646 | 7143 | C | 1772 | 1 | 174 | MWIFIFNKYYQHVKSPTMSRTGKS ATCDGCGMAAHCSRCWGLSWGLG EALSYSKNVS* |
| 1647 | 7144 | A | 1773 | 154 | 765 | RAGLEELTAAVMVRLNLCIVAVSQ NMGIGKNGDLPWPPLKNEFIYFQR MTTSSVEGKQNLVIMGKKTW\FSI PE/RRNRPFKG*EFNLVLSRELQGNL PQGA\HFLFQKF*D/AMPLKLTEQPE LANKVDMVWIVGGSSVYKEAMN HLGHLKLFVTRIMQDFESDTFFSEID LEKYKLLPEYPGILSDVQEGKHIKY KFEVCEKDD |
| 1648 | 7145 | A | 1774 | 1 | 676 | DRPNSGRPRAALAAGSTFPVLACSS AMAPKGSSKQQSEEDLLQDFSRN LSAKSSALFFGN\AFIVFAIPWLYW RIWHMDLFKSAVLYSVMT*LSTYL VAFAYKNVKFVLKHKV\AQKEGK DAVSK\EVTRKLFWKLDY*ERCSRE GRKD\ERILWK\KNEV\ADYEATNIF PIFYNNTLFLVLVIVASFFILKNFQ PHSVSFSRNYILSISG\SSGLIALFTG SK |
| 1649 | 7146 | A | 1775 | 99 | 362 | |
| 1650 | 7147 | A | 1776 | 3 | 403 | |
| 1651 | 7148 | A | 1777 | 184 | 360 | |
| 1652 | 7149 | A | 1778 | 1 | 885 | EFGTRWDFSMVAFADLDLRAGSDL KALRGLV\ETA AHLGYSVVAINHIV DFKEKKQEIEKPVAVSELTTLPIVQ GKSRIPIKILTRLTIIVSDP\SHCNCFER QLLRGARLYDVVAVF\PKGQEKSLF HIA\CTHLGCGDLVCITVTEETTIFT SKRPPINVAIDRGLAFDLALIPLLSR TPTMRKVYNFPSAPPILMPNLAKGK NVNYYLGGWQERAFREIR\GP\YDV |

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| | | | | | | GKS*ACLFGPFF*K*TPRVRVSTNCR AA\LLHGETRKTAFGHIISTVKKPRP\S EGDEDCLPASKKAKCEG |
| 1653 | 7150 | A | 1779 | 175 | 534 | DCSLPSVCHFPPLSPTHPTTHPPWG /CPSGGPEGLPIT*RHQVGSCPTAPPP VPAPSRQSDCGAVHSQDENTVNALI GGFLVLLHIMCNVVALTFYATIYED LCCTCNKYIEKAHTSVW |
| 1654 | 7151 | A | 1780 | 190 | 390 | TKRGAGEGNSKVVLGLQVGCQSQR GNHQGMFTWA/CCGKDSGGACSCSCL GV*CSWGQKSIRVSLWGF |
| 1655 | 7152 | A | 1781 | 805 | 1325 | ASKLEGSPCGKGGVGLGGCFPKRPE PRNHPHFVLWYLPQTRLEPKPLP PQLPSVG*KGPGPSFGLSLTAGPLP LQERLVPTQLLPVGKPGPGFPACA TSSGKPKLRPLCAKSTMP*THPPT VPKPPGQEA VENQAPMASEFPSPSP SVSGDLKPWGFRSFLCQGGAWS |
| 1656 | 7153 | A | 1782 | 1016 | 1560 | KDPELQASHFPCFSYCTPPAHFASLL DFAFSDPHLLGFLSSFLERSSI/CGKT DLSKTFSLD*SFGLNFSRLRESSYRP FGVQDAID*HPPAMFFSASQTLQGP SCGVPICAFIPAVPSTFQLPMFLWVR FLSLPSFSFPNPPVSSGSLFPHTPFL TTP/LPHG*LFPSAPPALHHATHFRT |
| 1657 | 7154 | C | 1783 | 68 | 223 | MSPSSVFFVXXXXXXXXXXXXXXXXXX XRASFIPPLDLXXXXFSLFQMKSI DF* |
| 1658 | 7155 | A | 1784 | 1373 | 1651 | LSVLCHCVCVCVCV/CCD*KGLHSY LFPWTWKKIFFYLFK*NLISSNHI*I NVKAYIVLYVN*ILKITKYMILLSTT |
| 1659 | 7156 | A | 1785 | 6 | 140 | |
| 1660 | 7157 | A | 1786 | 223 | 397 | QTPP*KSKQPFRTSS*DQVPSQP*PPI PPINNPPIPPPFGEVYYFEPILRKWV KGR |
| 1661 | 7158 | A | 1787 | 2287 | 2854 | |
| 1662 | 7159 | A | 1788 | 1 | 610 | SGRPFFFLSGGARATAQLAESWRG GQHLQSSPPPPASPGGPSSSDQRS PCSNARW/NTSIYSLVADGTC*D TALVGNKDP\PSIWAAIPGKTFLNIT PAEVGVL/VGKDWVKLLSLNGLDT GGPRNYNLLVPGDFHWLAGWGN* TVDL\QLKSIGGSP\TFNVIVTMTAK TLGLLMGKEGIHGNFIDK*CYEMAS HLQRSQY |
| 1663 | 7160 | A | 1789 | 157 | 610 | GYRKKQLRGDRRWAIHRITLTSR NVKSLEK\VCA*L**RRRKEKNLK S*KGPVVRMPTKT\LRITTKKTPCG*/ EGSKDRWDRFPD*GFHKRLHLTLH SSFLRFV*GRFTSFSYLRPGFEVGSS PFADALSQISIHTIDDQLKKKKKKK KI |
| 1664 | 7161 | A | 1790 | 1367 | 1582 | METRWESPDPDNFNIAPVTP*FCSNS D/CVLSVPDSSRLPRHFPPSHCTRKR PHLPTQQQPFKCALQEKWFF |
| 1665 | 7162 | A | 1791 | 122 | 344 | ALGPLPLFFPPSPLPVQKG*YSNQKL EGAGPGQGGFQPVFP*LGGTSNFP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FRKSPSQVQAH*PGSDEDPRL*EDP RPL |
| 1666 | 7163 | A | 1792 | 656 | 1068 | NQINFCLNGKYTYVCIDTLPLYMFN IHTLKHINTSVIISLEFAI*HKGQVEL HIKITYRSN*MWLGHNQRRN/LCPQ EGEEIPNEA*IFSIIKRQSWPGTVAH ACNLITLGG*DGRIS*DQVFKTSLINI VETPSLLKK |
| 1667 | 7164 | A | 1793 | 138 | 396 | |
| 1668 | 7165 | A | 1794 | 143 | 327 | CGVQLLPDRRRESRDIIVEL*AAVA AAGGNPDGKKGGGGWEAGQRKER KESEDPAEPDCV |
| 1669 | 7166 | A | 1795 | 23 | 483 | KAIVLLHICTEVISIILFNDFIQDKRP CRLFTCCSLLRSASPVSSAANMPEL FSSTSSSTVSWLSLSLSSSLSSCFLSFR FGNSSCMSFSIIIPFVRPEDWKRMLL AK*GPLMALMLCALFFSSSSRLKPL FMSTTILSLKYGGGVQDVGWQ |
| 1670 | 7167 | A | 1796 | 429 | 1394 | TISFEADIIHMYKT*ETD*TIFLEPYD YLLQLPAGKQVRTQT/LSQAFNHWA LKVPEAKLTDYLFEVDRLKFLGLMPS LLIADDIEDNSKLPTWAFVVAHSIYGI PSVINSANYVYFLGLEKVLTDHPD AAKLFTRQLELHHGQGLDIYWRD NYTCPT*EYKAMELQKTGGLFGLS KCLKHIVSDYQEYLKPLLNTLGLFF QIRDDYANLHSKEYSENKSFCEDLT EGKFSFPTIHAIWSRPESTQVQNILR QR TENIDIKKYCVHYLED\EGSF EYT RNTLKELEAKAYKQIDARGGEPLS LVA\LVKHLK*RCSKEGKWNNV |
| 1671 | 7168 | A | 1797 | 145 | 172 | GGCLLESVDTSHGQSLISASLNTK HPTGMHSTCWFHVELCGKGLGSRH TLKQHQSFA*SMPP/PPAPCHIVPQE PTS*VHPCWVFCVETG |
| 1672 | 7169 | A | 1798 | 197 | 378 | VLMSVLPALGYPPRSMWLYVRGLN ADTP*PPSTTFPLALPPSSTWNQ/PS* VHPLLGVCVET |
| 1673 | 7170 | A | 1799 | 32 | 377 | SSMPPTPGPSILSSLVIPVSPFHPCPP VLYLWPAPI/Y*KLLPVPDLAHSPPS TPTLHVSHYPMVGITLTPVPLFFIPS NSLPNGGDPEPSSDQVEPVQPGLLS LPSSKGSFCF |
| 1674 | 7171 | A | 1800 | 168 | 224 | |
| 1675 | 7172 | A | 1801 | 224 | 527 | CHQLRQELAIFTSFVILQLFSGHLDV YMQAWAQRPDKEYEDNK*FIEIKKI IQFTLISKRMK/YVGINLTR*VKDLH NENYKTLMEIEEDTSEWKDISCSW |
| 1676 | 7173 | A | 1802 | 22 | 430 | SPGCRRAESEKSQGSERGVGPSYRI WVGSGKLQSKGVVLWQAGAGVIR CSAGELLSQEKGFHKVMSSVKAGT SHLHFFCDSSVTSGHVDVYVQAWA QRPDRYSVHCSGDGCTKVSEITTKN LFM*PKTTCTPKTE |
| 1677 | 7174 | A | 1803 | 386 | 511 | |
| 1678 | 7175 | A | 1804 | 362 | 439 | |
| 1679 | 7176 | A | 1805 | 776 | 1376 | GAPWAFGGLPWVHGLAKEGVTAVI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AEHGLWNIGVHEGHGTLQLQHMH HYAVALRRHPFIQAQAQRGVLAG GGMGTRE*VRARGQPRVHSNNCH TGQNRYSVPSEGLWT*YLL*GPK MTQDAEQAGRDGGDDGGLALVGE ALLEAHRDAIEQALPWGLRQLSLTV SQIGGHTVGPVHFPGLSHIGEEHGL RGQLSTV |
| 1680 | 7177 | A | 1806 | 420 | 508 | |
| 1681 | 7178 | A | 1807 | 735 | 841 | |
| 1682 | 7179 | A | 1808 | 796 | 1123 | IQWICHNTISAPKNYLEISPHINNKQ F*KKI*KHFPFA*RT*SKKYLGINVQ SLRSLYLEIYK/SLIKMIKN/DT*RYN PY**FGKINIVK*LYNPM*FRFNTVPI KMPIS |
| 1683 | 7180 | A | 1809 | 137 | 303 | |
| 1684 | 7181 | A | 1810 | 122 | 385 | YPALEHILKAQAIQSRCGDCSCLPPS APWDHPGPTTP\SPGRRAAADPWHL SPIDGREHLR*VPVLPVTPPSPTLGH WVTDPSPGVGG |
| 1685 | 7182 | A | 1811 | 77 | 1181 | PLEKCYDLFSQNWSGFLPCFQEFQF QFKRILINRLKPDLEKSRKMGRK/R AEEYRQTFLTADV*RSPKKSRSRPRE SPKKAKKLEVIIGKPQSSSF*QRIR KRERTPATRA*SQ\KREKARRRSRSI DRGFERMR\SDVRNRLTSPSRSDR KGDRRDREREKENERGRRDRD YDKERGNEREKERERSRSRSKEQRS RGEVEEKKHREDKDDRRHRDDKR DSKKEKKHSRSRSRERKHSRSRSR NAGKRSRSRSKEKSSKHKNESKEKS NKRSRSGSQGRDTSVEKSKKREHSP SKEKSRKRS*/ASKERSHKRDHSDS KDQSDKHDRRRSPKYRTREPRKTSI KNKDETV*KYFVKCGSH*ILLND |
| 1686 | 7183 | A | 1812 | 1 | 585 | PLKRSDGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPVEKSAVTAL WGQA*TWMKVGGKALGK/RCWVV LPWDPKRSFEVLWGNLSQLP\DAVN GANP*R*KASMAKEKVLGCPLVNG PWLT/HWTTLKGHPLPHTEVSLHCD K\LRHGSCLKNFRAPGATVLGLCCLA HSLLAKEFNPKNLQGLPIQEKLVGW VVG |
| 1687 | 7184 | A | 1813 | 505 | 671 | QKNKVYFFFETYEIYWPGTVAHAC NPSTLGS*G/GWIT*AQEFETSLANM LKPCLC |
| 1688 | 7185 | B | 1814 | 277 | 480 | GTGHFYGRTPSDTNCQEYTHRKL CQIKSKADLVLMKNSKSLTRVIRNI LAPQDQNHQQNPLNSQFLQ* |
| 1689 | 7186 | A | 1815 | 32 | 1386 | VLLGPKAERTNSRRNYQRRDYFSA PRSITSNQSAKSSSSRGVYSAYQAP DIHECCHFRSASFLLDKMATPAVPV SAPPATPTVPAAVPASAPASVPAPT PAPAAAPVPAAAPASSSDPAAASAT TAAPGQTP\ASAQAPAQTPAPALPG PALPGPFPGGRVVRLHPVILASIVD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | \SYERRNEGACPS*SGTLFGKLVDK\ HSVE\VTN\CFSVPHNESEDEVAVD MEFAK\NMYETGIKKVSPNKLILG\ WYATGHDITEHSVL\IHEYYSREAP NPIHLTV\DTSLPGTGRMSIKAYVST \LMGIPLGRT/LWGVMTPLTVKY\ AYYDTERIRRLTLIMK\TCF*PPTRVI WTSQVDLQQEGGGIQLRNPGMPLS TSVANMPEGCTCLGKVSADNTIRK VGHFLMSL\VNQVPENRKPMTFET MLNSNINDLFMVITYLANLTQSRVIA LNEELVNL |
| 1690 | 7187 | A | 1816 | 273 | 748 | VIQNLFNKMDVGTGQVRVVHACNP RHFRRLRQEPKSGVQDQPDQHGET PSLKIQKLARR/GGVVHL*SQLLRR LKQENRLNPGGGGCSEPRSHHCTPV *VTQ*DSVPPAPRKKKMYVVLTKK FHIWHISFTLPNIKRSDSLRNRKVT NFSCYCSKVS |
| 1691 | 7188 | A | 1817 | 1 | 406 | LCQLETYPPISQCTASDFPGPVTAS WAIQEAARSGQAKAGA/GSATLS/M AYAGARFVFSLV DAMNGKEGVVE CSFVKSQETECTYFSTPLLLGKKGIE KNLGIGKVSSFEEKMISDAIPELKAS IKKGEDFVKTLK |
| 1692 | 7189 | A | 1818 | 1 | 1222 | FRQRAGAGQCGGRWSHFRVTSSCA CYVDAPPAPAMLSALARA VPSACS/ LARSFSTSA\QNNAKVAVLGASGGI GQPLSLLLKNSPLVSRLTYDIAHTP \GSGPQDLS\HIETKSRK*KAYLGW NSLPDCL\KGL*WW*VIPAGVPTKP GMDRD\DLFTTNATIVGTLTAACAQ HCPEAMICVIANPVNST/ISPITSKK VFKKAWGQHPQKKSSGVTTLNIVR AKTFVAELKGLDPAGVNVPIITGGH AGKTIIP LISQVHAYDPVRGFECTPK VDFP\QDQLAALTG\RIQEAGTEVV KAKAGA\GSATLSQCRNAGARFVF SLVDANELEKERCLWECSLPLSPQE TECTYFS\TPLL\LGKKGIEKKKAKT\ LGIGKSLPFEEK\MISDAIPELKA\SI KKGEDFVKTLK |
| 1693 | 7190 | C | 1819 | 876 | 1124 | MALGLRQRGIVSLAASITGPCPMSP APSPGTQVLLPTKRHPQVCLSHTC VEMRQVTKRLSAFKVRNKPDRFY SALLCSTE* |
| 1694 | 7191 | A | 1821 | 103 | 483 | |
| 1695 | 7192 | B | 1822 | 1 | 798 | MAFLDNPTILAHIRQSHVTSDDTG MCEMVLIDHDVDLEKIHPPSPMGDS GSEIQGSNGETQGYVYAQSVDITSS WDFGIRRRSNTESPKEPEQLRNLFIG GLSFETTNEKRSHCEQWGTLPCDV VMKDSNTRSGGFGFVITYATVEEV DAAMNARPHKRRKKYPLLGNNTN DKQLDLGPEKGRKHALNCHRMKP ALFSVLCEIKEKTGGATQAFAKENN QKAYKETYGVSHITRHDMLQIPKL AQNEKSQVPSIRSIQRLKII* |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1696 | 7193 | A | 1823 | 3 | 545 | |
| 1697 | 7194 | A | 1824 | 1 | 440 | VYLHLHSSQDRLLPMTVVVTMASAR VQDLIGLICWQYTSEGRKPKLNDN VSAYCLHIAEDDGEWTHDFTTLD NEPIHKFGFSTLALVEKYSSPGLTSK ESLFVR\INAAHGFSLIQVD\TQKVT MKEILLKAVKRRKGSQKVSGACD |
| 1698 | 7195 | A | 1825 | 293 | 2142 | GNWPTERMAFLDNPTILAHIRQSH VTSDDTGMCCEMVLIDHDVDLEKIH PPSMPGDSGSEIQSGNGETQGYVYA QSVDTSSWDFGIRRRSNTAQRLE LRKERQNIQCKNIQWK\ERNKQS AQELKSLF*KKNLSKEKPPISGKQSI LSVRLEQCPLQLNNPFNEYSKFDGK GHVGTATATKK\TDVYLPLHSSQDR LPMTVATMASARVQDLIGLIC*QYT SEGREPKLKDNVSDYCLHIAEDDGE VDTDFPPLDSNEPIHKFGFSTLALVE KNSSPGLTSKESLFVRINAAHGFSLI QVDNTKVTMKDILLKAVKRKKGFQ NVSGPQYRLEKHSEPNVPADLDSTL ESHSAREFCLVRENSRADGVFEED SQIDIATVQDMLSTLHYKSFPVSMI HRLRFTTDVQLGISGDKVEIDPVTN QKASTKFWIKQKPISIDSDLLCACDL AEEKSPS\HALF*LTYL\SNHDYKHS TFESDAATANEIVLKVNIL\ESRAS TAR\ADYFAQKQRKLEQTVRAFSFQ KEKEIPGSIEQLAFQPQILVPVASEP ACPGPSALRSPPGVLSFGGEAHPL GPLGTGAGGLFGEGVGGPLRREAA GDIA MGRKFALAMGF |
| 1699 | 7196 | A | 1826 | 436 | 917 | RLSSKLLHGAYQCFKAKIENYLLSW LNRKFRISFKKEKFSKAVCLKNDIW LGTVARDCNPNTVRLKWEDHLSPG I*DQPGKQ*DL/PSLQKNKKLPRHGG VHTLWSQLLGRRLRWENHLSLGDQG CIEVSSRHCTRAWVTEQDPI*KQLG PQGVYHHA WVIFCFFVEMQVSLFS RLVSNSWAQVILPLQPHSVGIAVTS HCTQPYVIL |
| 1700 | 7197 | A | 1827 | 46 | 573 | SQTPMGHFTEED\KATIT\SLWGK\W NVE\ DAGGE\TPGKGS\LVYP\WT\Q RFFD\SFGNLSSASAIHGQTPK\KAH G\KKVLTFLGTMP\TKHL\DDLKGHL LPKPEVNCTFDKLACGILEELSSFLG KMLLG*PVFGNP\IFGKRISPLEGARF FLGRKMGDLELASALVPSRLPLKPL GP |
| 1701 | 7198 | A | 1828 | 1 | 388 | |
| 1702 | 7199 | A | 1829 | 75 | 520 | TPERGSAYPRLLCGAPPGEATVIM SDQEAKPSTEDLGDKKEGEYIKLKV IGSGF\SEIHFKVKMTTHLKKL*ES YCQRQGVPMNSLRFL\FEGQRIAD\ NHTSNKNWGMEEEDVD*SFFREQT GGSFQQFRIFLFFFLSKSFFIF |
| 1703 | 7200 | B | 1830 | 78 | 236 | MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSDEKT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DK* |
| 1704 | 7201 | A | 1831 | 67 | 587 | IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALGQ IG\DKIMQVNGW\DMTMVTHDQ\A RKRL\TKR\SEEVVRLLG*RGSRMQ K\AVQQSMLFLRQPPSPCDSCLPPLC TVTPLPHSGPHLASADRWAPASEGL |
| 1705 | 7202 | A | 1832 | 3 | 420 | HLSGTSEVINKLLVQTPMGHFTEE DKAT\TSLWGK\VNVEDAGGETLG RLLVVYPWTQRF\DFSFGNLSSASAI \MGNP\KVKAHGKKVLTFLGEMPLK HL\DDLQGAFFAQA*SELALVDKPA MWD*GTSKLLGEMLLG |
| 1706 | 7203 | A | 1833 | 3092 | 3227 | ERQ/WPGTVAHACNPSTLGG*GGG AGIT*GQEFKTSANTVNPSSL |
| 1707 | 7204 | A | 1836 | 3 | 1088 | SMAA\VAESACICRWRRSCSTGQF EELLRLKAKSLLVVHF\WAPWAPQ\ CAQMNEV\MAELAKELP\QVSFVKL EAEGVPEVSEKYEISSVPTFLAFFKNS QK\NDRLGWVHMPQELTKKVQADM HLSGLLPTQALMEHL*RKILQPFGL EGNLT\SWLAPLAWLFYWKELPSK EPR\CGFSK\QMVEILHKHNIQASSF DIFS\DEEV\RQGLKAYSSWPTYPQL\ YGS\GELIGGLDIKELEASEELDTICP KAPKLEERLKVL\TNKASV\MLFMK GN\KQEA\CGFSKPN\SGKYLNSTW C*NLETFRILEDERKFGQGLKSLTP NW\PNIPLSLYVKGELVGGLDIVKE\ LKRKLGEFAAL*LRGEN |
| 1708 | 7205 | A | 1837 | 3 | 703 | VEFFSSQRAELYATPLTPAPGPNNGI PGWTLWLALPRPGNLRKGPGLSL QEVDEQPQHPLHV\TYAGAAV\DDE LGKVLTP\TQVKNRPT\SISWDGLD/S KGKLYTLVLTDPDAPKQGDPKY RE\WHHFLGWSTLKGQMTSATGTV LS\DYVGLGGLPKGTGLHR\YVWL V\YEQ\DRPLK\CDPHPSATRS\GDHR GKIQRWASLPVKK**SSRAPGGWAP CYPQPEVGMNQCAPKL |
| 1709 | 7206 | A | 1838 | 717 | 1390 | ASTTTSSVHCARTYMG\SVYNTPAR VRLRVGWRAADQLLLAASSTSAI VSTRALECAKM\QNAE\AADATLVFI GYVVPALATLYAAGATLPRSAGKD TPPGTGDHGPAGALGTQAAGGHRV HAVWALDATLSDPAGAHGHLAR EARGCTLPGGYCTL*RISPNSWSPA AL*HHFSTAT*TRASPASSNG**KSC PAG/APALLPGPHGGAAGAGVGGP ALLGET |
| 1710 | 7207 | A | 1839 | 1 | 310 | RTSPHSPRNILLLS/EPENADSLMLV DFEYSSYNYRGFDIGNHFCEWVYD YTHEEWPFYKARPTDYPTQEQLH FIRHYLA\EA\KKGETLSQEEQRKLEE DLLCM |
| 1711 | 7208 | A | 1840 | 3 | 375 | HYLA\EA\KKGETLSQEEQRKLEEDL LEMYSLKDEMGNLRKLL\ESTPSV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VFCHNDIHSSS*LHPPTPWISPGASR AGPWREEQRAEGPGDWAEPPESET VQETGLFLSLSRSPWLAGQSPVLCM |
| 1712 | 7209 | A | 1841 | 94 | 429 | |
| 1713 | 7210 | B | 1842 | 96 | 979 | XVGEEPREVLLRLYGAILQGVDSL LESVMFAILAERSLGPQLYGVFPEG RLEQYIPVRAQSYPLPKAPPPNP PVPNVCLHIPHPNPITTLIASWVQSR PLKTQELREPVLSSAAIATKMAQFHG MEMPFTKEPHWLFGTMER* |
| 1714 | 7211 | A | 1843 | 5 | 1463 | PEKPRPAGRGAERGRKEPSSESG AHPGLGPGRARAMAAEATAVAGS GAVGRCLAKNGLQQSKCPDTPKR RRASSLSRDAERRAYQWCREYLG AWRRVQTEELKVYPVSGGLSNLLF RCSLPDHLPSVGEEPREVLLRLYGAI LQGLDSLVLLESVMFAILAERSLGPQ LYGVFPEGRLEQY/IPTSWVQSRPLK TQELREPVL/SQAIATKMAQFHGM EMPFTKEPHWLFGVTMSRTLKQIQD RPPTGLPEMKLRGNVRLKDEMG NRKLLLESTPSPVVFCHNDIQEGNILL LSEPNADSLMLVDFEYSSYNYRG FDIGNHFCEWVVDLYSSEE/WPFH KKAGPPSPSPHQRRQVHFIRQLPLA RGK*KVESLPRRSQKKNWKE\DLL VRKSSRVMFWQSHFLWGLWS\ILQ\ ASMSTIEFGYLDLCPSLRFQ\FLLPS KKGQA*PSVHSCILDSTLPLLGFLE PPGQGPWRGGTTSRRPWRLG |
| 1715 | 7212 | A | 1844 | 143 | 762 | CRQERAVAPARRAMERIPSAQPPTV CLPKAPGLEHGDLPGMYPALMYQ MYKSRRGLKRSEDSKETYELPHRLI EKKRRDRINECIAQLKDLLPEHLKL TTLGHLEKAVVLELTLKHVKALTN LIDQQQLFKMHYA*LLIVF*L/SSFPV FILVLSRCLYL*SCYKYILYKIKKE NVSDVYLYNYLIHTVRKNECIPVFE EKNNFFFL |
| 1716 | 7213 | A | 1845 | 203 | 1507 | CRQERAVAPARRAMERIPSAQPPPA CLPKAPGLEHGDLPGMYPAHMYQ VYKSRRGIKRSEDSKETYKLPHRLIE KKRRDRRTNECIAQLKDLLPEHLKL TTLGHLEKAVVLELTFEH/V*KALT NLNLSSSRQKIAL/QSGLQAGELSG RNVETGOEMFCSGFQTCAREVLQY LA\KHENTRDLKVFASLSTHL\HRV VSELL/QGGTSRKPSDPASKVMDFR EKPSSPAKGSE\GPRKNCVPVIQRTF AHSSGEQSGSDTDTDGSGYGESEK GDLRSEQPCFKSDHGRRFTMGERIG AIKQESEEPPTKKNRMQLWDD\EGP FQLASDLNQLPPFGPTPQHQPFFCL PFYLIIPPSS/ATAYLPMLEKC\WYPTS VPVLYPGLNASAAALSSFMNPDKIS APLLMPQRLPSPLPAHPSVDSSVLL QALKPIPLNLETKD |
| 1717 | 7214 | A | 1846 | 628 | 1061 | AHRKSLYLCEACFPRSRASQETSGL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KEENWRLGRKTSKCRPGLSKKLGC ERKDRDCSG/CRKDEQQGPWEAPQ AARHSQKSRNARGRPFLEGGPGTE NR*QSFPPKNSREQGFNDPVGQSV EPLEQPLFPWEWQWPALAQDREL |
| 1718 | 7215 | A | 1848 | 88 | 953 | FQAPQLCYDSAFMISSVPSHILRV CFPCFHAHLRVCEFPFHAHLVCCE FPCFHAHLVCCEFPFHAHLVCCE PCFHAHLRVASVNFHFHAHLVCCE FPCFHAHLRVCEFPFHAHLVSVN FCFHIHLVCCEFSFHAHLRVCEFP FHAHLVCVSANFRVFTPTCASVNF FTPTCVCEFPFHAHLRVASVCEFP CFHAHLQVYEFPCFHAHLRVCEFP FHAHLRVCEFPFHAHLVCCEFP HAHLVCCEFPFHAHLVCCEFP AHLRVASVNFHFHAHLVCCEFP HAHLRVCEFPFHAHLVSVNFCFH IHLVCCEFSFHAHLRVCEFPFHA HLCVSAN/CPCFHTHLCVCEFP HLCL*ISVFSRPPASVCECL/CN/C FHAHLQ/CL*ISVFSCPPAGL*ISV FSCPPACL*ISVFSCPPVCL*ISV FSCPPACVCEFLCFHAHLVCDFP CFHAHQSATVLV |
| 1719 | 7216 | A | 1849 | 1 | 254 | |
| 1720 | 7217 | A | 1850 | 3 | 308 | |
| 1721 | 7218 | A | 1851 | 1 | 380 | IPTPLIGNFGPRGPRIRHERPQKR DDRREPSSFGKRRQ*DGTLCLRR CGS\KA\YHLQKSTCGKCGYPAK RKRKYNWSAKAKRRNTTGTGRM RHLKIV\YRRFRAWDFREGTTPK PK*GSLLQSSSS |
| 1722 | 7219 | A | 1852 | 41 | 544 | APSPRRPWGHFTEED\KAT\TSL WGK\VNVEDAGGE\TPGKGSLLV VYP\WTQRFDSFGNLSSAF\AHH GQTPKVKAHGK\KVLT\SLGDAIK \HLDDLKGTFQA*VNLHL*QSC NVDP\ENFQAPGEMLLVTR\VL AIHF\GK\EFTPGGCKASWAEDG \LAVGQWPCSSRYH |
| 1723 | 7220 | A | 1853 | 145 | 705 | SWRNRTVSNGSAVSASSVHLCFA ECKALCGERILTDGSDVSRPTIAA GGCNGTVKYL*QEVLTAPL\HDGP SHVGIPRSCPKPLDKRQAHLCVLA S\NCDEPTMYVKLVEAL\CAEHQ NQP*LRVD\DNKKLG\EWG*GLL LKFDREGGKPRKSWLG\CSCFS* FKDY\GKESQAKDVIV\EFKCKK |
| 1724 | 7221 | A | 1854 | 110 | 776 | SLASGPYL\THQQKVLGLYKRAL RHL\SWCVQRDKYRYFACLMRAF FEEHKK*KRIWAKATQL\LKEAR GKNFWYPVKHPKSQYILPLTSP LGGHPY*EDHD\CAYKVPRIGCL\ D\DWHPSE\KAMYP\DYFCQRRE QWKENLRRGKAWGTEGLSSLQE\ ETP\PG\GPLTESFAPWPEKEGD \LPPLW\WYIVTR\RRERPMLE RRPHLSCLQVKYVT EHGTC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1725 | 7222 | A | 1855 | 1 | 858 | |
| 1726 | 7223 | A | 1856 | 165 | 856 | PVSYHPRMCTGGCARCLGG\TLISL AFFGFL\ANILLFFPG\GKVIDDNDHL \SQEIWFFGGILGKRCL**SFPALVF LGA*RNNDCCG\CCGNEGCGKRFA\ MFTSTIFAVGWILGELGYSFIISAISI NKGP*NPSMAKK\TWGLPPSNDGD/ YILNDEGLNGTKCAREPLQCGFPGN LDPLSSILLGRREGIQMV\LCANQV\ VNGPPWGTLCGGTCQCCGCCGG\D GPVLNLRA |
| 1727 | 7224 | A | 1857 | 163 | 1322 | PGPYCGPVATMSLHGRRKEIYKYE APWTVYAMNWSVRPDKRFRWALG SFME\EHNNEGYLDGLDEERS*V\NS KNILDRPYPTNKVMWIPDTKGVYP DLLATSGDYLRVWRVGETETRLC LLNNKN\SDFCAPLTSFDWNEVDP YLLGTSSIDTTCTIWGLETGQVLGR LNL\VSGHVKTQLIAHDK\EVYDIAF SRAGGGRDMF\ASVGADGSVRMFD LRHLEHSTIYEDPQHHPLLRLCWT KQDPNYLATMAM\DGMEVVILDV RVPCTPVARLNNHRACVNGHLLW APHSS\CHI\CTAAG*PPGFSSWD\Q QMPRA\IEDPILAYTAE\GEINN\Q\ WA\SNSAPNWESPIC\YNNCPWRY ECSVGGA VPHEAGAFVFPASAPPPK |
| 1728 | 7225 | A | 1858 | 1 | 420 | REDRIQLWKPPYTDENKKVGLALK DRKNLLETRLHITGRELRSKIAETFG LQENYIKIVINKKQLQLGKTL EEQG VAHNVKAMVLELKQSEEDARKNF QLEEEEQNEAKLKEKQIQRTYRGL* ILAKRAAETVVDPEMTP |
| 1729 | 7226 | C | 1859 | 28 | 156 | MMYRLMSILTRHVSSLKSYILIHQK WTICCSWGLLPRKPGLV* |
| 1730 | 7227 | A | 1860 | 1 | 315 | |
| 1731 | 7228 | A | 1861 | 1 | 119 | |
| 1732 | 7229 | A | 1862 | 1 | 1477 | |
| 1733 | 7230 | A | 1863 | 3 | 1866 | PLQSGHSAGRGGSGVAQGW HKKK YLQAKMTKFLREERIQLWKPPYTD ENKKVGLALKDLAKQYSDRLECCE NEVEKVIEEIRCKAIERGTGNDNYR TTGIATIEVFLPPRLKK\DRKNLLET RLHITGRELRSKIAETFGLOENYIKI VINKKQLQLGKTL EEQGV AHN VKA MVLELKQSEEDARKNFQLEEEEQN EAKLKEKQIQRTKRGLEILAKRAAE TVVDPEMTPYLDIANQTGRSIRIPPS ERKALMLAMGYHEKGRAFLKRKE YGIALPCLLDADKYFCECCRELLDT VDNYAVLQLDIVWCYFRLEQLECL DDAEKKLNLAQKCFKNCYGENHQ RLVHIKGNCGKEKVLFLRLYLLQGI RNYHSGNDVEAYEYLN\RHVSSLKS YILIHQKWTICCSWGLLPRKHRLGL RACDGNVDHAATHITNRREELAQIR KEEKEKKRRRLENIRFLKGMGYST HAGQ\QILLSNPQMWWLND SNPET |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DNRQESS\SQENIDRLVYMGFDALV VAEPALRVFRGNVQLAAQTLAHNG GSLPPELPLSPEDSLSPATSPSDSAG TSSASTDEDMETEAVNEILEDIPEHE EDYLDSTLEDEEIIIAEYLSYVENRK SATKKN |
| 1734 | 7231 | A | 1864 | 1 | 727 | MVVWDADTQQVIPNGIQLAGLDKS HSGFALAPPTTLFSGGGGGGAKAT AAAGAGLASPGMKTNGGRCRIRAL CWSRREWRGAGEDTAAECPRPQPQ QHCLAPRFPVRLGTSPGQGWSGRG AGDLAKQYSDRLECCENEVEKVIEE IRCKAIERGTGNDNYRTTGATIEVF LPPRLKKDRKNLLETRLHITGRELR SKIAETFGLQENYIKIVINKKQLQLG KTL EEQGV AHN VKA \M \VLELKQSE EDARKNFQL\QEEEQNEAKLIEERL QRTKRGLAEILAKRAA\EPVVVPEMT PYLDIANQTGRSIRIPPSEKALMLA MGYHEKGRAFLKRKEYGIALPCLL DADKYFCECCRELLDTVDNYAVLQ LDIVWCYFRLEQLECLDDAEKKLN LAQKCFKN CYGENHQRLVHIKGNC GKEKVLFLRLYLLQGIRNYHSGND VEAYEYLNRRHVSSLKSYLIHQKW TICCSWGLLPRKHRLGLRACDGNV DHAATHITNRREELAQRKEEKEKK RRLENIRFLKMGYSTHAAQQVL HAASGNLDEALKILLSNPQMWWLN DSNPETDNRQESPSQENIDRLVYMG FDALVAEAAALRVFRGKVPVAAQT PAYNGGSL/FPPELPLS\AEDSLSPAT \SPSDSAGTSSA\STDEDMETEAVNE ILEDIPEHEEDYLDSTLEDEEIIIAEY LSYVENRKSSN*RCRIRALCWSRRE WRGAGEDTAAECPRPQPQHQHCLAP RFPVRLGTSPGQGWSGRGAGDLAK QYSDRLECCENEVEKVIEEIRCKAIE RGTGNDNYRTTGATIEVF LPPRLK KDRKNLLETRLHITGRELR SKIAETF GLQENYIKIVINKKQLQLGKTL EEQ GVAHN VKADGCLN |
| 1735 | 7232 | A | 1865 | 1 | 513 | PRVRNLSREWLCDRHLREKMFSSV AHLARANPFDTPHLQLVHDGLGD LRSSSPGPTGQPRRPRNLAAA VEE QYSCDYGSGRFFILCGLGGIISCGTT HTALVPLDLVK\CRMKVDPQKYK GIFNGFSVTLKEDGVRGLAKGWAP TFL\GYSMQGLLQVLAFYEVFKVLY |
| 1736 | 7233 | A | 1866 | 2 | 1296 | ALCEPQPFQSGSCVAILGRKMFSS VAHLARANPFNTPHLQLVHDGLGD LRSSSPGPTGKPRRPSQ/HMAAAPV EEQYSCDYGSGRFFILCGLGGIISCG TTHTALVPLDLVK\CRMKVDPQKY KG\IFNGFSVTLKEDGV\RLAKGW APTFLGYSMQGLCKFGFYEVFKSL YSNMLGE\ENTYL*RTSLYLAASAS\ AEFFADIALAPMEAAKVRIQTQPG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | YANT*EGISFPKCIKEEGLTSILQGG LLPLWMRQIPYTMN*SSPCLERTV A\LYKFV\VPK\PRRE*FKRQSRLVVT IW*QVTIARVFCANCFSPLEFLG*P VLD*GKKVSQCFLWVLQRD LGFK\ GV\WKGLFA\RII\MI GTLT\ALQWFI YYSVKGYFR\LRP\PPP\EMQES\LK KKLGVNSVVRIKAN CGLNLLVDPV FEESAKGTFIYLT V |
| 1737 | 7234 | A | 1867 | 127 | 433 | RPLESWIGLVRCNICRSPIAEAVFRK LVT DQ NISK NWRVDS AATSGYEIG NPPDYRGQSCMKRHGIPMSHVARQ DLNRKSNRVKTCKAKIELLSGYDP QKQL |
| 1738 | 7235 | A | 1868 | 2 | 535 | |
| 1739 | 7236 | A | 1869 | 551 | 1299 | PADPPRPSYYRHRTPPQAHWSRLRR SRLRRRGSHTRCPVGVGAGLRRRA GARLAVRLRASACGTPRCLGASAR GKMAEQATKSVLFVCLGNICRSPIA EAVFRKLVT DQ NISK N\WEGRQRG NFRWVIDSGAVSDWNVGRSPDPRA VSCLRNHGIHTAHKARQITKEVFP TFDYILCMDES NLARDLNRKSNRVK TCKS*KFELPWEL*SPQKQLIED\PY YGE*LWTLET VYQQ\CVR\CCRAFL\ EKAH |
| 1740 | 7237 | A | 1870 | 85 | 563 | SSF LDIVHVCNTPNVKKMVSGSSHK VIEQDLSIGDHPVTPVQSVYCKRS PKIPKIFVKVSKTNSETQIYLGWQV KIGFPNF*NPVAGILDR TKYRIFP*AP GIHKL GKYPREI*ASYV*KSPSTSMS TAALFPIAKPRAGP*MPTKGSWVK\ KIWYGQK |
| 1741 | 7238 | C | 1871 | 604 | 804 | MKRLRHLRXINNLA KITQPLSKTAL NLSPTQGGSKSRAILEFQLSRPGVPN PTLNWPSLNP FREPE* |
| 1742 | 7239 | A | 1872 | 64 | 73 | AFL*RWGSPCCPRAGLK/PP*P/PSI CPPRPPK PAGITRREPPGQAYFLII*F PSI*L |
| 1743 | 7240 | A | 1873 | 47 | 225 | NSHHVRGRPRCADSSSPSGDRGQPE AQPAPDSSAPEHAQEPGRAAVKRP DL*SHMTRRP |
| 1744 | 7241 | C | 1874 | 101 | 232 | MTMITPSSKLT LTKGNKSWSTAVA AALELVDP PGCRNSARGF* |
| 1745 | 7242 | A | 1875 | 66 | 723 | AILIILLSS EGLWSSDQHRLVGVDQS PPQGLCCHFSAMATSEQSICQARA SVMVYDDTSKKWVPKPG\QQGFSR INIYHNTASNTFRVVG VKFQDQQ\ V VINYSIVKGMKYNQATPPFPQWRD ARQVYGLNFASKEEATTF SNAMLF ALNIMNSQEGGPSSQRQVQNGPSPD EMDIQRRQVMEQHQQQRQEFLERR TSATGPILPPGHPSSAASAPVSCSGP SPPPPPPVPPPTGA\TPPPPPPL\ PAG GAQGSSHDES/SPCSGLAACH*LGPS LRRVPNGPEDASGGSSPSGTSKSDA NRASSGGGGGGLMEEMNKLLAKR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RKAASQSDKPAEKKEDSQMEDPS TSPSPGTRAASQPPNSSK\AGRKPW DRNNPLRNPLSSNLVRNPLLAKGPR KLRAPFSQQPHSRMKPAGS\VSDMA \LDAFDLD\RMKQEI*KEVVRELHK GERKEIID\AIRQEA*SGISRKKNLGH RAHPPTRTSFICSQRPRLM |
| 1746 | 7243 | A | 1876 | 1 | 668 | GERGVARHDRPRGTLREYKVVGR LPTPK\CHTPPLAYR\MRIFAP*SMSSL SPRF\WYFVSQKKDEESLQWRFSY CAQVFEKSP\LRVK\NFGIWLRYDS RSG\THNMYREYRDLDHPQAPVHP SCLTRDNGVAPAPAA/HEAHFHFRI ERLEEIAGQQDCRRPGCSKQFPRIS RFKFPAAAPGSLRRQDKPRF\TTKRP KTFKLVQGPSSGVCQNKQTQETPR |
| 1747 | 7244 | A | 1877 | 1 | 1059 | |
| 1748 | 7245 | A | 1878 | 87 | 260 | |
| 1749 | 7246 | A | 1879 | 1 | 1254 | |
| 1750 | 7247 | A | 1880 | 160 | 615 | PSLNTYVTSP\SENFSARYRNHSND LTCVHTELQNKTKLTVLEGDILDEP FLKRACQ\DVSVNHTACHIDVFGVT HRESIMNVNVKGRVAWGGDKARW GNEDQKEGQEGKRSLSIEHLLCSGP SDFADHYQLGELKAAIFSFIDEKTRT EQ |
| 1751 | 7248 | A | 1881 | 53 | 1338 | CPLQGHPRVTLESDDLPSIFCFLVSD SCYFGLATMGWSCLVTGAGLLGQ RIVRLLVEEKELKEIRALDKAFRPEL REEFSKLQ\NK\TKLTVLEGDILDEPF LKESLARDRLRSIIHTACFHLMSFGV \THREFF\MNVQC*KVPSSC*EACVQ ASVPVFIYTSSIEVAGPNSYKEIIQNG HEEEPLEN\WPAPYPRSKKLA\KKA VLAANGWNLKNGGALYTALRPM YIYGEGRFLSVSINEALNNGILSS VGKFST\NPNVYVGNVAWGHILAL RALQDPKKAPSIRGQFYIISDDTPH QSYDNLNYTLASKEFGPPPLDSRWAS FPLSLMYWIGFLLGNNR*GFLLRPIY TYRPPFNHRHSSHCNN*ALFHLLFIKE GFSEILGVLRLPLTAGGGKAKAGKR VGSWVWVPFVDPAPQGRNLEVPRIQ |
| 1752 | 7249 | A | 1882 | 3 | 575 | HSLFGTSEVINKLLVPDAMGHFTEE D\KATITSLWGK\NVNVEDAGGE\TP GKGSLVVYP\WTQRF\DF\SFGNLSS ASAI\MGKPPKSKAHGKKVLTFLGT MPTKHLE*FSRGTFCPSLK*TCTC*Q ACMWDPGGTFKLPGENVAGLTVFG QSHFRQKNFTPEGARFFLGRKMGD LELASALVPSRLPLKPLGP |
| 1753 | 7250 | A | 1883 | 1 | 960 | GRPAPEDGGPLSLPNAAMARGPKK HLKRVAAPKHWM\LDKLTGVFAPR PSTGPHKLARECLPFII\LRNRLKYA LTS\DEVKKICMQRFIK\NDGQVR\TD ITYPAGFMDV\ISIDKDGREFSVL/Y LIDTQGVRFCL*HRJTP*GRAKVQSC AKMRKILLWAPKGIPSSWVTHDAR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NHPATPDPPSSKVN*YHFRLDLETG KDYLISSKFDTW*PCVMVTGGAN LGRNWVLITN\RRHPGIF*PLVHVK DANGNKLLATSDFSNIFWLLGKGN KPWISL\PRGKGIPPHHLLLEERDKRL AAKQSSWVKWGPWVTWSDLLVP |
| 1754 | 7251 | A | 1884 | 1 | 1218 | FFQNSARGAGAGWQLPWTRFVWT SGLLEINE\TLVIQQRGVRIYDGEEDI KFDAGTLLLSTHRLIWRDQKNHEC CMAILLSQ\VFIEEQ\AAGIGKSAKI VVHL\HPAPPNKEPGPFQSSKNSYI KLSFKEHGQIEFYRRLSEEMTQRRW ENMPVVSQSLQTNRGPPQGRIRAVGI VGTERKLEEKRKETDKNISEAFEDL SKLMIKAKEMVELSKSIANKIKDKQ GDITEDETIRFKSYL\LSMGIANPVT RETYGSGTQYHMQ\LAQQL\AWNIA RVPLEERGIMSLTEVYCLVNRARG MELLSPEDLVNACKMLEALKPLR LRVFDSGVMVIELQSHKEEMVAS ALETVSEMGS\TS*EFAKLVGMSVL LAKERLLLAEKMGHLCRDD\VEGL RFYPNLFMTQS |
| 1755 | 7252 | C | 1885 | 179 | 361 | MPKVCVFNHFLKTSSERDLFALMN TVGKKHSIMSEKGRSKKFLHLIDSK KNEDPHLDGTL* |
| 1756 | 7253 | A | 1886 | 2 | 913 | RRLLLFGWARS\GAVSLGSAGVSSS GFLTAPH\SRRLTAAAAAAGGAWRF EAERHRGWGAEEEQPEGGA\CPG TERPCAMAYAYLFKYIIGDTGGGR\ SCLLLQFTDKRFQPSAMTLTNGVEF GARMITIDGKQIKLQIWD\TAGQES\ FRSITR\SY\YRGAAGALLVYDITR\R DTSTHLTTWLEDARQHS\HFQHGS LCLLG\NKSD\AESRKE/VSKKRKEGE SFLQPRNHGLHLPWKTSC\KNCFPM* KEAFINTSKRN\FIEKIQ\EGVFDINNE A\NGIKIGP\QHAATNATHAG\NQQG QQAGGGCC |
| 1757 | 7254 | A | 1893 | 138 | 426 | FIHSHCCIVFRLFIHFS\HPKVIHSPIN SLLRIFQF*AIMNSTV*NILIHVFW*V YTFPF\GINPKKGIARL*GVYIFSFSIY CQTVFQSDCKKAPF |
| 1758 | 7255 | A | 1894 | 45 | 1057 | FLVFLVETGFHHVAQAVLELLASSD PPALAPPKCWDYRCELLRLAEFCFL RTEFWYLLFFFFWRRSLALSPRLEC SGANL\THCNLR/LPGFKQFCSLSLS SWDYRCMPPHLATFFVF/SVETGFH RVAQASLELLSSGSLPALA/FPKCW DYRAKATV/WSPGVSSFILGL*TS* FHSLEPYLHAWKT\TSHLPTKEALT W/VSHTAKTKHLWILVSILMEF*VA LIS/SFFLGPGGK*T*VTAPQCPSLGQ DTLS*FLHAACTRSVPYPGLA/CGPS LWLTRVLLPTPP*QQHNP/DTLEKT SFPGPHWIL*/TPQPSLSETPAPKVPP FPAFGSIPTHEEPGLP |
| 1759 | 7256 | A | 1895 | 2 | 289 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1760 | 7257 | A | 1896 | 1 | 397 | |
| 1761 | 7258 | A | 1897 | 1 | 410 | STMISPVLLIFSSFLCHVAIAGRTCPK PDDLPFSTVVPLKTFYEPGEEITYSC KPGYVSRGGM\RKFCPLTGLWPIN TLKCTPRVCPFAGNLRKMGAVRLIT DFLNYSPTRFSSLLTWGFILEWAL DS\AKCIEGG |
| 1762 | 7259 | A | 1898 | 19 | 1215 | CQCDSSSTMIFSRCSLLFSSFLCHVAI AGRTCPKPDDLPFSTVVPLKTFYEP G\EEITYSCKPGYVSRGGIEESLSCPL VTGTVGPFNTSGNVTPRVCPF\AGIFR KMGGRTLITTF*NYPNTDPVFSLLTL GF*FWNGALDFWPSCTGGKGKWS P\ELPGLVAPIN\CPPPSIP/TGFATLH VLLRPFRLGNNSPPIGDTAVFECLA HNMAMFG\NDTIT\CTTHGKLDLNY PECRGSKMPPFPHQDPDNGIW*TYP CQNPNTLFTRVKAPHLGLPHDGIFS GMGPRKEIEC*PQTWKGKPSWPLA PSW*KPSLVKGTVPVKRPTVV/YPQ GERVKDSREKFKEWECLHG**KFLS FCKNKEKKCSYTEDAQCIDGTIEVP KCFK\EHSSLAFWKT\DA\SDVKPC |
| 1763 | 7260 | A | 1899 | 58 | 446 | |
| 1764 | 7261 | A | 1900 | 1 | 954 | MGEVSGTSDCTDDQCRQVKKALEG GKAARGHRSKIKIRFFRPGGLGPGP AITAVAGMPRVYIGRLSYQAREHA V\ERLLNGHAKILEVDLKNYGFVE FDDLRLDADDAVYELNGKDLGGERV IVEHARGPRRDGSYSGRSGYGYR RSGRDKYGPPTRTEDRLIVEN\LTR CSWQDLKDYMRQAGEVTYADAHK GRQKMKGVIEFVSYSMDMKRALEKL DGTEVNGRKIRLVEDKPGSRRRRSY SRSR\SHSRSRSRSRHSRKSRSRSGSS KSSH\SKSRSRSRSGSRSRSKSRSRSQ SRSRSKKEKSRSPSKDKSRSRSHSA\ GKSRSKSKDQAE\EFQNDNV\GK PKSRSPSRHKS\SKSRSRSQERRVEE GRKRGSF*QGQ/EAQEKSLRQSRSR\ SRSKAGSR*PVDRSRSKSKDKRKS KRSREESRSR\SRSRSKSERSRKRGS KRDSKAS\SCKKKKKEDTDRSQSR PSRSV\SKEREHA/RSLESSQREGRG ESENAGTNQEDPGPGPRSM\SKSKP NLPIRMHRSKIKSQASKTPISGPMR SR\ASRSP\SRSRSKSRSRSQSRSR KKEKSRSPSKDKSLQPQP |
| 1765 | 7262 | A | 1901 | 3 | 180 | |
| 1766 | 7263 | A | 1902 | 227 | 440 | GMHNVCYVAVNE*FCGFIIR*SLAE RRQIS*EFQLFKFTLCLELILARRAC RESMA\$PVAGSWSHFPEREF |
| 1767 | 7264 | A | 1903 | 2 | 438 | HEELDTSERKIEFDSASGTY\TYLNI GDAHFEEPQSLWNVADLVHQSPPE EKAPLDLSCPQNLFTPK\QEIQWIRI GA\NVSNFTFAP\STIIFHLGHA\AM LGLMYVYWTQLNMF\QTLKYLAIL GSVTFLAGNRMLAQQA\VKRTAH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1768 | 7265 | A | 1904 | 1 | 1660 | |
| 1769 | 7266 | A | 1905 | 156 | 2369 | PVLKTHPGPQSLPRVPGVPCGGLLE PLSRAEVSPRFLRRDLLGGMAPP SSTVFLALTIISTWALTPTHTLTK HDVERLKASLDRPFTNLESAFYISV GLSSLGAQVPDAKKACTYIRSNLDP SNVDSLIFYAAQAISQGLSGCEISISN ETKDLLLA/VSE/DSSVYPRSYHAS WQL*SGLLGLSLWAVPKESTQVAL NWL VFKQ GKETVLA/TVQALQTAS HLSQQADLR SIVEEIEDLVARLDEL GGLYLQFEEGLETTALFVAATYKA /LMDH/VGTE/PSIKE/DQVIQLMNAI FSKKNFESLSEAFSVA/SGVA/VLS HNRYHVPVVVVPEGSASDTHEQAI LRLQVTNVLSQLTQATVKLEHAK SVASRATVLQKTSFTP/VGIVFELNF MNVKFSGG*CDF/LVEVEGDNRYIS/ NTVELRVQDPPTVEGITNVDLSTV/ DKDQSIAP/QTTRVTYPAKAKGTFH SAGQATRNFGVLVSSW*DVNTGVAE LTPHQTFVRLHNQKTGPGSGCLFAE PGQQGTCYKFELDTSERKGLNLTSR SGTYTLYLIIG*CQL*RTQILWKCGL MWVIKFP*GKEASFDCLCSQEPFSL PKQGNFRHLFPGRP*GRRAPPWCP NTFTAPESFFGPLL/LCFLRLLWIRD WVPKCLPTFTFCFLSTIIFHPWDM LAYAGTSMYVY*TQAQPCSQTLEVP WPILGQCDRFLAGQSGMLAPARQV KRIAAEQSSRLAKYRTLRTAH |
| 1770 | 7267 | A | 1906 | 37 | 404 | PQLSRCRSECMYVNPTVVM TSMGQ ATWSDPHKAKTMLNRIPLGKFAGE SGGSPASVVPAPVPCALGRGGRER WAAASFLYAPDPRPAHEVEHVVN AILFLLSDRSGMTTGSTLPVEGGFW AC |
| 1771 | 7268 | A | 1907 | 271 | 1086 | YTQCPGIEPVCVDLGDWEATERAL GSVGPVDLLVNNAVALLOPFLEV TKEAFDR*ACEGGTSGRGCPGGRS SPNL*PGSVPRPLDPLRVNLRAVIQV SQIVARGLIARGVPTGPS*NVSSQC FPAGQ*TNHSVLLLPTKGVPLDMLD QG*WAL/ELGPHKLSRCRSGVNAIV NPHSGG*RSMGPGPPWSDPHKIAKI MLNRIPLGKFAGESEVEHVVNAIL FLLSDRSGMTTGSTLPVEGGFWAW LSSLHTPQAPWACFILTPNPSNKT |
| 1772 | 7269 | A | 1908 | 2 | 305 | ARESGSLVAPRSRPPWEHGLPGEHS *DAPRPHKSPTLPWLPHLHLSKEAL DTHQRSQHE/ECMPLYKFTPTSEKR PQLMLPLPEQQCEQLCRFGSTPVTW A |
| 1773 | 7270 | A | 1909 | 2 | 529 | GTVAACGACYWLLGLMAVRASFE NNCEIGCFAKLTNTYCLVAIGGSEN FYSVFEGELSDTIPVVHASIAGCRIIG RMCVG/TEEILADV LKVEVFRQTVA DQVLVGSYCVFSNQGLVHPKTSIE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DQDELSSLLQVPLVAGTVNRGSEVI AAGMVVNDWCAFCGLDTTSTELSV VE |
| 1774 | 7271 | A | 1910 | 18 | 889 | GVQGTVAACGACYWLLGLMAVRA SFENN\CEIGCFAKLTNTYCLVAIGG SENFYSVFEGELSDTIPVVHASIAG CRNIGRMCVGN\NRHGLL\VPNNTTD Q\ELAQHISATGLPRHSGRFRAGWKE RFLSLWGNFFNHLAIDYVGLGSNQ D\LDKGRQEEISGQMLFKGWVFRQ TV\ADQVLVES\YCVFSNPGRWVP SPRPFQ*RPRLNELSSISFKVPL\VAGT C*TKGSEVICLLGMGGEMNWCA\FC GPGTPNPAQSCQVVEECLQS*NEAP ALAPIANRACGNSL\IDSLT |
| 1775 | 7272 | A | 1911 | 132 | 440 | |
| 1776 | 7273 | A | 1912 | 149 | 389 | FSWV*REIFSFLISLIFIYETFSKLIKIF QDHPLQKTYN\YNVLMV\PKPQGGLP NTALLSLVLMAGTFFFAMMLRKFK NSS |
| 1777 | 7274 | A | 1913 | 3 | 153 | |
| 1778 | 7275 | A | 1914 | 94 | 593 | LVVFSSPSQSWERTECLGFLQIFQD HPLQKTYN\YNVLMV\PKPQGGLPNT ALLSLVLMAGTFFFAMMLRKFKNS SYFPGKLRRVIGDFGV\ICILIMVLV DFFIQDTYTQKLSVPDGF\KVSNSA RGWV\HPLGLRSEFPIWMMFASAL PALLVFILIFLESQITT |
| 1779 | 7276 | A | 1915 | 115 | 3015 | TTGHSGPRHGAAGGCSLASAVLP PGGSGDLVDSYLRWGWS\PSQPS LSGHFPQDDYEDMMEENLEQEEYE DPDIPESQMEEPAAHDTEATATDYH TTSHPGTHKVYVELQELVID\ERIPD LQWMEAAPLR\QLDENLGENGAW GRPHLSHLTFWSLLELRRVFTKGT LLDLQETSLAGVANQLLDRFIFEDQI RPQDREELLRALLLKHS\HAGELEAL GGVKPAVLTRSGDPSQPLLPQHSSL ETQLFCEQGDGGTEGHS\PSGILEKSP PDSEATLVLVGRADFLEQPV\LGFR LQEA\AELEAVELPVPIRFLVLLGPE APHIDYTQLGRAAA\TLMSEVFRID AYMAQSRGELLHSLEGFLDCSLVLP PTDAPSEQALLSLVPVQRELLRRRY QSSPAKPDSSFYKGLDLNGGPDPL QQTGQLFGGLVRDIRRRYPY\LSDI TDAFSPQVLA\AVIFIYFAALSPAITF GGLLGEKTRNQMGVSELLISTAVQ GILFALLGAQPLL\VGFGSPLL\VFEE AFFSFCETNGL\EYIVGRVWIGFWLI LLVVLVVALRGVASLVRFIS\RYTQ EIFSFLISLIFIYETFSKLIKIFQDHPL QKTYN\YNVLMV\PKPQGGLPNTALL SLVLMAGTFFFAMMLRKFKNSSYF PGKLRRVIGDFGV\PI\ILIMVLV\DDF IQDTYTQKTSQVPDGF\KVSNSARG WVIHPLGLRSEFPIWMMFASAL\PC LLVFILIFLESQITTLIVSKPERKMKV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GSGFHLDLLLVVGMGGVAALFGMP WLSATTVRSVTHANALTMGKAST PGAA\AQIQEVK\EQRISGLLVAVLV GLSILMEPILSRIPALVFGIFYMGV TSLSGIQLFDRILLFKPPKYHPDVP YVKRVKTWRMHLFTGIQIICLAVL WVVKSTPASLALPFVLILTVPLRRV LLPLIFRNVELQCLDADDAKATFDE EEGRDEYDEVAMPV |
| 1780 | 7277 | C | 1916 | 20 | 202 | MAAIKYLGISAILYYKYKCPRGQGN QPEELGTGSILCGNFSGLMLFPVQM YTVKKAYRAV* |
| 1781 | 7278 | A | 1917 | 1 | 493 | |
| 1782 | 7279 | A | 1918 | 214 | 612 | |
| 1783 | 7280 | A | 1919 | 287 | 847 | SDRPTMAPGVARGPTPYWRLRLG GAALLLLLIPVAAAQEP PGAACSQN TNKTCEECLKNVSLWCNTNKA CLDYPDTSVLPPASLCKLSSARWGVC WVNFDAIITMSVVGGLLLGIA\NC CCCCRRKRSRKPDRSEEKAMR\ER EDR\WILQEERRAEMNTRHDEIRKK\ YGLFKEENPYARFENN |
| 1784 | 7281 | A | 1920 | 61 | 515 | |
| 1785 | 7282 | A | 1921 | 1 | 2175 | |
| 1786 | 7283 | A | 1922 | 3159 | 3441 | |
| 1787 | 7284 | A | 1923 | 36 | 387 | |
| 1788 | 7285 | A | 1924 | 64 | 408 | |
| 1789 | 7286 | A | 1925 | 1 | 10514 | |
| 1790 | 7287 | A | 1926 | 64 | 601 | VNNILGLGHTFWALLASPKMEHKE VVL LLLFLKSGQGEPLDDYVNTQ GPSLFSVTKKQLGAGSREECAAKCE EDKEFPAGAF\QYHSKEQQCVIMA ENRKSS\INRVRDAVLFGKGKCLF RVQDLGMERTTEGRCPKQKMASPC QKWEFHFPADLGQTFPFIFVFIYCK VVPLCL |
| 1791 | 7288 | A | 1927 | 173 | 491 | AGEARWESQSAHLKPEFGGPTGPN NAQSPPREADAQQVWREPPGPASK APHSPVGYSSPGHESHLPGDDPA KDGSCPP\PFPLGIEAPVPGPRKRIR TCCCMN |
| 1792 | 7289 | A | 1928 | 1 | 735 | |
| 1793 | 7290 | B | 1929 | 1 | 1026 | MRARRLPWALTIVAELGWD TQGG DQTSPGGNDRMSMEAECSTTVSP LSCSIPTGCGQTREEVSARATPPPSL GASLLQTLTPDTHCTGVSATIMSML VVFLLWPFSSSTLAKHKRIHTGE KPYKCEECKAFSRSTLAKHKRIH TGEKPYKCECKAFRQSSSTLTKH KJIHTEKPYKCECDKAFKRLSTL AKHKIHHAGEKLYKCEECKAFNR SNLTIHKFIHTGEKPYKCEECKAF NWSSSLTKHKRIHTREKPFKCECK KAFIWSSTLTRHKRIHTGEKPYKCE ECKKAFSRSTLTKHKTIHTGEKPY KCECKGKLLSTPQPLLNK* |
| 1794 | 7291 | A | 1930 | 1 | 2832 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1795 | 7292 | A | 1931 | 98 | 3867 | PAGIGRATAKMPGTPGSLEMGLLTF RDVAIEFSPEEWQCLDTAQQNLYR NVMLNRYRNLAFLGIALSKPDLITY LEQGKEPWNMKQHEMVDEPTGICP HFPQDFWPEQSMEDSFQKVLLRKY EKCGHENLQLRKGCKSVDECKVHK EGYNKLNQCLTTAQSKEVFCGKYL KVIFYKFLNSNRHTIRHTGKKCFKCK KCVKSFCIRLHK\TOHKCVYITEKSC KCKECEKTLWSSTLTNHKEIHTE KPYKCEECGKAFKQLSTLTTHKIIC AKEKIYKCEECGKAFLWSSTLTRHK RIHTGEKPYKCEECGKAFFSHSSTLA KHKRIHTGEKPYKCEECGKAFFSHS ALAKHKRIHTGEKPYKCKECCGAF SNSSTLANHKITHTEKPYKCKECD KTFKRLSTLTCHKIHHAGEKLYKCE ECGKAFFNRSSNLTIHKFIHTGEKPY KCEECGKAFFNWSSSLTKHKRFHTR EKPFKCKECCGKGFIWSSTLTRHKRI HTGEKPYKCEECGKAFFRQSSTLTCHK KIIHTGEKPYKFECCGKAFFRQSSTLT CHKIHSREKPYKCKECCGKAFFQFS TLTTHKIIHAGKKLYKCEECGKAFFN HSSSLSTHKIIHTGEKSYKCEECGKA FLWSSTLRRHKRIHTGEKPYKCE CGKAFFSHS\ALAKHKRIHTGEKPY KCKECCGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTCHKIHH AGEKLYKCEECGKAFFNRSSNLTIHK FIHTGEKPYKCEECGKAFFNWSSSLT CHKRIHTREKPFKCKECCGKAFFWSS TLTRHKRIHTGEKPYKCEECGKAFFS RSSTLTCHKTIHTGEKPYKCKECCGK AFKHSSALAKHKIHHAGEKLYKCEE CGKAFFNQSSNLTTHKIIHTKEKPSKS EECDKAFFWSSTLTEHKRIHTREKPY KCEECGKAFFSQPSHLTTHKRMHT GEKPYKCEECGKAFFSQSSTLTTHKII HTGEKPYKCEECGKAFFRSSTLTTEH KIIHTGEKPYKCEECGKAFFSQSSTLT RHTRMHTGEKPYKCEECGKAFFNR SKLTTHKIIHTGEKPYKCEECGKAFFI SSSTLNGHKRIHTREKPYKCECGG\ KAFFSQSFN\TLTGHKRLHTGEKPYK CGECGKAFFKESALTCHKIHTGEK PYKCEKCCGAFFNQSSILTNNHKKIHT ITPKIHTREKPYKYKECGKSFNRSS FTKHKVIHTGVKLYKCEECGKSFF WSSALTRHKKIHTGQQPYKQEKFG KAFFNQPSHLTTR |
| 1796 | 7293 | A | 1932 | 590 | 891 | |
| 1797 | 7294 | A | 1933 | 1 | 1527 | |
| 1798 | 7295 | A | 1934 | 13 | 1668 | PESKMAGSRHRGLRARVRPLFCAL LLSLGRFVRGDGVGGDPAVALPHR RFEYKYSFL\GPHLVQSDGTVPFWA HAG\AISSSDQIRVAPSLKSQRGSV WTKTK\AAFENWEVEVTFRTVTRG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RIGADGLAIWYAENQGLEGPFVFGS ADLWNGVGIFDFSFDNDGKKNNPA IVIIIGNNGQIHQNDGASQALAS CQRDFRNKPYPVRAKITYVQNTLA TVMINNGWFTPDKNDEYFCAKVEN MIIPAQGYFGISAATGGLADDHDVL SFLTFQLTEPGKEPPTPDKEISEKEK EKYQEEFEHFQQLDKKKEEFQKG HPDLQWQPAEEIFESVRDRELRO VFEGQNRHLEIKQLNRQLDMILDE QRRYVSSLTEEISKRGAGMPGQHG QITQQLDTPVKTQHEILRQVNEM KNSMSVEPVLVSGMQHPGSIAGGV YGTTQHFIDIKELHIVKRDIDNL VQRNMPASNEKPKCELPFPSCSLST VHFQIFVVVQTVLFIGYIMYRSQQ EAAAKKILLTTIFLCTSSICVQNDVV LREFKYLNCFIV |
| 1799 | 7296 | C | 1935 | 238 | 360 | MGGLGLSLRSLSSASPAXFRPAHAP VGAAGLGPASPQGPL* |
| 1800 | 7297 | A | 1936 | 1 | 1656 | |
| 1801 | 7298 | A | 1937 | 83 | 260 | |
| 1802 | 7299 | A | 1938 | 1 | 678 | |
| 1803 | 7300 | A | 1939 | 1 | 1097 | |
| 1804 | 7301 | A | 1940 | 1 | 1706 | MQLLLAECMGQSGPPGAVCHCQR VWQARAVRRSKRPVPSTTQGLKSV GAWRGSGRQLHLQPQYRIHWVKP AGLLSLVGTMENICVWPSDCKYTN RHSVSSRLLDSLKRDYAGKPQPI KSERRNPPSYAMAAAQLRDSEETG GSEFVFAEKTLRKCVKCPQVELENV AFAKDAEESRDAQRLGHWWPCIME TLSNASGTFAIRLLKILCQDNPSHNV FCSPVSISSALAMVLLGAKGNTATQ MAQALSLNTEEDIHRAFQSLTEVN KAGTQYLLRTANRLFGEKTCQFLST FKESCLQFYHAELKELSFIRAAEESR KHINTWV\SKKTEGKIEELLPGSSID AETRLVLVNAIYFKGKWNEPFD YTREMPFKINQEEQRPVQMMYQE ATFKLAHVGGGLRAQLEL\LPYARK ELSLVLLPDDGVELSTVEKSLTFE KLTAWTKPDCMKSTEVEVLLPKFK LQEDYDMESVLRHLGIVDAFQQGK ADLSAMSAERDLCLSKFVHKSFVE VNEEGTEAAAASSLWVVAECCME SGPRFCADHPFLFFIRHTRANSILFC GRFSSP |
| 1805 | 7302 | A | 1941 | 3 | 428 | ETLERIKNNDPKLEEVNLNNIRKIPI TLKAYAEALKENSIVVKFSIVGTRS NDPVAYALAEMLKENKELKTLNVE SNFISGAGILRPGEALPYNTYLVEM RSDNQSQPPGKNVEMEIVSMLAEKN ATLLRVR*HFSQQDAR |
| 1806 | 7303 | A | 1942 | 1 | 1258 | ALARPLPAGAPRPPASICPPAPVP QPASAPAPQLCVRVLLSTEIQETQTS SSTMSYRRELEKYRDLDEDEILGAL TEEELRTLENELDELPDNPALLPAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LRQKDQTTKAPTGPFFKREELLDHLE KQAKEFKDREDLVPYTGEKRGKV WVPKQKPLDPVLESVTLEPELEEAL ANASDAELCDIAAILGMHTLMSNQ QYYQALSSSSIMNKEGLNSVIKPTQ YKVPDDEEPNSTDVEETLERIKNND PKLEEVNLLNIRNIPIPTLKAYAEAL KENSIVKKFSIVGTRSGDGVAYAL AEMLENKVLKTLNVESNFISGAWI LRLVEALPYNTSLVEMKIDNQSQPL GNKVEMEIVSMVEKDPHHFLKFGL PPYPSKEPRLR\ASTAMMNTIALVR EIRRLAAPDLGPSFPKCRSGV |
| 1807 | 7304 | A | 1943 | 2 | 382 | EIAHQIIEQQMG/EG*NFVAIESVV*K IVTEQQTGQKIQIVTALDHNTQGKQ FILTNHDGSTPSKVILARQDSTPGK\ VFLTTPDAAGVNQLFFTTPLDSAQ HLQDVMGAVTCEGCKGFFKRSIRK N |
| 1808 | 7305 | A | 1944 | 240 | 454 | |
| 1809 | 7306 | A | 1945 | 1 | 1851 | |
| 1810 | 7307 | A | 1946 | 128 | 512 | TAPLAAGRPPGDALGPRPLAVGVK GTPWPPPPTRSLVSPPSVSYYRFCAL LTPASGADATVPRLPLVDWGALRE ERLKKADGMWDRDSRRRELSVFG ACALATGRSGERRS*RSQGGVEGSE GRAAAL |
| 1811 | 7308 | A | 1947 | 1 | 705 | |
| 1812 | 7309 | A | 1948 | 124 | 1583 | IMATIEEIAHQIIEQQMGIVTEQQT GQKIQIVTALDHNTQGKQFILTNHD GSTPSKVILARQDSTPGKVFLTTPD AAGVNQLFFTTPLDSAQHLQLLTD NSPDQGPKNVFDLCVVCGDKASGR HYGAVTCEGCKGFFKRSIRKNLVYS CRGSKD\CIINKHHRNRCQYCRLQR CIAFGMKQDSVQCERKPIEVSREKS SNCAASTEKIYIRKDLRSPLTATPTF VTDSESTRSTGLLDSGMFMNIHPSG VKTESAVLMTSDKAESCQGDSTL ANVVTSLANLGKTKDLSQNSNEMS MIESLSNDDTSLCEFQEMQTNGDVS RAFDTLAKALNPGESTACQSSVAG MEGSVHLITGDSSINYTEKEGPLLSD SHVAFRLTMPSPMPEYLVNHYIGES ASRLFLSMHWALSIPSFQALG\QEK QP*SLVKAYWNEFLTGLAQCWQV MNVATILATFVNCLHNSLQQDAKV IAALIHFTTRAITDL |
| 1813 | 7310 | A | 1949 | 6 | 2028 | KILRTLTPQKYPRTESSLRRESRSHM PTAFLNLSCRSAPQSTRGSRGTVAS APDAGGSRAQKRREIMATIEEIAHPI IEQQMGIVTEQQTGQKIQIVTALD HKTQGKQVILTNHDGSTPSKVILAR QDSTPGKVFLTTPDAAGVNQLFFTT PDLSAQHLQLLTDNSPDQGPKNVF DLCVVCGDKASGRHYGAVTCEGC KGFFKRSIRKNLVYSCRGSKDCIIN KHHRNRCKYCRLQRCIAFGMRQDS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VQCERNPLEVSREKSSNCAASTEKI YIRKDLRSPLTATPTFVTDSESTRST GLLDSGMFMNIHPSGVKTESAVLM TSDKAESCQGDSTLANVVTSLANL GKTKDLSQNSNEMSMIESLSNDDTS LCEFQEMQTNQDVSRFDLAKAL NPGESTACQSSVAGMEGSVHLITGD SSINYTD\KEGPLLSDSHVAFRLTMP SPMPEYLVNHYIGESASRLLFLSMH WALSIPSFQSGRGKEN\SISLVESLLG IELFTLGLAQCWQVMNVATILA\TF VNCLHNSLQQDKMSTDRRKLLME HIFKLQEFCSNMVKLCIDGYDYAYL KAIVLFSPDHPSLENMEQIEKFQEK AYVEFQDYITKTPDD\TYRLSRLLL RLPALRLDGGCTITEELFFKGLIGNIR IDSVIP\HILKMEPADYNSPIIGHSI |
| 1814 | 7311 | C | 1950 | 65 | 286 | MDYCNTFLPSNPETVFGDIMPRV NK PDLGTALSRGFTHEINKTYLSHLKL GSQKTHFWFIISFYAHLTLIIYP* |
| 1815 | 7312 | A | 1951 | 15 | 82 | |
| 1816 | 7313 | A | 1952 | 2 | 1934 | CVQAATSLSVGICPLPGPGSPPPWY PGVSVNVWIFKQIDDEGDLRLINK EVLSGVVVISKDSVQHOGVSLTME GTVNLQLSAKSVGVFEAFYNSVKA QLRRSVQATGLEERPALPERLQQEG SEEAGGLSGAEALPRRARGSPIQII NSTIEMVKPGKFPSPGKTEIPFEFPLH LKGKLVLYETYHGVFVNIQYTLRC DMKRSLLAKDLTKTCEFIVHSAPQK GKFTSPVDFTITPETLQNVKEHS HQ TEAGQQRAFQRFRSALRGGRLTAR ADNSSSSNVAQGSQKSGHPCSRPSS VLPQQRQVCRVKRALLPKFLL/RRT SQLNKLCHHAATNGRAGGGELGSR HQKRGAAAGARGDPGQQSRP*P*L* KTRGRRGSKSKSVAVP*Q*PRV*GK VCR\SYARDATEIQNIQIADGDVCR GLSVPIYMFVPRFLTCTPTLETTNFKV GKWHSPSPHGPMPGAAQRQGLL WVTELRTCPSVPQCQGLPQAIQLR ACCP SAAQQNLVKELLCRTGDTPT GSPGACGTSTVTWNTQTTHISVDM GRPQPQVGTD SKAPSTAELPQCGA QHRVPSAHTMPFPPLLTLGKEMVL VCRQDQQGSPISAEESVEKESCLLK EFEVNIVVLLHPDHLITENFPLKLCR I |
| 1817 | 7314 | A | 1953 | 262 | 1274 | ATAGREGKGRGPQPSGEAPLVSLGS RAATSGGCCGELEMTGLDIKSKR ANKVYHAGEVL SGVVVISKDSVQ HOGVSLTMEGTVNLQLSAKSVGVF EAFYNSVKPIQIINSTIEMVKPGKFPS GKTEIPFEFPLHLKGKLVLYETYHG VFVNIQYTLRC\DMKRSLLAKDLT KTCEFIVHSAPQKGKFTSPVDFTIT PETLQNVKERALLPKFLLRRTS\QLN KLCHHAATNGRAGGGELGSR\HQK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RGAAAGARGDVRVCR\SYARDAPE IQNI\QIADGDVCRGLSVPIYMFPR LFTCPTLETTNFKVEFEVNIVLLHP DHLITENFPLKLCRI |
| 1818 | 7315 | A | 1954 | 2 | 236 | DRCLMLKQGSEAWLTSISIEPPAPPV YQAPCQSCPEPPGAHEPSDSPHHTP VHPPPE\TRTPVLPQRAVPPPRSSM S |
| 1819 | 7316 | A | 1955 | 760 | 925 | HLEYLPTYANSSYS\WPSSVAHTCN PSTLGGRGGRITGGQEFKTSVANIT KPCLY |
| 1820 | 7317 | A | 1956 | 32 | 487 | SRRHGSSLWGKVNVEDAGGETLGR LLVVYPWTQRFDFSFGNLSSASAIM GNPKVKAHGKKVLTSLGDAIKHLD DLKGTFAQLSELHCDKLHVDPENF KLLGNVLVTVL\AIHF\GKFTPEVQA SW/QEDGDWSGQCPVLQIPLSSLPM MQSFQG |
| 1821 | 7318 | A | 1957 | 41 | 638 | APSPRRPWGHFTEEDQGLLSTSLWG KVNVEKCKWKEKTPGKGSLVVYP\ WT\QRFDF\SFGNLSSAF\AHGQTP KVKAHGK\KVL\TFLGRCQQSTLDD LKGTFAQL\SELHCDKLHVDPENFK LLGNVLVTVL\AIHF\GKDFTPGGC RASW\QKMGD*SGQCPVLQIPLSS L\PMMQSFSRIRLLFLQAITNNKSISA KRSP |
| 1822 | 7319 | A | 1958 | 3 | 227 | |
| 1823 | 7320 | C | 1959 | 171 | 366 | MHTPSVEKPSCGSQLFVYIRKFWKK RNLVKVLNMTTSSVTEDVPLYPEW CMLWRYPASRPNVRKP* |
| 1824 | 7321 | C | 1960 | 332 | 421 | MEEKIFSQPGMVAPT\CN\STLGGQG RWIT* |
| 1825 | 7322 | A | 1961 | 322 | 1145 | RFSKSPDSDGAQLVSPSGSRTRQQV ELAATPTQCSTLLSPWASDGTGCHG AAGRSSGRLRPTGALRWVPLHFPS PARGDSQARSLPTRA\AASADSSLPG CGRREVCGSRAPAGG/PPLAPAPPA APVPASAAAQPPAPAWAYEQVWA GRGALRSPSASSGEA\ADDSYGVA GRWGRPVQDSRLGTAGEGIAGRES WGSVTSWVLGSHMVKFGLV\AELGI CETQDWRRGSEGGAGEFGAVAIHC IGTWVADNAVTCPLLNTTQLEIPFG VQFWML |
| 1826 | 7323 | A | 1962 | 30 | 2814 | LPRAKVEGAPRAPSPQDPGVPPRAP SPRSPSPALRALPAPLSPRSP\DEPM ARPRAREPLL\ALLPLAWLAQAG LARAAGSVRLAGGLTLGGLFPVHA RGAAGRACGPLKKEQG\VRLEAM LYALDRVNADPELLPGVRLGARLL DTCSRDTYALEQALS\SFVQALIRGRG DGDEVGVRCPPGVPPLRPAPP\ERV VAVVGASASSVSIMVANVLR\LFaip QISYASTAPE\SDS\TRYDFFSRVVP DSYQAQA\MVDIVRALGWN\YVSTL ASEGNYGESGVEAFVQISREAGGVC |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | IAQSIKIPREPKPGEFSKIVIRRLMETP NARGIIIFANEDDIRRVLEAARQANL TGHFLWVGSDSWGAKTSPILSLEDV AVGAITILPKRASIDGFDQYFMTRSL ENNRRNIWFAEFWEENFNCKLTSSG TQSDDSTRKCTGEERIGRDSTYEQE GKVQFVIDAVYAIAHALHSMHQAL CPGHTGLCPAMEPTDGRMLLQYIR AVRFNGSAGTPVMFNENGDAPEGRY DIFQYQATNGSASSGGYQAVGWQA ETLRLDVEALQWSGDPHEVPSSLCS LPCGPGERKKMVKGVPCCWHEA CDGYRFQVDEFTCEACPGDMRPTP NHTGCRPTPVVRLSWSSPWAAPPL LAVLGIVATTTVVATFVRYNNTPIV RASGRELSYVLLTGIFLIYAITFLMV AEPGAAVCAARLFLGLGTTLSYSA LLTKTNRIYRIFEQGKRSTVPPFISP TSQLVITFSLTSLQVVGMIAWLGAR PPHSVIDYEEQRTVDPEQARGVLKC DMSDLSLIGCLGYSLLLMTCTVY AIKARGVPETFNEAKPIGFTMYTTCI IWLAFVPIFFGTAQSAEKIYIQTTLT VSLSLASVSLGMLYVPKTYVILFH PEQNVQKRKRSLKATSTVAAPPKG EDAEAHK |
| 1827 | 7324 | C | 1963 | 334 | 387 | MKCYIYIMTLVLLIV* |
| 1828 | 7325 | A | 1964 | 1 | 489 | |
| 1829 | 7326 | A | 1965 | 152 | 717 | VESIEDVGNHRTDHGADMISIHVEE ENAFILDTLAKKQWKGPDDILLGMV YDTDDASFkWVDNSNMTFDKWT VQDDEDLVDTCAFLHIKTGEWKK GNCEVSSVEGTLCCTAIPYKRKYL DNHILISALVIASVTILTVLGAIIWFL YKKHSDSRFTTVFLTGPQLPYMEN CVLVVGEENEYPVQFD |
| 1830 | 7327 | A | 1966 | 3 | 614 | LLFFPSAKMALETGPKDLRHLRACL LCSLV/KGTIDQFEYDGCDCYAYL QMKGNR\EM\YDCTSSSFDGIIAM MSPED\SWVSK\WQAKSSNFKP\GV YA\SVVTGRLAPKIR/VRELKSR\G VALQIPGDTANKDLAKMQGCQHLC SPPPCLCIISCSWNLNEQNFQILPTLQ FRLSSTVERAAHHFIILSSLDYRWG GRDLGWVD |
| 1831 | 7328 | A | 1967 | 66 | 407 | |
| 1832 | 7329 | A | 1968 | 2 | 1272 | CPWPESTGQSGVTSSKARPSLAERW AGPAKKKRKGVEHGPAIREAGLM KRLSS/LGDLLTSPEIEVLFTDIKVR THCPKSLPGTETVQIELSSFFLNILG GKKKKQSWEQEGCHLKDFGDLST PVPKDDLNNLIVNPRSVGLANQEL AEVVSRAVSDGYSCVTLGGDHSLAI GTISGHARHCPDLCVVWVDAHADI NTPLTTSSGNLHGQPVSFLLRELQD KVPQLPGFSWIKPCISSASIVYIGLR DVPPEHFILKNYDIQYFSMRDIDR LGIQKVMERTFDLLIGKRQRPIHLSF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DIDAFDPTLAPATGTPVVGGLTYRE GMYIAEEIHNTGQRNTTENFDTSSQ TLTEGLLSALDLVEVNPQLATSEEE AKTTANLAVDVIASSFGQTREGGHI VYDQLPTPSSPDESENQARVRI |
| 1833 | 7330 | A | 1969 | 212 | 460 | |
| 1834 | 7331 | A | 1970 | 1 | 1223 | TVVECLSPA WHEESSGGRWRS LPA SNRAEPLPWRFSVL RIMSLRGSLSR LL\QTRVRSILKKS VHSVHVIGAPFS QGQKRKGVEHGPA AIREAGLMKRL SSLGCHLKDF/GQDLSFTPVPKDDL YNNLIVNPRSVG\LANQELAEVVSR AV/SQDGYSCVTLGGDHSLAIGTISG HARHCPDLCVWVDAHADINTPLT TSSGNLHGQPVSFLLRELQ\DKVPQ LPGFSWD/IKPCISSARIVYIGLRDVY PPEHFILKGTMDIQYF SMEEILDR L GIQEGHGNGTFDL\LIGKRQRPIHLS YDIDAFDP THAPAHRT\PVVGDITYR EAMYIAEKIHNTG LLSALDLVEVN PQLATSEEEAKTTANLAVDVIGLPS LWVQTREGGAYWSYDPTFPTPSSP\ DESENQARVRI |
| 1835 | 7332 | C | 1971 | 162 | 425 | MVGPSLHAGXXXVYIPRFLYIRSWL PCIFFSGGVTVG NIGRQLAMGVPEK PIVIESSKPXILE SXGRFLEENLXLVD YXKGLSFFLK* |
| 1836 | 7333 | A | 1972 | 89 | 308 | |
| 1837 | 7334 | A | 1973 | 2 | 454 | |
| 1838 | 7335 | A | 1974 | 570 | 1418 | PMPRLHDHFWSCSCAHSARRRGPP RAIAAGLA AKVGEMII VFVSGPSLM AVLSASDADPAPRGRSA VKSGPYP GSPYPNTWHHSLMQKSLV LFSVGE VLALVLNLLQIQRNVT LFP EEVIATI FSSA WWPV\CCGTAPADVGLLYPC IDSHLGEPHKFKERMGQVSMRCIAV FVGINHASAKLDFANNVQLSLTLAA LSLGLWWTFDRSRSG LGLGITIAFL ATL\ITQFLVYNGVYQYTSPDFLYIR SWLPC\IFFSGSVTVGNIGRQLGYG VFLEKPHSD |
| 1839 | 7336 | A | 1975 | 1 | 287 | KFQERGIIQIKYPP/RAFTLSHTHTRH AHIQAPTVTNQTP/DFP/RPRR*ESSS SSEGANSFLKIMT*RQSSSPKEKDV RPATSTTSCSM LLSILFIG |
| 1840 | 7337 | A | 1976 | 1 | 166 | |
| 1841 | 7338 | A | 1977 | 37 | 448 | GGCTCPCSRWQGSPPQAPAGLPPL ASGPAPSASASPQSGGPIPLH/VR*E SSSSSEGANSVCSSRSCSLAETFS*S AHCLE*NLTPSPSFYETPLSVVSLA LVVSSGGRPV LGPCAESPGRGWV ASPWSSGWSP |
| 1842 | 7339 | A | 1978 | 45 | 249 | |
| 1843 | 7340 | A | 1979 | 77 | 3801 | KGGVFAHDLVPLPFQGTDSPPRAP PGRGVPLPPGALTMNTRD\TPRVAE TSHHLKIFLPKLLLECLPRCPLLPE RLRWNTNEEIASYLITFEKHDEWLS |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | CAPKTRPQNGSILYNRKKVKYRKD GYLWKKRKDGKTTREDHMKLVQ GMECLYGCYVHSSIVPTFHRRCYW LLQNPDIVLVHYLNVPALEDCGKG CSPIFCSISSDRREW LKWSREELLGQ LKPMFHGIKWSCGNGTEEFV EHL VQQILDTHPTKPAPRTHACLCGGGL GSGSLTHKCSSTKHRIISPKVEPRAL TLTSIPHPHPPEPPPLIAPLPPELPKA HTSPSSSSSSSSSGFAEPLEIRPSPTS RGGSSRGGTAILLLTGLEQRAGGLT PTRHLAPQADPRPSMSLAVVVGTEP SAPPAPPSPAFDPDRFLNSPQRGQTY GGGQGVSPDFPEAAEAHTPCSALEP AAALEPQAAARGPPQSVAGGRRG NCFFIQDDDSGEELKGHGAAPPISP PPSPPPSPAPLEPSSRVGRGEALFGG PVGASELEPFSLSSFPLMGELISDE APSIPATPQLSPALSTITDFSP EWSY PEGGVKVLITGPWTEAAEHYSCVF DHIAVPASLVQPGVLR CYCPAHEV GLVSLQVAGREGPLSASVLF EYRAR RFLSLPSTQLDWLSLDDNQFRMSIL ERLEQMEKRMAEIAAAGQVPCQGP DAPPVQDEGQGPGEARVVVLVES MIPRSTWKGPERLAHGSPFRGMSLL HLAAAQGYARLIETLSQWRSVETG SLDLEQEVDP LNVDHFCTPLMWA CALGHLEAAVLLFRWNRQALSIPDS LGRPLPSVAHSRGHVRLARCLEELQ RQEPSVEPPFALSPPSSSPDTGLSSVS SPSELSDGTF SVTSA YSSAPDGSPPP APLPASEMTMEDMAPGQLSSGVPE APLLLMDYEATNPKGPLSSLPALPP ASDDGAAPEDADSPQAVDVIPVDM ISLAKQIIEATPERIKREDFVGLPEAG ASMRERTGAVGLSETMSWLASYLE NVDHFPSTTPSEL PFERGRLAVPSA PSWAEFLSASTSGKMESDFALLTLS DHEQRELYEAARVIQTAFRKYKGR RLKEQQEVAAAVIQRCYRKYKQLT WIALKFALYKKMTQAAILIQSKFRS YYEQKRFQQSRRAAVLIQQHYRSY RRRPGPPHRTSATLPARNKGSFLTK KQDQAARKIMRFLRCRHRMRELK QNQELEGLPQPLAT |
| 1844 | 7341 | A | 1980 | 1 | 4333 | MQVQDDGVNLIPFAKCSRVSRSPP PRLPSQSLRPM PQRYGDVFWKNLN QRPTPTWLEEQHIPPM L RATGCSQL GLYPPEQLPPPEMLWRRKKRRPCLE GMQQQGLGGVPARVRAV TYHLED LRRRQSIINDTDSPPRPLRPGVTLPP GALTMNTKDTTEVAENTRPLKIFLP KKLLECLPRCPLPPERLRWNTNEEI ASYLITFEKHDEWLSCAPKTRPQNG SILYNRKKVKYRKDGYLWKKRKD GKTTREDHMKLVQGM ECLYGCY VHSSIVPTFHRRCYWLLQNPDIVLV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HYLNVPALDCGKGCSPIFCSISSDR REWLKWSREELLGQLKPMFHGIKW SCGNGTEEFVSVEHLVQQILDTHPTK PAPRTHACLCSGGLGSGSLTHKCSS TKHRIISPKVEPRALTLTSIPHAHPPE PPPLIAPLPPELKAHTSPSSSSSSSSSS GFAEPLEIRPSPPTSRGGSSRGGTAIL LLTGLEQRAGGLTPTRHLAPQADPR PSMSLAVVVGTEPSAPPAPPSPAFDP DRFLNSPQRGQTYGGGQGVSPDFPE AEAAHTPCSALEPAAALEPQAAAR GPPQSVAGGRRGNCFFIQDDDSGE ELKGHGAAPPISPPPSPPSPAPLEP SSRVGRGEALFGGPVGASELEPFSL SSFPDLMGELISDEAPSIPAPTPQLSP ALSTITDFSPESWYPEGGVKVLITGP WTEAAEHYSCVFDHIAVPASLVQP GVLRCYCPALPLPYTQKSALLGDLK DHQSDRLAALLSTSVFSPSLYSSIQH VSHEVGLVSLQVAGREGPLSASVLF EYRARRFLSLPSTQLDWLSLDDNQF RMSILERLEQMEKRMAEIAAAGQV PCQGPDAPPVQDEGQGPGEARVV VLVESMIPRSTWKGPERLAHGSPFR GMSLLHLAAAQGYARLIETLSQWR SVETGSLDLEQEVDPNVDHFSCTP LMWACALGHLEAAVLLFRWNRQ ALSNPDSLGRPLPSVAHSRGHVRLA RCLEELQRQEPSVEPPFALSPPSSSP DTGLSSVSSPSEL\TDGTFSVTAAYS SAPDGSPPPAPLPASEMTMEDMAPG QLSSGGPEAPLLMDYEATNSKGPL SSLPALPPASDDGGGPEDADSPQAV DVIPADMISLAKQHEATPERIKREDF VGLPEAGASMRERTGAVGLSETMS WLASYLAENVDFPSSTPPSEL\PFER \GRLGLSLTAPSWAEFLSCIPPVGKI GKLIFALLTLASD\QEQRLEYEAARVI QTAFRKYKGRRLKEQQEVAAAVIQ RCYRKYKQFALYKKMTQAAILIQS KFRSYEQKRFQQSRRRAAVLIQQH YRSYRRRPGPPHRTSATLPARNKGS FLTKQDQAARKIMRFLRRCRHRH SALPFKTHRPLSVTPKMADLLGSILS SMEKPPSLGDQETRRKAREQAARL KETTRARETTESGVS |
| 1845 | 7342 | A | 1982 | 1 | 145 | |
| 1846 | 7343 | A | 1983 | 1 | 419 | |
| 1847 | 7344 | A | 1984 | 3 | 532 | PRASRSRPTGLREAAGSGPREAPRR SGCKSPGLGTVAMLRPKALTQVLS QANTGGVQSTLLLNNEGSLLA\YS GLRGTTDAPGSPAAIAISNIWA\AYG PETGTQAFNEDNLQ\IILHGTCMGG AVLGHSPELANLSCLLYCIAKEDRG AFGNCFKAKGPGLLGGSYLEEPLTQ VAAS |
| 1848 | 7345 | A | 1985 | 2 | 555 | |
| 1849 | 7346 | A | 1986 | 90 | 323 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1850 | 7347 | A | 1987 | 1 | 4695 | |
| 1851 | 7348 | A | 1988 | 81 | 523 | SCLCRDRACLTSLPVSFQVQGVGSK GWRDVTTFSGKAEGPLDSPSEGH YQNSGLDHFQNSNIDQSFWETFGSA EPTKTRKSPSSDS\WTCADTSTER\R SSDSWEVWGLASTNR\NSNSDGV GGEGTKKAVPPAVPTDDGWDNQ W |
| 1852 | 7349 | A | 1989 | 1187 | 1720 | QNQSRDKMRDLREGQMEPPKSELI GWGGGETSRWVRGGASPPPVALSP LFLITWSGHKDLK\DLKVRGLRGLE APRVNVWETEANQAGLQPLGPAT IGLRPRERPGPGRVGREGGPAWPLG EFGIPGVGLRARHQHELRRWRPGR ASPRPERKAAWKGGQPGQPAGPADG RAARSRG |
| 1853 | 7350 | A | 1990 | 738 | 1086 | GTASENLGCKILKHRQQLRKVYP VVLHILSYRGSHSRKKNWGRLLNI LKTFFFLGGGGDGSCWQRPGWELQ WALFSGSLQSPPGFKQFSCSLLS SWEYRCTPPCLANFCIFQ |
| 1854 | 7351 | A | 1991 | 1 | 340 | LGEGRATAVEALPGPSLDHWYRSA GEEKDGP/VYCAAQHLRGRSLPKA WPPPPSSLPVLTDQKSR/YPGHEAH DQGG\WDARQSIIRKVVDPETGRTR WGAFLTYTTGSGSVG |
| 1855 | 7352 | A | 1992 | 1 | 142 | |
| 1856 | 7353 | A | 1993 | 58 | 328 | LKKKGKEKAEAAQVVEALPGPSLDQ WHRSAEEEEGPVLTDEQKSR/YPG HEAHDQGG\WDARQSIIRKCGGPLR RGAPGLLKGDGEGPKRKS |
| 1857 | 7354 | A | 1994 | 120 | 416 | LFFGESSRLTVLEDLKNVFPQVAV FEPSKAEIFHTQKAPLVFLATGFYPD HVELSWVNGKEVHSGVSTDPPQ LMEQAALNDSRYCLSSRLRVSATF |
| 1858 | 7355 | A | 1995 | 1 | 977 | VKLPSCPDPAMGTSLLCWMALCLL GADHADTGVSQNPРНITKRGQNV TFRCDPISEHNRLYWYRQTLGQGPE FLTYFQNEAQLEKSRLSDRFS PKGSFSTLEIQRTQGGDSAMYL CAS SIGAGLPSSNQPHFGDGTRL SILED LNKVFPPEVAVFEPSEAEISHTQ KAT LVCLATGIFPDHVELSWVNGKEV HSGVSTDPPQLKEQPALNDSRYCLS SRLRVSATFWQNPРНHFRQVQFY GLSENDEWTQDRAKPVQTIVSAEA WGRADCFTSVSYQQGVLS\ATIL YEILLGKATLYAVLVSAVLMMAMV KRKDF |
| 1859 | 7356 | A | 1996 | 2 | 883 | FVSQLSPEKVVCGHHLKMLSLLLLL LGLGSVFSAVISQKPSRDICRGTSV KIECRSLDFQATTMFYRQFPKKS SL MLMATSNEGSKATYEQGVKDKFL INHASLTLSTLTVTSAHPEDSSFYICS ARESTD PKNEQYFGP\GTRLTVLE DLKNVFPPEVAVFEPSEAEISHTQK ATLVCLATG\FFPDHVELSWVNG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KEAHSGVSTDPOPLKEQPALNDSRY CLSSRLRVSATFWQNP RNHFRCQV QFYGLSENDEWTQDRAKPVQTIVS AEA WGRAGEWGLGRCLLEIR |
| 1860 | 7357 | A | 1997 | 195 | 1133 | PQHGGHFPRKIKSCSWQARPLEDEA TLGQCGVEALTTLEVTRPACLEVKS MVPWPVLEKVRGQTPKVAKHGEK KKKKTGRAKRRMQYNRRFVNVVP TFGKKKGTTFTKIFVGGLPYHTTDA SLRKYFEGFGDIEEAVVITDRQTGK SRGYGFVTMADRAAAERACKDPNP IIDGRKANVNLA YLGAKPWCLQTG FAIGVQQLHPTLIQRTYGLTPNYMY PPAIVQATVVIPAAPVPSLSSPYIEYT PASPAYAQYPPATYDQYPY\AASPA TVRSFVGYSYPAAVPQALSAAAPA GTTFLQYQAPHVQPD RMH |
| 1861 | 7358 | B | 1998 | 60 | 378 | NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCSKIH FISPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX* |
| 1862 | 7359 | A | 1999 | 1 | 437 | DPRATEGMVVADKTCQKSTGR LPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNLDFLRP YTVPNKKGTRLGRYRCEKGT TAVL TEKITPLEIEVLEETVQTMDTS |
| 1863 | 7360 | A | 2000 | 2290 | 2481 | |
| 1864 | 7361 | A | 2001 | 3 | 860 | FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKL\PRPRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCSKIH FISPNIYCCGAG\TAA DTAMTTQLISS\NLKLHSL\STGR L P RV\VTANRMLKQMLFRYQGYIGAA LV LGGVDVTGPHLYSIYPHGSTD K VP\YVTHGFLAPLAAMAVFEDKFR P\D\MEEEEA\KNLVSEDSPPQFP PPS WRIFND\LGSGSNIDLCVISK\NKLDF LRP\YTVPNKKGTRLGWRYRCEKG VTAVLTEKIPLLWST |
| 1865 | 7362 | A | 2002 | 1 | 340 | RQGTIVAISSIQGKMSIPFRSAYAAS KHATQAFDCLRAEMEYQIEIVTVI SPGRSC/VEVAQDVLAAGKKKKD VILADLLPSLAVYLRTLAPGLFFSL MASRAR*ERKSKNS |
| 1866 | 7363 | A | 2003 | 56 | 385 | RPWTSSPPQSPCCSAAWASSASS GCCSGCAGRPTCGMLWW*SQAPA QGRSPVEVAQDVLAAGVKKKKDVI LADLLPSLAVYLRTLAPGLFFSLMA SRARKERKSKNS |
| 1867 | 7364 | A | 2004 | 2 | 409 | |
| 1868 | 7365 | A | 2005 | 1 | 1092 | |
| 1869 | 7366 | A | 2006 | 50 | 1101 | LTMVSPATMKSLPKVKAMDFIT\ST AIL\PLLFGCLGV\FGL\FRLQWVR GKAYLRNAV VVITGATSGLGKECA KV FYAAGAKLVLCGRNGGALEELI\ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RELTAS\HATKVQTHKPLLGGPSDL TDSGAIVAAAAEESFSCF\GYGRHY FVNNAGISYRGTVTMDTVTDVVKR VMETNYFGPVALTALLPSMIKRR QGHIVAIISSIQGKMSIPFRSGICQPS KHATQ\AFFDCLAVPEMEQYIEIV TVISPG\YIHTNLS\VNITADGSRYG V\MDTTVTSPGPESPVEGGPRMFLAC LWGKKK\KDV\TLADLPALPLAVY\ LRTLAP\GLLPSSLPLPRAQKRAGN PKNSLVL |
| 1870 | 7367 | A | 2007 | 75 | 461 | |
| 1871 | 7368 | A | 2008 | 3 | 426 | DAWVCLSPAFILLELCAARV*EGLP NRVHRTEEVNHVDFYAFSYYYDLA GGAGPIDAEKGGSLVVGDFEIA TKY VCRTLETQSQSSPFSCMDLTYVSL LQEVGFPRSKVLKLRKIDNVYTT WAPGAIFHYIDSLNRQKS |
| 1872 | 7369 | A | 2009 | 3 | 421 | QALGNRGVVSRRGWRPGRWRPGRG SPKDRLPAPRKRALVSVGVAERA VHETPTLTHETFKALKPGLSAYADD VEKSAQGIRELLDVAKQDIPDF*K ATPLILK/ATAGLRLLPKKAQR*LA K\GKEVFKAWLFFEGNDW |
| 1873 | 7370 | A | 2010 | 337 | 769 | PLALCLAPAASLHELCAAKVSEVLH NRVHRTEEVKHVDFHAFSYYYDLA AGVGLIDAEKGGSLVVGDFEIAAK YVGVTVSVKGRVSSPVCRTLETQP QSSPFSCMDLTYVSLLLQEFGFPRS KVLKLRKIDNVETSWALGAIF |
| 1874 | 7371 | A | 2011 | 2 | 486 | |
| 1875 | 7372 | A | 2012 | 176 | 1643 | MKKGIRYETSRKTNIFQQPQHGP WQTRMRKISNHGSLRVAKVAYPLG LCVGVFIYVAYIKWHRANATQAFF SITRAAPGARWGQQAHSPLGTAAD GHEVFYGIMFDAGSTGTRVHVQF TRPPRETPTL/TAHETFKALKPGLSA YADDVEKSAQGIRELLDVAKQDIPF DFWKATPLVLKATAGLRLLPGEKA QKLLQKVKEVFKASPFLVGDDCVSI MNGTNE\GVSAWITINFLTGSLKTPR RSNVGMLDLGGGSTQIVFLTHVEG TLQASPPRYLTALRMFNRTYKLYC YSYLGLGLMSARLAILGGVEGQPA KDGKELVSPCLSPSFKGEWEHAEVT YRVSGQKAAASLHELCAARVSEVL QNRVHRTEEVKHVDFYAFSYYYD LAAGVGLIDA\KGGSLVVGDFEIA AAKYV/CVRTLGETQP\QSSPFSCMD LTYVSLLLQEFGFPRSKVLKLRKID NVETSWALGAIFHYIDSLNRQKSPA S |
| 1876 | 7373 | A | 2013 | 21 | 119 | PGWPQTPDFKRS/PPLWPPKVLGLQ V*ATAPGPK |
| 1877 | 7374 | A | 2014 | 1420 | 1627 | IGLNPSSVPSTFFSYSPQFTEGVPP/P GMERP/PFPWEQRPTGWSFFSPCPQ TP\SPPTSEHGTPPNWPKC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1878 | 7375 | A | 2015 | 447 | 775 | QIPKEHLHHP/PQTSHSNRPLR/P/GN RPNPESPTGSPPECCSCLAPRGS WGDPNPLQRTPGAGKVAGGPFPPP TQQSPGKALCINLKGFAAIKLLD NVLQPSSALGFL |
| 1879 | 7376 | C | 2016 | 49 | 519 | MYGKGKSNSSAVPSDXQAREKLAL YVYEYLLHVGAQKSAQTFLSEIRW EKNITLGEPPGFLHSWWCVFWDLY CAAPERRETCEHSSEAKAFHDYPFM SPRYPGGPRPLRIPNQALGGVPGS QPLLPSGMDPTRQQGHPNMGGPMQ RMTPPRGMVP* |
| 1880 | 7377 | A | 2017 | 1 | 1155 | |
| 1881 | 7378 | A | 2018 | 56 | 1416 | WVDRCVTVGAALGTSMYGKGKS NSSAVPSDSQAREKLALYVYEYLL HVGAQKSAQTFLSEIRWEK\NITLG EPPG\FLHSWWCVFWDLYCAAPER RETCEH\SSEAKAFHDYSA\AA\PS VLG\NIPPGRWACQLGPVTTTRGSFQ PFMFTFGYPG\GPRSPLRV\PNQALG G\VPGGQPLLPSGMDSTRQQ\GHPN MGGAMQR\MTPPRGMVPLGPQFLT PWLSLQNYGGA\MRP\NALGGPG MPGMEQGSRCGRPW\PNPTNA\NSL PFSSAFSWNLLGPPGGGGPPG\TP\I MPSSSRFQPTSGDNMYTLMNAVPP GP\NRPNF\PMGP\GSDGPMGGGLGG MESHMMNGSLGS\GDMAISIKNSPN N\MSLSIQ\GIPK\DDGAMGANFLN PFQSESYSPSKPYKCVFPFGLFMKP TVSQPFPELRTENYSSTSVPVKQR NLSHTKPTFLFPALSPLL |
| 1882 | 7379 | B | 2019 | 162 | 349 | LEELEEEELDLVLLRAFCLLLSW DVEAEQFLEVSFLLFFLFS DPRPRD RLRLLERLREPT* |
| 1883 | 7380 | A | 2020 | 2 | 353 | SSSDGRKKRGKYKDKRRKKKKKKR KKLKKKGKEKAEAAQQVEALPGPSL DQWHR SAGEEEDGPVLTDEQKSR/ YPGHEAHDQGG\WDARQSIIRKV DPETGRTRWGAFGLTYTTGSGSVG |
| 1884 | 7381 | A | 2021 | 1 | 142 | |
| 1885 | 7382 | A | 2022 | 404 | 946 | PVCACPRPEQGTKVYLFPSWLSLT FSLHREKQAEGRGEEEDASSASS SSSSSSSSSSSSSSSSSDGRKKRGK YKDKRRKKKKKKRKKLKKKGKEKA EAQQVEALPGPSLDQWHR SAGEE DGPVLTDEQKSR/YPGHE\THDQGG\ WDARQSIIRKCGGPLRRGAPGLLKG DGE GPKRKS |
| 1886 | 7383 | A | 2023 | 3 | 634 | |
| 1887 | 7384 | A | 2024 | 131 | 546 | VAGTPGRHPHTRLIFPVFCRGGVFL CFPGWSFFFFKPSDLD SFHLEMIHPR CESWKMPGALPM/YCSP/CCLLVLL KDQGGGASTGVRRRKESWLPAPHS STVQVTQEGWREQSREL PKTECQL GWFLFLLQPYSR SRFY |
| 1888 | 7385 | A | 2025 | 363 | 578 | RPYPCLSPR SSSSTNPLSS**LNKIPS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LPSSWEKW*IPPKNNCLSLNPSPPS LAPSLDDIKEGLSWKKKKK |
| 1889 | 7386 | A | 2026 | 166 | 191 | KNVIHQSKNCVFVKLLDQIHNFPLS TLLHVIVDLFLGLFGVPE/CSDP*RLP GTPPYQPAPARQPAPADHRQWPVPQ RGPEASG |
| 1890 | 7387 | C | 2027 | 358 | 405 | MSSREGARDGGEGRLS* |
| 1891 | 7388 | C | 2028 | 306 | 347 | MSPGRGPGMEGRG* |
| 1892 | 7389 | A | 2029 | 2 | 358 | QCGGIRFWRAPVFLVLSWSPQDGIT GEEPDTSHDPRHLHQASSCPAHPPLP PTQSCSSCQGWLCPPQGCPPGGPRT A/CIVPWPSFVASAATQERGQCPL DPLSPNQTRALHLSGTSGK |
| 1893 | 7390 | B | 2030 | 1043 | 1146 | MPSSVSWGILLLAGLCLVPVSLAE DPQGDAQAQKTDTSHTDQDHPTFNK ITPNLAFAFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEASPVISGASKRA KKQINGKMGETLLKSKDPRKEDFT LDQVTTVKGAYDEAFRACTSSHX * |
| 1894 | 7391 | A | 2031 | 2 | 402 | SQTQREPTMVLSPADKTNVKAA/W GMFLSFPTTKTYFPHFDLSHGSQAQV KGHGKKVADALTNAAVHVDMPN ALSALSDLHAHKLRVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR |
| 1895 | 7392 | A | 2032 | 9 | 509 | NSARATDSERTHHGARLLPDKTNV KAAWGVKGAHAGEYGAELERM FLSFPTTKTYFPHFDLSHGFAQVK GATAKKVA\DALTKAAVHVDGHA QTALSALSGPATAHKL\RVGPGSTF KLLASHLPCWLTGRPPSPAEPQPLA VARLPWNKVPGLLVEAPLLEPSK |
| 1896 | 7393 | A | 2035 | 413 | 674 | CRSDRWAKEHRGKRGQDSSKDVM ARLMEAPKQTAQYFFIFYFFETKSY SVTQAGVQWLDLGSQRPPPGP\SD SPASASRAWPQTAH |
| 1897 | 7394 | A | 2036 | 2525 | 2734 | LTNGTESTPPRPPTPSRCSRQCPES VGPPFCSPFCVPAHFKLLPWTFQG TVISSPQIISSSSVCAFF |
| 1898 | 7395 | A | 2037 | 168 | 392 | NKSFFPPSSSFDLSILNTFSFPLTLSSL RSGPTHHTHTHAN/THHTHTHTHT HTPSSPDQAHPHTLTDNWWSTL |
| 1899 | 7396 | A | 2038 | 216 | 528 | AGEKLGAGDTSWRVVWPAACT PGRVERVGWCRV\GPADPSGGLTPG \ACGASWQGPFSWAKDLQPGGSW WPVWPTRPFLDLGSSGLLIWVHK WPWGVCVYV |
| 1900 | 7397 | A | 2039 | 37 | 424 | RWNFLATTPSAVFRVWEAQMLTCE RWPTLSGRRQTYLLLPFAP*PQTGC WSPDGSRLLFVLEPLIYSLSPER CGEGKGALEVQSQQRLWQICLRQ QYRHQMVRRLGERLTPWSGTPVG NVWLCL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1901 | 7398 | A | 2040 | 1 | 442 | PEFRVDDFVLRYPAYESSPGTELRECGL/WPFRPGVCRLQTSCEPWINLPVLQLTKDPLKTPGRLDHGTRTAFIH HREQVWKRCINIWRDVGLFGVLNEIANSEKEVFEWVKTAGSWALALCRWASSLHGSLFPHLSLRNEDLIAEF |
| 1902 | 7399 | A | 2041 | 722 | 1395 | CLCLGLWACQS\CILIWTL\DPSTLFTRPSSG\CAQVLSHPGHTPVTSLAWAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLWSPDGSKI LATTPSAVFRVWEAQMWDLWRRWPTLSGRCQTGCWSPDGSRLFTVLGEPLIYSLSPERCGEKG\ALEVQSQ QRLWQICLRQQ/YTRHQMVRRLGLERLTPWSGTPVGNVWLCFMKGKAAQGLPGW |
| 1903 | 7400 | A | 2042 | 1 | 418 | MPEQEPTAEQLS*IAAENEDEHSV NYKPRAQKSIQEIQLDKDDESLRKYKRALGRVAVSADPNVPNVVAPGRVRLLPQALSATTPGRPSLTQPGT NKGPSAHIAESRLLCLPRPIPLRVVSARLRQRRLSLLLF |
| 1904 | 7401 | A | 2043 | 1 | 525 | LSQQASLESF*KHFFCLKEVVEYRIKISFRVNREIVSGMKYIQHTYRKGVKID\KTDYIVGSYWPRAEYEFLTPKS PRWTASPTPSVLQSGAPLGHQYLLP PSVPSSGHWPVCSPRLLVPPLLGR PSLTLPGTNKGPSAHIAESRLLCLPR PIPLRVVSARLRQRRLSLLLF |
| 1905 | 7402 | A | 2044 | 354 | 487 | |
| 1906 | 7403 | B | 2045 | 61 | 516 | KSIQEIQLDKDDESLRKYKEALLGRVAVSADPNVPNVVVTGLTLVCSS APGPLELDLTGDLESFKKQSFVLKE GVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMGVSYGPRAEYEF LPRPIPLRVVSARLRQRRLSLLLF* |
| 1907 | 7404 | A | 2046 | 11 | 328 | |
| 1908 | 7405 | A | 2047 | 1 | 507 | LTFVCSFRPVPLYDLRSNLDCKNQ SFLFKEAVDYRIKISFRFHPKYISLI*\YIQHTYSK/GVKIDKTDYMLGSY/GP RAEYEFLLTPVEEAPKGMLARGSYS IKSRFTDDDKTDHLSWEWNLTISIY CLRPCRPWATGLAPVPPGSQCHPR QAFDPARNKQGTKCTHC |
| 1909 | 7406 | A | 2048 | 1 | 327 | TAEQLAQIAAENEDEHSVNYK/PP AQKSIQEIQLDKDDESLRKYKEALLAPLAVSADPNVPNVVVTGLTLVCSS/APGPLELDLTGDLESFKKQSFVL KEGVECTVGP |
| 1910 | 7407 | A | 2049 | 1 | 452 | |
| 1911 | 7408 | A | 2050 | 3 | 868 | SHFVLDVIPGVGHLTLPQRMPLSRN RGGGEERRCPPWSPFGAPLQPTLLL RSAPPLGIQVQGLSPSRPQVSRPRLS LSMAEQEPTAEQLAQIAAENEDEHSV NYKPPAQKSIQEIQLDKDDESL RKYKEALLGRWPFSADPNVPNVV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VTGLTLVCS\SAPGPLELDLTGDLAE SFKKQFVLCLEGEVEYRIKISFRFNP RDNCPGMKYIQHTYRKGVKIDKTD YMGVSYG\PRAEGSFELTPVEEAP\ KGMLA\RGSYSIKSRFTDDDKTDHL SWEWNLTIKKDWKD |
| 1912 | 7409 | A | 2051 | 1 | 618 | TLLVPQDSERTHPWLLSPADK\ITNV KGPPGGKVGAAHVRSMCAEALER MFLSFPTTKTYFPHFDLSHG\SAQV\ KGHGKKVADALTNVAHVDDMP N\ALSAL\SDLHAHKLRVDPV\NFKL LKPLACLVDPPGAHLPAEFQPLAV ATSSLGQSFLGFLWANLKFEQIPV KLGSLGWAMLSLPLWAFPPAPPPLS CTRTPVVFEIKS |
| 1913 | 7410 | A | 2052 | 3 | 398 | |
| 1914 | 7411 | A | 2053 | 1773 | 3913 | FEQNTKLDQAQQAPEDHYPISLLLP SHMAIGLLMAQEGHCKDSSAMGEE AHHPLTPATPPFPLSPDWGHMQPD FFVPVAVPAVFRGPPQLQCHGRRLF LNSPCAQKSSSGLVVEPGLSRTLLE MVKLTSMRGQFLEAQIPTGISLTLO YQLYQKQTNKNMSYSFVFLKWW ALGQRRAGYPSLEDADSRFRNGS RSFLITVIGITLTVEIVTSGMMKGTR VRWSGAGNEGMMGLEEGRNERSV KEAPPRRAVEAQPKDRTWDVGKG QGTEGEGRGLEVEGQQHQGSEPGTI PFSVSWGVLALLAGLCLVPSSLVED PQEDAAQKTDTSHTDQGDWEDLA CQKISYNVTDLAFDLYK\SWLIYHN QHVLVTPTSVAMAFAMLSLGTAKA DTRTEILEGLNVNLTETPEAKIHECF QQVLQALSRPDTRLQLTTGSSLFVN KSMKLVDTFLEDTKKLYHSEASSIN FRDTEEAKQINNYVEKRTGRKVV DLVKHLKKDTSALVDYISFHGKW KDKFKAERIMVEGFHVDDKTIIRVP MINHLGRFDIHRDRELSSWVLAQH YVGNAFFILPDPKMWQLEEK TYSHLENIQRAFDIRSINLHFPKLSIS GTYKLRVPRNLGITKIFSNEADLS GVSQEAPLKLSKAVHVAVLTIDEK GTEATGAPHLEEKASKYQTVMFN RPFLVIIKEYITNFPLFIGKVVNPTQK |
| 1915 | 7412 | A | 2054 | 3 | 409 | PGPVVVSNNSSAHGSQRTSGPESSM KIYCCPEMVEYQKKGKSLDSEPSVP SAKPPSPEKTAPVASTPSSTPIPALS PTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLY |
| 1916 | 7413 | C | 2055 | 235 | 366 | MRIPETKPLTRNGSEVKELAHSSPQ DNQNDQMSFFIVLLPRNG* |
| 1917 | 7414 | A | 2056 | 3 | 484 | STTPTATQPTSLWQLAVQSPGQSNQ TTNPKLGKASEEEMAEPGLGWWE NR*LSLGHRA\PSFPSPPAVSIASFVT VKRPGVTGENSNEVAKLVNTLNTIP SLGQSPGPVVVSNNSSAHGSQRTSG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PESSMKGTIT*KTLSSQSFKNINKVF VVSELYTQK |
| 1918 | 7415 | A | 2057 | 2 | 4256 | FVHGSMADTDLFMECEEELEPWQ KISDVIEDSVVEDYNSVDKTTTVSV SQQPVSAPVPIAAHASVAGHLSTST TVSSSGAQNSDSTKKTLVTLIANN AGNPLVQQGGQPLILTQNPAPGLGT MVTQPVLRPVQVMQNaNHVTSPPV ASQPIFITTQGFVRNVRPVQNAMN QVGIVLNVQQGQTVRPITLVAPGT QFVKPTVGVPQVFSQMTVPVRPGST MPVRPTTNTFTTVIPATLTIRSTVPQ SQSQQTKSTPSTSTTPTATQPTSLGQ LAVQSPGQSNQTTNPKLAPSFPSPP AVSIASFVTVKRPVGTGENSNEVAK LVNTLNTIPSLGQSPGPVVSNSS AHGSGRTSGPESSMKVTSSIPVFDL QDGGKICPRCNAQFVRVTEALRGH MCYCCPEMVEYQKKGKSLDSEPSV PSAAKPPSPEKTAPVASTPSTPIPAL SPPTKVPEPNENVGDAVQTKLIMLV DDFYGRDGGKVAQLTNFPKVATS FRCPHCTKRLKNNIRFMNHMKHHV ELDQQNGEVDGHTICQHCYRQFSTP FQLQCHLENVHSPYESTTKCKICEW AFESEPLFLQHMKDTHKPGEMPYV CQVCQYRSSLYSEVDVHFRMIHED TRHLLCPYCLKVFKNQNAFQQHYM RHQKRNVYHCNKCRLQFLFAKDKI EHLQHHKTFRKPKQLEGLKPGTK VTIRASRGQPRTPVSSNDTPPSALQ EAAPLTSSMDPLPVFLYPPVQRSIQK RAVRKMSVMGRQTCLECSFEIPDFP NHFTYVHCSLCRYSTCCSRAYAN HMINNHVPRKSPKYLALFKNSVSGI KLACTSCTFVTSVGDAMAKHLVFN PSHRSSILPRGLTWIAHSRHGQTRD RVHDRNVKNMYPPPSFPTNKAATV KSAGATPAEPEELLTPLALPSPAS TATPPPTPTHPQALAPPLATEGAEC LNVDDQDEGSPVTQEPELASGGGG SGGVGKKEQLSVKCLRVLVLFALCC NTEQAAEHFRNPQRRRRLRRFQ ASQGENLEGKYLSEAEKLAEWV LTVQREQQLPVNEETLFQKATKIGRS LEGGFKISYEWAVRFMLRHHLTPH ARRAVAHTLAPKDVAENAGLFIDFV QRQIHNQDLPLSMIVAIDEISLFLDT EVLSSDDRKENALQTVGTGEPWCD VVLAILADGTVLPTLVFYRGQMDQ PANMPDSILLEAKESGYSDDEIME LWSTRVWQHTACQRSKGMVMD CHRTHLSEEVLAMLSASSTLPAVVP AGCSSKIQLDVCIKRTVKNFLHKK WKEQAREMADTACDSVLLQLVL VWLGEVLGVIGDCPKLVQRSFLVA SVLPDPDGNINSPTRNADMQKELIA SLEEQLKLSGEHFESSTPRPRSSPEE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TIEPESLHQLFEGESENE\SFYGFEEA DLDLMEI |
| 1919 | 7416 | A | 2058 | 3 | 824 | |
| 1920 | 7417 | A | 2059 | 1 | 1077 | MLSGVGGFVLGLLFLGAGLFIYFRN QKAEESFVSALSIDLSGGGNMALLS MVCLKFPGG\SCMAALTVTLMVLS SPLALAG\DTR\PPVRLRKTEDEPLG CVLSGLRVGPDSVFPGGRFCNRIVL VPPARFLEQVKHECHFFNGTERVRF LDRYFYHQEEYVRFDSDVGEYRAV TELGRPDAEYWNSQKDLLEQKRAA VDTYCRHNYGVGESFTVQRRVYPE VTVYPAKTQPLQHHNLLVCSVNGF YPGSIEVRWFRNGQEEKTGTVSTGL IQNGDWTFTQTLVMLETVPRSGEVY TCQVEHPSLTSPLTVEWRARSESAQ SKMLSGVGGFVLGLLFLGAGLFIYF RNQKGHSGLQPTGFLS |
| 1921 | 7418 | A | 2060 | 2 | 867 | GRVGLPAALAPGPVLFSSMVCLRLP GGSCMAVLTVTLMVLSSPLALAGD TRPRFLEYSTSECHFFNGTERVRYL DRYFHNQEENVRFDSDVGEFRAVT ELGRPDAEYWNSQKDLLEQKRAA VDNYCRHNYGVVESFTVQRRVHPK VTVYPSRTQPLQHHNLLVCSVSGF YPGSIEVRWFRNGQEEKTGTVSTG LIHNGDWTFTHTLVMLETVPRSGEV YTCQVEAPRA*QAPLTVEWRARS ESAQSKMLSGVGGFVLGLLFLGAG LFIYFRNQKGHSGLQPRGFLS |
| 1922 | 7419 | A | 2061 | 3 | 940 | RNFRVDPRVRREEGFIVLPERDLPA SLAPGPVLVSSMVSLKLPGGSCMTA RTVSLMVLSSPLALAGDTRPRFLW QPKRECHFFNGTERVRFLDRYFYN QEEVRFDSVDVGEYRAVTELGRPDA EY\WNSQKDLLE\QRRAA\VDTYC RHNYGVGESFPVQRR\VEPKVTVY PSKTQPLQHHNLL/VFCVSGFYPGS IEVRWFLNGQEEKAGV\VPQALION GDWTFQTW\VMLETVPRSGEGLHC QSE\HPGVTSLLTVEWRARSESAQS KMLSGVGGFVLG\LLLPLGPGLFIY FRNQKGHSGLQPTGFPELKCR |
| 1923 | 7420 | A | 2062 | 25 | 384 | EFHRLRENPPMVAVSCPTKTNVKG PPGGKVGAAHVRSMCAEALERMFL SFPT\TKTYFPFHD\SHG\SAQVKGP RQRRWPNALTKRRGAPLDDMP\NT ALSALSDLHAHKLRVDPVQLSSS |
| 1924 | 7421 | A | 2065 | 47 | 353 | AGRVRILWDCVEVDLTGAGQSV EASRHAEVVRNRCHWAPQLFSL FAPGWGG\GEGRVGDGGAVGWFP PQPPSSPPGVMPCPHDRRGTEPGRD LVPAQ |
| 1925 | 7422 | A | 2066 | 3 | 692 | KRLPKMAEVQVLVL\DGRAHSSLG\ RLAGHRGLNQVLLGRK\VVVVVRCE G\NISGNFYRNEVKVPWLFPSKRM NTNPSRRPLTTSGAPSRI\FWRTVRG MLPHKTQAEAKA\LDRL\KVFDGI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PPPYGQEKSGMVVPAALKVVRLK PTRKFCLIFFFSGGGAL\AHQVVGWK YQAVTAPLEE\KRKREKPRFHYRK KENSIMRL\RKQAREETWRKKIDKY TEVLKTHGLLV |
| 1926 | 7423 | A | 2067 | 1 | 2091 | |
| 1927 | 7424 | A | 2068 | 384 | 4189 | ERTSPAMITSELPVLQDSTNEATAH SDAGSELEETEVEKGRIRGRPP STNKKPRKSPCEKSKIEAGIRGAGR GRANGHPQQNGEGEPVTLFEVVKL GKSAMQSVVDDWIESYKQDRDIAL LDLINFIIQCSGCRGTVRIEMFRNM QNAEIIRKMTEEFDEDSGDYPLTMP GPQWKKFRSNFCEFIGVLIRQCQYSI IYDEYMMDTVISLLTGLSDSQVRAF RHTSTLAAMKLM TALVNVALNLSI HQDNTQRQYEAERNKMIGKRANER LELLQKRKELQENQDEIENMMNSI FKGIFVHRYRDAIAEIRAICIEIGV WMKMYSDAFLNDSYLKYVGWTLH DRQGEVRLKCLKALQSLYTNRELF KLELFTNRFKDRIVSMTLDKEYDVA VEAIRLVTLILHGSEELSNEDCENV YHLVYSAHRPVAVAAGEFLHKKLF SRHDPQAEELAKRRGRNSPNGNLI RMLVLFFLESELHEHAAYLVDSLW ESSQELLKDWECMTELLLEEPVQGE EAMSDRQESALIELMVCTIRQAEEA HPPVGRGTGKRVLTAKERKTQIDD RNKLTEHFIITLPMLLSKYSADA EK VANLLQIPQYFDLEIYSTGRMEKHL DALLKQIKFVVEKHVESDVLEACS KTYSLCSEETYIQNRVDIARSQID EFVDRFNHSDVLLQEGEEADDDDI YNVLSTLKRLTSFQNAHDLTKWDL FGNCYRLLKTGIEHGAMPEQIVVQA LQCSHYSILWQLVKITDGSPSKEDL LVLRKTVKSFLAVCQQCLSNVNT VKEQAFMLLCDLLMIFSHQLMTGG REGLOPLVFNPDTGLQSELLSFVMD HVFIDQDEENQSMEGDEEDEANKIE ALHKRRNLLAAFSKLIYDIVDMHA AADIFKHMYKYNDYGDIIKETLSK TRQIDKIQCAKTLILSLQQLFNLVQ EQGPNLDRTSAHVSIGIKELARRFAL TFGLDQIKTREAVATLHKDGI EFAF KYQNQKGQEYPPPNLAFLEVLSEFS SKLLRQDKKTVHSYLEKFLTEQMM ERREDVWLPLISYRNSLVTGGEDDR MSVNSGSSSSKTSSVRNKKGRPPLH KKRVEDESLDNTWLNRTDTMIQTP GPLPAPQLTYTVLRENSRPMGDQI QEPESHEGSEPYFLHNPQM QISWLG HPKLEHLNPKDITGMNYMKVITGA RHAALCLMEEDAEPFEDVMMSSR SQLEDMNEEFEDTMVIDLPPASRN RRERAELRP\DFVDSAAIIEDDSGFG MPMF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1928 | 7425 | A | 2069 | 1 | 2661 | |
| 1929 | 7426 | A | 2070 | 1 | 1454 | |
| 1930 | 7427 | A | 2071 | 1 | 2364 | |
| 1931 | 7428 | A | 2072 | 1 | 1368 | |
| 1932 | 7429 | A | 2073 | 114 | 1473 | VKGDRFGALRFNDPCAGIKLPMTFF TELEKTTLKFIWNQKRARIAKSILSQ KNKAGGSTLPDFKLYYKATVTKTA WYWYQNRDIDQWNRTGPSEITPHT YNYLIFDKPEKNKQWGNDSLFNKW CWENWLAICRKLKLDPFLTPYTRIN SRWIKDLNVRPKTIKTLEENLGITIQ DIGMGKDFMSKTPKAMATKDKIDK WDLIKLKSFCTAKETTIRVNRQPTK WEKIFATYSSDKGLISRIYNELKQIY KKKTNNPIKKWAKDMNRHFSKEDI YAAKRHMKKCSSSLAIREMQIKTT MRYHLPVRMAIHKKSGNNRCWRG CGEIGTLLHCWWDWKL VQPLWKS VWRFLRDLELEIPFDPAPILLGIYPN DYKSCCYKDTCTRMFIVALFTIAKT WNQPKCPTMIDWIKKMWHIYTME YYAAIKNDEFM/SFVGTWMKLEIIL SKLLQEQTCK |
| 1933 | 7430 | B | 2074 | 1 | 1890 | MDKFLDITYTLPRLNQEEVESLNRPI TGSEIVAINSLPTKKSPGPDGFTAEF YQRYKEELVPFLLKLFQSIEKEGILP NSFYEASILIPKPGRDTTKIENFRPIS LMNIDAKILNKILANRIQQHIKKLIH HDQVGFTPGMQGWFNICKSINIIQHI NRTKDKNHMISIDA EKA FDKIQQH FMLKTLNKL GIDGTYLKMIRTIYDK PTANIILNGQKLEAFPLKTGTRQGCP LSPLLFNIVMELLARAIRQEKEIKGI QLGKEEVKLSLFADDMIRIKYLGIO LIRDMKDLFKENYKPLLNEIKEDTN KWKNIPCSWVGRINIVKMAILPKVI YRFNAIPIKLPMTFFTELEKTTLNFI WNQKRARTAKSILSQKNKARGIML PDFKLYYKATVTKTAWCWYQNRD IDQWNRTEPSEITPHIYNYLIFDKPD KNKQWGKDSL FNKWCWENWLAIC RKLKLHPFLTPYTTINSRWIKDLNV RPKTIKTLEENLGNTIQDIGMGKDF MSKTPKAMATKAKIDKWDLIKLKS FCTAKETTISVNRQPTKWEKIFATY SSDTGLISRIYNELKQIYKKKTNNPI NKWAKDMNRHFSKEDIYAAQKHM KNAHHHWPSEKCKSKHNEIPSHTS* |
| 1934 | 7431 | A | 2075 | 1 | 2676 | MKAIEIKMFFEINENKDTTYQNLWD AFKAVCRGKFIALNAHNRKQERPFI DTLTSQLEKEKQEQTSHKASRRQE MTKIRAELEKEIQKTLQKINESRSW FFERINKIDRPLARLIKKKREKNQID AIKNDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDITYTLPRL NQEEVESLNRPI TGPEIVAINSLPTK RSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYEASILIPKPG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RDTTKKENFRPISLMNIDAKILNKIL ANRIQQHIKKLIHHDQVGFIPGMQG WFNIRKSINVVQHINRTKHKNHMII SIDA EKAFDKIQPFMLKTLNKL SID GTYLKIIRATYDKPTANIILNGQNLE AFPLKTGTRQGHPLSPLFNIVLEVL ARAIRQEKEIKAQNLLKLISNFRKVS VYKINVQKSQAFLYTNNRQTESQIM RELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLNEIKEDTNKWKNIPCS WIGRINIVKMAILPKVIYRFNAIPIKL PTTFFTELEKTILKFIWNQKRAHIAK TILSQKNKAGGIMLPDFKLYYKATV TKTAWYQYQKRDIQWNRIELSEII PHIYNHLIFDKPDKNKKWGKDSVF NKRCWENWLAICRKLKLDFTLTPY TKINSRWIKDLHVRPKAIKTLEENL GITIQDIGMGKDFTSKTPKAMATKA KIDKWDLIKLSFCTAKETTIRVNR QPTKWEKIFAIYSSDKGLISRIYKEL KQIYKKKTNNPIKKWAKDMNRHFS KEDIYAANRHMKKCSSSLAIREMQI KTTMRYHLTPVRKAIKKSGNNRC WRGCGEIGTLLHCWWDCCLVQPL WKTWVQFLRDLELEIPFYPAIPLGI YPKDY |
| 1935 | 7432 | A | 2076 | 1 | 3045 | MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAIINSLPTKKISPGPDGFTAE FCQRYKEE/LEKEGILPNSFYEASII PKPASDTTKKENFRPISLMNINAKIL NKILAKQIRQHIKKLIHHDQVGFIPG MHGLFNICKSVNIIQHINRTNDKNH MIISIDAEKPFDKIQHFMLKTLNKL AQNLLKLIGNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMNEFPFTIASKR IKYLG IQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCSWEKTTLKFI W/NQKRAHIAKSII SQKNKAGGITLP DFKLYCKATVTKTAWYQYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWGKDSL FNKWCWENWLAIC RKLKLDPFLTPDTKINSRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHMKK CSSSLVIREIQIKTTMRYHLTPVRMA IIKKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVIIIHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLP CSSAC RRPVIGLQLVMINSGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLTA PL GSTPQAAVCRGPRGRELRAAPADS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HLFQRDLWPFNKVIVHGEKGSNQTSQGLLNTGSEMTIVLENPKYHSGPPVRVSPDGGQVIEVLADPSYTGPTALLNVFFAFQCNFYFDHIPENC GFSDPSDPQNLQKGEGCPSLVRASTAPPQEKATEQPLLCKTTESPFGMTVGPCTDETLDHGAPSKHVPGTAHNELALLDLRVKSAGSAAVHHKLKVLHWRSLSNNKGTGRLYEQVA |
| 1936 | 7433 | A | 2077 | 1 | 2142 | |
| 1937 | 7434 | A | 2078 | 1 | 1551 | MRFKEKIHLHNIKEPSEAAASADGGA VASYPDLAKIVDEGRYKAEVMQLRCGWRAPASDCVHSVA VVGVD SVLEVLARAIRQEKEIKGIQLGKEEVKLSLFADDMIVYLENPTVSAQNLLKLISNFSRVSGYKINVQKSQAFLYTNNKQTESQIMSELPFTIASKTIKYLGIQTRDVKDLFKENYKPLLNIKEDTNKWKNIPCSWIGRINIVKMAILPKVIYRFNAIHIKLPMTFFTELEKTTLKFIWNQKGVHIAKSILSKKNKAGGIMLPHF KLYYKATVTKTAWYQYQNR YTDQCNRTEPSEIHPHIYNHLMFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLDPFLTPYTKINSRWIKDLNVRPKPIKTLEENLGITIQDIGMGKDFMSKT PKAIATKAKIDKWDLIKLSFCTAKETTIGVNRQPTTELEKIFAIYSSDKGLI SRIYKELKQIYKKKNPIKKWVKDMNRHFSKEDIYAVNRHMKKCSSSLVIREMQIKTTMRYYLTPV |
| 1938 | 7435 | A | 2079 | 1 | 1458 | GLSGDLLGAHQLPDVLGCVQPLPD LLLPPQNLLALQSLQDDLLWALDPAAPWAMDRGAATQWAVGPVSDPWVMEAVASLPSAMDLD SAAQPTWLLGAASLLVTDQPM DQPSADQLAEFPDLLSKVSQSLRIKYLGIKLTRNVKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKVIYRFNAIPIKLPMTFFTELENTTLKFIWNQKRACIAKSILSQKNKAGSIMLPDFKL YHKATVTKTAWYQYQNRDIDQWNGTEPSEIMSHIYNYLIFDKPEKNKQRGKDSLFSKWCWENWLAICRKLKLD PFLTPYTKINSRWIKDLNVRPKIHTLEENLVNTIQDIGMGKDFMSKTPKAMATKAKIDKWDLIKQSFCTAKET TIRVNRQPTTEWEKIFAIYSSDKGLISRIYKELQQIYRKKTNNPIKKWAKDMNRHFSKEDIYAANRHMKKCSSSLAIREMQIKTTMRYHLTPV |
| 1939 | 7436 | A | 2080 | 1 | 2028 | |
| 1940 | 7437 | A | 2081 | 2 | 1547 | |
| 1941 | 7438 | A | 2082 | 3 | 1945 | |
| 1942 | 7439 | A | 2083 | 1 | 2124 | |
| 1943 | 7440 | A | 2084 | 1 | 2250 | |
| 1944 | 7441 | A | 2085 | 2 | 2483 | GKYYKLSSGTAPTCVSLGWGLARG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DSAAPALGSRTSACAPCSHGWTWKL SLEPSDRLSPCDRSSEEATHAPHRL LALVASLPWSRLPLLAPQSHSEAEA TSQPTGVENHHQKTRYVKAGGPVI CRSLPESRGFLWASEGRKCMIGSW AAMGRLRKSTISSRFGPQTLAGTGR PQAIPVLKKHSDAVLLGVCFLKLLH QHHQELGENADSQTLPTQTHWEFILS EDYNKMTVPVKNYQVLEVLARAMR QEKQIKSIQLGKEEVKLSVFADDMI VYLENPIVSAQNLLKLISNFSKVS KINVQKSQAFLYTNNRQTESQISEL PFTIPSKRIKYLGIQLTRDVKDLFKE NYKPLLNEIKEDTNKWKNI PCSWV GRINIMKMAILPRVIYIFNAISIKLPM TFFTELEKTTLKFIWNQKRARIAKTI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRGVDQWNRIEPISEII PHIHNLIFDKPDKNKKWGKDSLFT KWCWENWLAICRKLKLDPFLTPYT KINSTWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKETTIRVNRQ PTEWEKIFTIYPSDKGLIPRIYKELK QIYKKKSNNPIKKWAKDINRHFSK EDIYAANRHMKKCSSSLVIREMQN KITIR/YHLTPVRMAIIKSGNNRDM DEAGNHHSQTIARTENQAPYLLTH RWELNNENTWTQVEEHHTLGPIVG VICRKVFPNGSGPSKPSGLHFSQPLP QVTSVVAKITIVPWEMKLIAMGVQ DELNIAFHKNHLLMNDTTIHMTPIYI QPAPKS |
| 1945 | 7442 | A | 2086 | 1 | 2622 | |
| 1946 | 7443 | A | 2087 | 853 | 2831 | YPESTMNSNKFTRKKQTTPSKSG*R I*TDTSQKKTFMQPKDT*KNAQHH WSLEKCKSKPQ*DTISHQLEWRS LK SQDRKD*QSTLLAILKKKGQKNQI DT/IKNDKEGITTDPREIQTIREYYK HLYTNKVENLEEMDKFLDTYTLPT LKQKKEVKTLNRPITGSEIEAIINSLP T/KKSPGPDRTAEFYR/DIRSSGQG NQARERNKGYSIRKRGSIQVPVCR* HHCIFRKPHHLSPKSS*ADKQLQQS LRIQNQSAKITSIPHQ*QTNREPNHE *TPIHNCFKENKMPRNPTYKGCEGS LQGELQTTAQ*NKRGHKRMEEHSM LMDRKNQYRENGHTAQGNL*IQCH PHQATNDFFHRIGKNYFKVHMEPK KSPHRQVNPKEQSWRHHTT*LQ TILQGYSNQNSMVLVPKQRHRPME QNRAPGNNTIHLQLSDL*QI*QKQE MGKGFPI**MVLGKLANHM*KAET GSLPHILYKN*FKMD*RLKC*T*NH KNPRRKPRQYHSGHRHGQGLHD*N TKSNGNKSQN*QMGSN*TKELLHST RNYHQSEQATYRMGENFCNLLI*Q RANIQNLQRT*TNLQDKNKQPHQK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VGKGYEQTLLKRRHLCSQKTHEKM LIITGHQRNANQNHNEIPSHTS*NGD H/SNQVRKQQVLERMWRN |
| 1947 | 7444 | A | 2088 | 1 | 4954 | MVFSIDAQKAFDKIQHRFMLKTLN KLGIDGTYLKIIRAIYNKPTGNIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIRQEKEIKGIQLGKEEVK LSLFADDIIVYLENPIVSAQNLLKLI GNFSKVSGYKINVQKSQAFLYTNN RQTESQIMSELPFTIASKRIKYLGIQL TRDVKNLFKENYKPLLNEIKEDTDK WKNIPCSWIGRIHIVKMATLPKVIY RLHAIHIKLPMTFFTELEKTTLKFIW NKKRARIAKSILSQKNKGGGITPPDF KLYYKATVTKTARYWYQNRDIDQ WKTREPSEIIPHIYNHLIFDKPDKNK KWGKDSL FNKWCWENWLAICRKL KLNPF LTPYTKINSRWIKDLNIRPKT IKTLEENLGNTIQDKGVGKDFMSQT PKAMATKAKIDKWDLIKLSFCTA KETTIRVNRQPTWEKIFAIYSSDKG LISRIYKELKQIDKKKANNPINKWA KDMNRHFSKEDIYAANRHMKKSSS SLAIREMQIKTTMRYHLTPVRMVII KKSNNSEGLNPGYKGFPTIHWAPL PVAQSKDSGLASLNSDPDIPSMLEC SLKAPQLYRSKNVGQVFISSASQAF TKKARIYARLRVSQALKTLCKSSCH DGWSFERLARIQEVSLPISPDILCSE AYHYGTPQWLVAATGTAQTFLLEL NQKSQQYQKQEQTHSKASRMQEIT KIRAELEIETRKTLOKIDESRSWFF ERINKTDRPLARLTQKREKNQIDA IKNGKGDITDPTGIQITIREYYKHL YAKKLENLEEMDKFLDTYTLPRLN QEEVDSLNRPITGAEIVAIINSLPTKK SPGPDGFTAIFYQRHKEELVPFLK LFQSIEKEGILPNSFYEASIIIPKGR DTTKKENLRPISLMNIDAKILSKILA NRIQQHIKLIHHDQVCFIPGMQGW FNIRKSINVIQHINRAKDKNHMISID AEKAFDKIQQTFMLKTLNKLIGDGT YFKIIRAIYEKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPIVSAQNLLKLISNFSKVS GYKIYKIDVQKSQAFLYTNNNDKQ ESQIMSELPFTTASRIKYLGIQLTR DVKDLFK\ENHKPLLNEIKEDTNKW KNIFIPCLWVGRINIVKMAILPKGIY RFNAIPIKLPMTFFTELEKTTLKFIW NQKRARITKSILSQKNKAGGITLPDF KLYYKATLTKTAWYWYQHRDINQ WNRTEPSEIIPHIYNHLIFDKPDKNK KWGKHS LFNKWCWESWLDICRKL KLDPYTKFTPYTKINSRWIKGLNVR PKTIKTLEDKPIQVFNTIQDIGMGKD FMSKTPKAMATKAKIDKWDLIKLK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SFCTGKETTIRVNRQPTWEKIFAIY SSDKELISRIYKELKQIYKKK\TNMPI KKWAKDMNRHFSKEDIYAANKHM KK\CSSSLAIREMQIQTMMRYHLTPV RMANIKKSGNNRCWRGCGEVGTLL HCWWD CNLVQPLWKS VWRFLRDL ELEIPFDPAIPLLGIYPKDYKSCCYK DTCTRMFIVALFTIAKTWNQPKCPT MMDWIKKMWHIYTM EYYAAIKND EFMSFVGTWMKLEIILSKLSQEQT KHRIFSLIGGN |
| 1948 | 7445 | A | 2089 | 93 | 225 | |
| 1949 | 7446 | A | 2090 | 133 | 849 | PVWPKWSGWPLLMRSFAPARIATV VIGGVVAMAAVPMVLSAMGFTSV GIAASSIAAKMMSTAAIANGGGVA AGSLVAILQSVAWLYSSSHQEPLRK STPDPKATELTRAGMEASALTSSAV TSVAKVVRVAS/GSCVVLPLARIAT VVIGGVVAMAAVPMVLSAMGFTS VGIAASSIAAKMMSTAAIANGGGV AAGSLVAILQSVAWLYSSSHQEPLR KSTPDPKATELTRAGMEASALTSSA VTSVAKVVRVASGSAVVLPLAALS PNISLLRPLLGALEASSFMLGSLTGT LFCNLEMGNRLRKWRGSQCGSTHR MFFWFPARIATSCDWRSCGPMAGC ANGCSSAMGLQLRAGIALVLP |
| 1950 | 7447 | A | 2091 | 161 | 1344 | TCPVLRHYSTMSSHKGSAVAQGNG APASNREADTVELAEGLPLEEKGK RVIANPPK\AEEEQTCVPVQEEEE VRVL\TLPLQAHAMEKMEEFVYK VWEGRWRVIPYDVLDP\WLKGND\ YLLHGRPPMPSPFRACFKSIFRIHTE TGNI\WTHLA/LGFVLF\FLGILTML RPNMYFMAPLQ/EKKVVF\GMFFLG AVLCLSFSWLFHTAYCHFGGVFSTF PQRELFKGLLLLNMGELWSPGLYY SFYCSP\QPARLIYLSIVCVLG\ISANV AQWDRFATPKH\RQTRAGVFLGLG LSG\VVPTMHFTNRWRALSKATTV GQ\MGWFFLMAV\MYITGKLAFNAA RIPERFFPGK\FDIWFQSHQ\FHVL\ V\AAAFVHFYGS/VSNLQEFPLTGL EGGL |
| 1951 | 7448 | A | 2092 | 2 | 1419 | RLRDPYRSSRLCRRGASRTSSAARS RSRSPA VEGCNRSPGAPQAPARRR RPSRGAPGRAMVKVA\FNSALAQK EAKKDEPKSGEEALIPDAVAVDC KDPDDVVLVGQRRACGWRMCFGL AFMLAGVILGGAYLYKYFALQPDD VYYCGIKYIKDDVILN/ESPSADAP AA\LYQTIE\ENIK\IFEERRSLNFISVP VPEF\ADSDPAKIVQDFNRKLTAYL DFNL\DKCYVIP\LNTSMCYATPKTL LELLIN\IKAGNLFALSPYLD\SMRHM GYLLDR\ENIDHLGF\FIYRLCHDK\ ETYKLATRRKLFKGIQKREGQQLF SAISGIFENKFAVETLICSW |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 1952 | 7449 | A | 2093 | 1 | 669 | |
| 1953 | 7450 | A | 2094 | 267 | 550 | GRTMMFGAKRRQEEWEKVRKPED PEECPEEVYDPRSLYERLQEQKDRK QQELRGTVSNCKNM\VRG\LEDEET TFLDEVSRQQELIEKQPKRRRT |
| 1954 | 7451 | A | 2095 | 1 | 418 | |
| 1955 | 7452 | A | 2096 | 272 | 383 | |
| 1956 | 7453 | A | 2097 | 118 | 379 | RSGGGRGRRGPEVLHLKHPMLKRP DFLYRKPF SRGWEHGPPSRKSHLL/ GAPPPFPKFFCHLC*APSPFRVLSPY QKRIHLVPPTQLH |
| 1957 | 7454 | A | 2098 | 1 | 276 | |
| 1958 | 7455 | A | 2099 | 1 | 341 | |
| 1959 | 7456 | A | 2100 | 1 | 450 | ACPYLALNSSMFCPDLILPTCLISST GFVGEGKFLQGFKSLSPGSLWLSEG LDYFLSVPGDQYDVCAICLDEYED GDKLRVLP CAHA YHSRCVDPWLTQ TRKTCPIK\QPVHRGPGDEDQEE\ ETQGQEEGYEGE\PRDQP\ASERTPF LG |
| 1960 | 7457 | A | 2101 | 238 | 525 | |
| 1961 | 7458 | B | 2102 | 178 | 373 | XLPOPLRGPLAHS DPERPAPFASSLF IGVLGTTKTRKKLKGKEEGDERGS KGTNPALRKDPTFGF* |
| 1962 | 7459 | A | 2103 | 634 | 1940 | SGVDISFFELVFLPRRPHVAGKWDL GGGWDPGIPKGGAGRAQNSASAPC YQDARPPQPLSSRCHAPLQPFPLPV VVA AVLWGSGPDPGASFRATS\DH NCQHGFADLPALFGATLSLEGPGQ LALGEPHPDNACSPIAPPPAPVNGS VFIALLRFD CNFDLKV LNAQKAG YGAAVIHNVNSNELLKMVWNSEEI QQQIWIPSVFIGERSSEYLALFVYE KGARVLLVPDNTFPLGYLIPFTGIV GLLVLAMGAVMIARCIQHR\KRLQ RNRLTK\EQLNQIPTQTNQKRDQ\Y DVCAICLIEYEDGDKLR\VFPGAHA YH\NRCVDPWLTQTRKTCPIK\Q PVHR\GPGDEDQEEETQGQK\EGDE GE\PR\DH PASERTPLL\SSPTLPTS\ FGFLRPKFPLVFS LGP\STD PPLSPPS SPCYPGLITPHTYTFG |
| 1963 | 7460 | A | 2104 | 25 | 527 | EFHRLRENPPMVA VSCPTKTNVKA\ AWGKVGAHAVRSMCAEALERMF LSFPT\TKTYFPHFDL\SHG\SAQVKG ATGKKVADALTNAVAN\DDMPN VAVRPEATLHAHKLRVDPVNFKL LKPLACLVDPGPAHLPRPSFTPGGA TSSLGQSFLGFLKHRCLNLPNYR |
| 1964 | 7461 | A | 2105 | 262 | 364 | |
| 1965 | 7462 | A | 2106 | 3 | 1265 | PRPGLRAPDAPGSAPRERAQPRDPR AGQVRRLDGD KARPRAQLRRESG GAESVTRPLRAASPAPPRAAAA MSEKPKLGRRAPSASLSARCRAPR CCSCRARRPRIPPOQCPRSVFACSSP ESLLVGVALSPGIALGAGSCVECTE SAREQASGVTPKGRALRGLAPVSST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AVLPGRPSRPRYSPTSPHRVPAIASP SVRPPLSFVSPQSCPQCAPTPTHRAP CAPTASIASPGVRPPLPIAPPGVPRP LPITPPMEGVKTENDHINLKVAGQD GSVVQFKIKRHTPLSKLMKAYCER QGLSMRQIRFARFDGQPNQWKLDDL STAGDWKDEDTIDVFPSSKTGRCA GEQPWQGTVSRGPVPKPGPSILALL LNGEHGDHADHKGVCGNSRTFTT MIFLSLMYFKLQLKTISAGMNL |
| 1966 | 7463 | A | 2107 | 4 | 408 | |
| 1967 | 7464 | A | 2108 | 1 | 465 | PACGYVPALSSASKSRSALGFPLPR CPRGRVDPELAALWPLLQCCCQLL QMGCFLGLGPAI*SPHPHQSHSLGI DRS*FQNAQSPPGFCVSCGPLREVS VCLP*PG*ARCCLGCSFGSGHSRLG NTAQ TANQCILPQASSTLCC*LHPQ NLVCP |
| 1968 | 7465 | A | 2109 | 126 | 488 | |
| 1969 | 7466 | A | 2110 | 1 | 5586 | |
| 1970 | 7467 | A | 2111 | 68 | 310 | TDLPTQNMVFTFSSNWG/TVRQVLS /YSCTRETLQHRELDKTRARGPE*GS VVLTSPLWSPCRKCATGTYHGSPI CQSSGGGR |
| 1971 | 7468 | A | 2112 | 2 | 630 | FFFFSDLLNFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*KPVNSSPSSVFVFCVASP AYRRSSSFSRISFSVSGICPWWSR DGEVGTTFPSQFAKGRKGLIRGGP QHPLRLSPGPIEEQK*GLVSPKARLG ISPCQLCPGFWSYLADSVSPPPGGSC SGCTVPGSSHNVPVSHPSGPACGV RTALSSA |
| 1972 | 7469 | A | 2113 | 331 | 754 | NFLKTNNVWSKWTHVLSQFWYQG FILFCLGSIVKCTEIDSSICTE\PSHTK QHMLGGKNQTLNS/DPQGVKCSG* EAM*PRGGISQKDNMGEMNGTT TTKTFCFIFMPGEDQGCSSCVSTRTT RKSQVQKSRGTISRYFHK |
| 1973 | 7470 | B | 2114 | 110 | 225 | XLGRPQLAGSLRSRFPISGMRGEFFT QDCQRNAGREELQGRLSIQSFPILA LGPDDSCETKTGMDKLS* |
| 1974 | 7471 | A | 2115 | 83 | 287 | SLLKCSGVIVLRRPLGYGQVMK* PGAAY*GRTG*SHPFFSTDWSTDGTG VRKSIWCHRNCRWESPS |
| 1975 | 7472 | A | 2116 | 167 | 397 | EPLLALLKSGEVAPARQEATGLGEA KCSCAMGLSGPKTQPQEGCEERRL QSKR*SSGDPGWGDEGHWPTPNRS CLL |
| 1976 | 7473 | A | 2117 | 1 | 540 | FCHLQIYYFISSESLGSQQGCKAK WQ*LKGPEQSWCWEGPAWTGRRG GDLNIQG*NTSNSSPSSVFVICVTSP AIRKLLNLSLGLSLKFLGSPVGGT AGMGKSVPLSPSQVCCGFRSFNHQ AGHAPGCTVPGSSP*CVSRVQHPSG PCMWWVTYPALSLSFNKSCQCPWVFP LPTMPPG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 1977 | 7474 | A | 2118 | 1 | 3121 | RQEAELARMGFDLQNVWIVSHINS NYKLCPSYPQKLLVPVWITDKELN VASFRSWKRIPVVVYRHLRNGAAI ARCSQPEISWWGWRNADDEYLVTS IAKACALDPGTRATGGSLSTGNNDT SEACDAFDSSLTACSGVESTAAPQ KLLILDARSYTAAVANRAKGGGCE CEEYYPNCEVVFVGMANIHAINSF QYLRAVCSQMPDPSNWLSALESTK WLQHLSVMLKAAVLVANTVDREG RPVLVHCSDGWDRTPOIVALAKILL DPYYRTLEGFQVLVESDWLDFGHK FGDRCGHQENVEDQNEQCPVFLQW LDSVHQLLKQFPCLFEFNEAFLVKL VQHTYSCLYGTFLANNPCEREKRNI YKRTC SVWALLRAGNKNFHNFLYT PSSDMVLHPVCHVRALHLWTAVYL PASSPCTLGEENMDLYLSPVAQSQE FSGRSLDRLPKTRSMDDL SACTS SPLTRTSSDPNLNNHCQEVVRVGLEP WHSNPEGSETSFVDSGVGGPQQTV GEVGLPPPLPSSQKDYL SNKPKSH KSCSPSYKLLNTA VPREMKSNTSDP EIKVLEETKGPAPDPSAQDELGRTL DGIGEPPEHCPETEAVSALS KVISNK CDGVCNFPESQNSPTGTPQQAQPD SMLGVPSKCVLDHSLSTVCNPPSAA CQTPLDPSTDFLNQDSSGSVASISH QEQLSSVPDLTHGEEDIGKRGNNRN GQLENPRFGKMPLELVRKPISQSQI SEFSFLGSNWDSFQGMVTSFPSGEA TPRRLLSYGCCSKRPNSKQMRATGP CFGGQWAQREGVKSPVCSHSHNGH CTGPGGKNQMWLSSH PKQVSSTKP VPLNCPSVPPLYLDDDG LFPFTDVI QHRLRQIEAGYKQEVEQLRRQVRE FQ\MLRDIRHWCAPPAEPPMDYEDD FTCLKESDGS DTEDFGSDHSEDCLS EASWEPVDKKETE VTRWVPDHMA SH\CYNCDCEFWLAKRRHHCRNCG NVFCAGCCHLKLPIPDQQLYDPVLV CNSCYEHIQVSRARELMSQQLKKPI ATASS |
| 1978 | 7475 | A | 2123 | 3 | 259 | FPHRAGPILSSFQVPQRWL VGGFGR NCIAGGESVWDR TNKYTRN* AQE WGMFSWSLDGHLGESIIRGRSNTG ALSCPWPLGHL P |
| 1979 | 7476 | A | 2124 | 1171 | 1784 | KLYLSVL YKGEAKV VLLKPA\YDV SSFSFF\QRPTVQE\FM TFSQLIVER S/SRKGTRASVKEQDYLCHVYVRN DSL AG/VVVIADNEYPSRGGPF TLL\ EKVLDEFSQAKSHRIDWPVGIPWL TIHYPALDGHL SRYQNPRE\ADPMT KVQAELDETKIILHNT PWESLLERG EKLDDL VSKSEVLGTQSKAFYKTA RKQNSCCAIM |
| 1980 | 7477 | A | 2125 | 2 | 262 | RGNWVFLHTTEFSLTRSLISFN SCFI TRLECSGAITAHCSLDLLGSS/QSPTS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PSRVAGTTGVCHHTQLIYLKQFFLE MRSPFVAQLV |
| 1981 | 7478 | A | 2126 | 36 | 376 | PFDPAVLTAKA AVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVAL\LVHLSRGGA EVQIFAPD VPQMHVIDHTKGQPSGESRCGGGI GTCFLSTSHGAAFF |
| 1982 | 7479 | A | 2127 | 3 | 724 | LAAASAFTPLCPVCRTSPSQRALHL CVPRPAGRVSLVLSGCGVYNGTDIH EASAILVHLSRGGA EVQIFAPDVPH MHVNDHTKGQPSGESMNVLTES ERIRRGKITDLANLSAANHDA AIFP GGFGAAKNLSTFAVDGKDCKVNKE VERVLKEFHQAGKPIGHSLKDLPGH CPGRPLKWSLRKRCLRAPEGGPC CSRVTAGVKVSPMVSTSGSRPCQRS VPWMSAQREEMALSSVTD |
| 1983 | 7480 | A | 2128 | 172 | 1020 | PSDPAVLTA MA AVRALVASRLAAA SAFTSLSPGGRTSPSQRALHLSVPRP AARVALVLSGCGVYDGT EIH EASA\ ILEHLSRGAEDHIFAPDVPHMHVI DHTKGQPSGESRNVLTESARIARG KITDLANLSAANHDA AIFP/GEGFG AAKNLSTFCRWTKICKVNKEVER VLKEFHQAGKPIGLCCIA PVLA AK VLKGVEVTVGHEQE EGKWPYAG TAEAILALGAKHCVK EVVEAHVD QKNKVTTT PAFMCETALHYIHDG\ GAMVRKVLELTGK |
| 1984 | 7481 | A | 2129 | 1 | 416 | IQYRSDLELHSITMKKGGVLFLLGII LLVLIAAHGTPVVRKGRCSCHITNQ GTIHLQSLKDLKPFGPSQCKIDIIA TLKNGIQTCLNPD SAD\VKELIKKW EKQVSQKKKQKNGKKHQKKKVLK VRKSQRSRQKKT |
| 1985 | 7482 | A | 2130 | 2 | 81 | |
| 1986 | 7483 | A | 2131 | 2 | 130 | |
| 1987 | 7484 | A | 2132 | 1 | 524 | RPRIRHEPQTQREPTMVLSPA\DKTK AQRPPRLKLGA TPGEYGGEPLER\ VLFPPPTPKPYFPH\DL SHG\SAQVK GATAKKVA\DALTKAVAHVDGHA QTALSALSDLHGAQAFGWDPVNF QASLSHLPCLGEPWAGPPSPA EFHP LAVARLPWGQSFLGFLKHRCLNL PNYR |
| 1988 | 7485 | A | 2133 | 388 | 654 | GLFFVLQFFFLFCFVFLRSHSVSQAG VHWC RHGSAAST/SPGSSDPPTLAS\ KVLGVTDMSHCTWAESYFFTKMGS SPVVACACSSSYLGG |
| 1989 | 7486 | A | 2134 | 384 | 622 | INAPPRCPQLC\TSEVCAME/CPQRV PAGPCPGCPRGNLLIHAPSNRPGTTS QINDPQPFLRICFWGSPKTPSHRHS FFF |
| 1990 | 7487 | C | 2135 | 44 | 340 | MKCSQPXRCHFQSD FQKCAPCPRA QTHWLEPPGRVQTISSMRNAQKGF ADSIRLWRLPASGVGVVVSPEGAG DPSHLLDPPGHSAPYSPAPRQLSRV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | P* |
| 1991 | 7488 | C | 2136 | 2413 | 2829 | MFPRRACATCPNLKRACVCAPLRP RFGTSRVWCACLLPSPEPTGSVNI FYVPLPSGLLSTSAPGSRASGVGV LEGARGSFSSPWTLPGHFWSLFPSS LGSLSRCPLGKGQDEALVQGALGW GQRAWTPAQCSVDNG* |
| 1992 | 7489 | A | 2137 | 69 | 332 | YQVLKTDKNMSRISFFPFLRKGLAL SPRMECSGAITAHCSLRISQSQ/DDP/ AHVSLSSWGLQGTCHHTQLIFLFF VGDEGLCCPGVRS |
| 1993 | 7490 | B | 2144 | 73 | 358 | XVPGSRGPETKLWDDFSMSQATKR KHVVKEVLGEHIVPSDQQQIVRVLR TPGNNLHEVETAQQQRFLVSMPSK YRKNIWIKRGDFLIVDPIEEGEK* |
| 1994 | 7491 | A | 2145 | 80 | 201 | |
| 1995 | 7492 | A | 2146 | 498 | 748 | FLPRRGDNDSSYPQ/WTKACRRRRRT CW*T*TWIRSGQRKMWSCGRRSL TTCMPRTRTAARLMACGSGSWRR SGPSCGRLSP |
| 1996 | 7493 | A | 2147 | 1 | 1764 | MTTSQKHRDFVAEPMGEKPVGSLA GIGEVLGKKLEERGFDKAYVVLGQ FLVLKKDEDLFREWLKDTCGANAK QSRDCFGCLRE/WCAKSRPAAEVSE LKADSKEGPQAQGPQEERTGL |
| 1997 | 7494 | A | 2148 | 842 | 1186 | FLPRRGDNDSSYPQ/WTKACRRRRRT CW*T*TWIRSGQRKMWSCGRRSL TTCMPRTRATTTWRSKNLALSCP SMTKSLKSGHIPSAWSRAARLMA CGSGSWRRSGPSCGRLSP |
| 1998 | 7495 | A | 2149 | 526 | 1158 | SCGLSLIKMTTSQKHRDFVAEPMGE KPVGSLAGIGEVLGKKLEERGFDKG L/YVVLGQFLADIEKMKTSFREWLK DTCGANAK\QSRDCFRMPFEKWCE ALLVDALLGKFSIPPAPQSRSLASRS RDSSPCPSYEGKD\CYC\RTHL\RRYF RGSFGEFSPLNHFQLFFGILRSWHAF PRPFFPWVPSWVTVYQLFLEWDFP GPIPHPHPHFQSV |
| 1999 | 7496 | A | 2150 | 150 | 446 | HEGLLLKLRLSDVYFLLFFETRSCF VAHAGVQWHHYNLSL/T/PPGTMPF PPLLASQVAGSTGMNHQAQIKKTF FGENMILLCCSGWLSGIFVLYSLY |
| 2000 | 7497 | C | 2151 | 203 | 427 | MNFVRSIWMAQSTILLTARGXATLI IAISFLAPXLAQSVHAVSSFQSQAD LLNGQCGFQQSSEPQPHVHTTSS* |
| 2001 | 7498 | A | 2152 | 1 | 1065 | |
| 2002 | 7499 | A | 2153 | 597 | 1292 | QTFSNTIFLLTRHKQHSMLVPMNT PGVKIIRPLSVFGYTDNFHGGHFEIH FNQVR\VPATNLILGEGRGFEISQG RLGPGRIHHCMRTVGWAERLLQI MCERATQRIAFKKKLYAHEVVAH WIAESRIAIEKIRLLTLKAAHSMDTL GSAGAKKEIAMIKVAAPRAVSKIVD WAIQVCGGAGVSQDYPLANMYAI TRVLRADGPDEVHLSAIATMELRD QAKRLTAKI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2003 | 7500 | A | 2154 | 1694 | 1886 | ASDSRVPAAGIS/PSAPFPTQLSPRRS PPSPPPPPQSPGLGIFSPKASPVGILHL FKTLFCILNV |
| 2004 | 7501 | A | 2155 | 1002 | 1480 | MLLLKTTERFEVSVCMACTYV\SNL GKKQRSVSFLASGLMRVSTGPELRL HHSFVLTGDVGRRICRLLVGLFTKG DTSSKRV\HPFSPGP\CFLLCDLAR\V GSSPKJNRVPHFTRTQTSTQRSCTVF VWQRCSLVGPFQVTVFTMYFHHS RSISRFS |
| 2005 | 7502 | A | 2156 | 1 | 1623 | RLPFVDVDARVYADAPAKLLLPL AFWELAVRLRGAEAAASERQVYSVA VKLLLHPAFQSCLLLTLLGLWRTT PEAHASSLGAPASAAASFLQDLHRY GEGDSLTLQQLKALLNHLDVGVGR GNVTQHVQGHRNLSTCFSSGDLFT AHNF\SEQLRIGSSELHEFCPTILQQL DSRACTSENQENEENEQTEGRPSA VEVWGYGLLCVTVISLCSLLGASV VPFMKKTLYKRLLLYFRALAI GTLL LKRLFQLIPGAVWFQPLEDYVVS KSAVVFGGFY\FFFTEKILKILLKQKNE HHHGHSHYASESLPSKKDQEEGVM EKLQNGDLDHMIPQHCSSELDGKA PMVDEKVIVGSLSVQDLQASQSAC YWLKGVRYSDIGTLAWMITL\SDGL HNFIDGLAIGASFTVSVFQGISV AI LCEEFPHEL GDFVIL\LNAGMSIQQA LFFNFLSACCCYLGLAFGILAGSHFS ANWIFALAGGMFLYISLADMFP EM NEVCQEDERKGSILIPFIIQNLG LLTG FTIMVVLTMYSGQIQIG |
| 2006 | 7503 | A | 2157 | 1 | 604 | MGTRWEPGWRAPLAPAAQARSS GRAAPAAGSERARERERDGGSVGG GGSSSAIPSERAADAHGEDSGAYR WERANRPFSNNCCCLAFYLGMEEA RWLYAGLFCVYGASLIAIATHVPLF GSQIKAE/DPSGDSAPAAHLPPQPAQ /PHLPQAQLMLTGSQLAGHPLGMR WSMATQHAGCVSQRCLFPMTVG CSQGNILWSL |
| 2007 | 7504 | A | 2158 | 22 | 1358 | VHFSMGAPEIRMSKPLEAEKQGLDS PSEHTDTERNGPDTNHQNPQNKTSP FSVSPTGPSTKIKAE DPSGDSAPAAP LPPQPAQPHLPQAQLMLTGSQLAG DIQQLLQLQQLVLVPSHHLQPPAQF LLPQAQSQPGLLPTPNLFQLPQQT QGALLTSQPRAGLPTQPPKCLEPPS HPEEPSDLEELQFARTFKQRRIKLG FTQGDVGLAMGKLYGNDFSQTTIF RFEALNLSFKNMCKLKPLLEKWL N DAETMSVDSSLPSIQLSSPSLGF DGLPGRRRKKRTSIETNVRFALEK SFL ANQKPTSEEILLIAEQLHMEKE VIRV WFCNRRQKEKRINPCSAAPML PSPG KPASYSPHMTVPQGGAGTLPL SQAS SSLSTTVTTYILSCGDAPPQ PDSWR GWGRGRGCAPPQFHPLCHS PTPGH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HQQHKPQPLKAATRLSACQA |
| 2008 | 7505 | A | 2159 | 3 | 452 | |
| 2009 | 7506 | A | 2160 | 9 | 633 | NSARATDSERTHHGARLLPDKTNV KAAWGKVGAGAHAGEYGAEALERMF LSFPT\TKTYFPFHD\LSQRSAQVKG ATGKKVADALTNAVA\HVD\DMPO TALSGPEATLHGAQSFGVDPVQLSS SLSHWPAWLTGPAHLPRPSFNPW RLQRLPWGQSFLGFLVEEPLLEPSKI PVKAWKPSGWPCFLCPFASPGQGP SLSWNPYPRWSFE |
| 2010 | 7507 | B | 2161 | 55 | 372 | MERFLMDGFQPQQLSTYALTLYKH TATVDGKTILVADINVTQKSFNFAK KFSPLPLYFVSAADGTNVVKLFNDAI RLAVSYKQNSQDFMDEIFQELENFS LEQEEEN* |
| 2011 | 7508 | A | 2162 | 552 | 1809 | QLRGRGASRKWSALRRELGRRAWF ESAQSPDWRQGPGRPSVPGLSSP HSEPHPEMAEDKTKPSELDDQGYD ADDNVKIIICLGDSAVGKSKLMEFL MDGLYPSRFEVLLVPVGLPTLMYQ CPTAHPFVPAAQEGGLDFWDTAGQ DTLSSPPTPHPSMELVPVCSQPQQLS TYALTLYKHTATVDGKTILVDFWD TAGQERFQSMHASYYHKAHACIMV FDIQRKVITYRNLTSTWYTELREFRPEI PCIVVANKIDDRPMSYLLSTADINV TQKSFNFAKKFSLPLYFVSAADGTN VVKVWLTAEVASKLFNDAIRLAVS YKQNSQDFMDEIFQELEVGVQVHISG GMEETAPLQG*GLQPSRVTLA*VCP TKCIRAAVEQMGGQASPATLFTNF SLEQEEEDVPDQEQQSSSIETPSEE |
| 2012 | 7509 | A | 2163 | 807 | 1389 | EPMAENKTKPSELDDQGYDADDNV KIIICLGDSAVGQSKLMEFLMDGFQ PQQLSTYALTLYKHTATVDGKTILV DFWDTAGQERFQSMHASYYHKAH ACIM/LDINVTQKSFNFAKKFSLPLY FVSA\ADGTNVVKLFNDAIRLAVSY KQNSQDFMDEIFQELENFSLEQEEE DVPDQEQQSSSIETPSEEVASPHS |
| 2013 | 7510 | A | 2164 | 3 | 923 | RAARTRAEPEVECAAARAGPAGVV RERAESRHGGRRAGADPQRPWSLQ PSLGT\AHRDNTLPSLGPGLSTARS QWAKNKTKPSELDDQGYDADDNV KIIICLGDSAVGKFKLMEFLMDG\ FQPPQLSTYALTLYKHTATVDGRTI LVDF\FHTAGQERFQSMHASYYHK AHA\CIMVFDVQRKVITYRNLTSTWY TELSGSRPEIACIVVANKIDADINV TQKSFNFAKKFSLPLYFVSAA\DGT NVVKLFNDAIRLAVSYKQNSQDFM DEIFQELENFSLEQEEEDVPDQEQQS SIETPSEEAAASPHS |
| 2014 | 7511 | A | 2165 | 1 | 2715 | |
| 2015 | 7512 | A | 2166 | 1 | 2256 | |
| 2016 | 7513 | A | 2167 | 339 | 1086 | IQMNRFL\LM\SLYLLGSVARGTSSQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PNELSGSIDHQTSVQQPLPGEFFSLEN PSDAEALYETSSGLNTLSEHGSSEH GSSKHTVAEHTSGEHAESEHASGEP AATEHAEGEHTVGEQPSGEQPSGE HLSGEQPLSELESGEQPSDEQPSGEH GSGEQPSGEQASGEQPSGTILNCYT CAYMNDQQKCLRGEGETCITQNSQQ CMLKKIFEGGKLQFMVQGCENMCP SMNLFSHGTRMQHCCRNQSFCKNI |
| 2017 | 7514 | A | 2168 | 2 | 425 | |
| 2018 | 7515 | A | 2169 | 2 | 169 | GRVGDTLKAGINAVERRSNRCNGN SGFEGQSRYPSSGMSAKELCEND DLSTSLVLDPYLGFQTHKMNTR*FG S |
| 2019 | 7516 | A | 2170 | 2 | 227 | |
| 2020 | 7517 | A | 2171 | 177 | 1400 | LNAPGSQLSVGMKGLGESKNMVV NGRRNGGPLSNDHQQNQSKLQHTG KDTLKAGKNAVERRSNRCNGNSG FEGQSS/RYPVSYGMTAKELCEND LATSLVLDPYLGFQTHKMNTSAFPS RSSRHF\SQSDSLSHNNPVFRPIKG RQEELKEVIERFKKDEHLEKAFKCL TSGEWARHYFLNKNKMQEKLKE HVFIYLRMFATDSGFELPCNRYSS QNGAKIVATKEWKRNDKIELLVGCI AELSEIEENMLLRHGENDFSVMYST RKNCAQLWLGPAAFINHDCRPNC FVSTGRDTACVKALRDIEPGEEISC YYGDGFFGENNEFCECYTCERRGT GAFKSRVGLPAPAPVINSKYGLRET DKRLNRLKKLGDSSKNSDSQSV/SA LNTDADTTQEKNIASK |
| 2021 | 7518 | A | 2172 | 3 | 114 | |
| 2022 | 7519 | A | 2173 | 328 | 471 | |
| 2023 | 7520 | A | 2174 | 1 | 190 | |
| 2024 | 7521 | A | 2175 | 2 | 132 | SGLGRLPGPWQEAGSSRGPSGDM AGVKALVALSFSGAIGLTF/LHMLG CALEDYGVYWPLFVLIFHAISPIPHF IAKRVTYDS DATSSACRELAYFFT GIVVSCLWISPVILARVALIK\WGAC GLCV/VAGNAVIFLTIQGFPIFGRG DDFSWEQWGYWTDFS |
| 2025 | 7522 | A | 2176 | 191 | 479 | NTSLPNPSEVSHSSLRLDSGGAEAF VGGGTGVLKKPEGAGPAAPS/LGW RPRG*APHRTGSAQPPTAVPCR/PGA LGEDSSPGPPGALGGLGVIPQPSM |
| 2026 | 7523 | A | 2177 | 1920 | 2524 | TQYPPAEQRSQTLMDQVFALPLNSL CAQSSKTLNCKTQCHPCSILCKNLL KNKCLILHSRFTIQTAFEGGQLRI PLFPKPKVRSSQFQASVLELRRSQ PFVGGGTGVLKKPEGAGPAAPTSG WRPRGEAPHRTGTAQPPTAVPSGG RIWGKIPLPGPPGALEGVGFPSASPR FQLQPRCLKLDAGRRLRSGSKPHVK HL |
| 2027 | 7524 | A | 2178 | 239 | 380 | |
| 2028 | 7525 | A | 2179 | 34 | 202 | EPTTRQTLYMLITFTPHNHLVRETSS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VPFEQMKN*GSERFNTLSKALQTISAKTRI |
| 2029 | 7526 | A | 2180 | 1 | 1566 | |
| 2030 | 7527 | A | 2181 | 574 | 1949 | KSKCRFPEGLSEGFGPMRKEALSSG SVQEA EAMLDEPQEQAEGSLTVYVI SEHSSLLPQDMMSYIGPKRTAVVRG IMHREAFNIIGRRIQVAQAMSLTE DVLAAALADHLPEDKWSAEKRRPL KSSLGYEITFSLNPDPSKSHDVYWD IEGAVRRYVQPFLNALGAAGNFSV DSQILYYAMLGVNPRVYSASSSYIF GHAQLPHVINPVESRLGSSAASLYP VLNFLLYVPELAHSPLYIQDKDGAP VATNAFHSPRWGGIMVYNVDSKTY NASVLPVRVEVDMVRVMEVFLAQ LRLFLGIAQPHLPPKCLLSGPTSEGL MTWELDRLLWARSVENLQATT LTSLGAASWARSATLFIKGRRGHLE VLQRL LAPVQKSAEELASGHLADLP LSPAREAVTSSELAFFDPSLLHLLYF PDDQKFAIYIPLFLPMAVPILLSLVKI FLETRKSWEKA |
| 2031 | 7528 | A | 2182 | 76 | 419 | |
| 2032 | 7529 | A | 2183 | 71 | 350 | AFIPAMAELIQKKLQGEVEKYQQQLQ KDLSKSMGRQKLEAQLTENNIVK EKRYESQLRDLERQSEQQRETLAQ LQEFQRAQAAGAPGKA |
| 2033 | 7530 | A | 2184 | 175 | 1032 | GLLPHLGPRVQRLPRLSLSTLPCSLT RCPHPFLLPQIHHLTRIVGIGGTFDV SKLPFLSSPDLSKSMGRQKLEAQL TEYNIAKEVRDWDLWGEEGPVLA MVLITYVPSLHQELALLDGSNVVFK LLGPVLVKQELGEARATVGKRLDY ITAEM*VFIPPPCAAPCDASEPLE*R C*TIAEQLSIVAPSPVPPTLSFPF*PP FFSLPWISRFSTYLFLAFSTLHSESY* FLPFCLSPSLLSKRYESQLRDLERQ SEQQRETLAQ LQEFQRAQAAGAPGKA |
| 2034 | 7531 | A | 2185 | 112 | 520 | AFIPAMAELIQKKLQGEVEKYQQQL QKDLSKSMGRQKLEAQLTENNIV KEELALLDGSNVVFKLLGPVLVK QELGEARATVGKRLDYITAEIKRYE SQLRDLERQSEQQRETLAQ LQEFQ RAQAAGAPGKA |
| 2035 | 7532 | A | 2186 | 635 | 1015 | GGQKHPTGLLKPPANTAATMPKRRK AKGDAKGDKAKVKDEPQRRSARLS AKPAPPKPEPGLKKASIAKKGEKL/P KGRKGGKADA\GKGLGNNPAKNPR LPLHFQFQKAE\GTGGLPSEMFIFES SGTYW |
| 2036 | 7533 | A | 2187 | 302 | 471 | TLSHRVLVEAQSREQLAALKKHHE EEIVHHK\KEIERLQKRNL SRHK\QK DSKLLKH |
| 2037 | 7534 | A | 2188 | 3 | 399 | LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLGRV/WGVRTMQA RFGSDQSENFTGPRAHP/RKAG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GALGKREQAEEERYFRAQSREQLA ALKKHHEEE\VHHKKKE\ERLA FERHKQK\KMLKH |
| 2038 | 7535 | A | 2193 | 2 | 406 | ARAEMSRVALAVLALLSLSGLEAI QRTPKIQVYSRHPAENGKSIFLKCY VSG\FHPSDIE\VDLLKNGKE/RLKK VEPSDLS/FSAKDWSFYLLPYTEFH PQLKKDGVCPARVN\HVTLSAPARL VK\WDRRHVKQHQ |
| 2039 | 7536 | A | 2197 | 319 | 393 | WL/TPVIPTLWEAEVGGSFHRSSR |
| 2040 | 7537 | C | 2198 | 84 | 290 | MLPSKGLSFFSLQHLRDSRSLFPM SMITMLELECCRASSNHEVRWLKX HXVSQICSLICFPXMLTIRA* |
| 2041 | 7538 | A | 2199 | 2 | 743 | PRVRSESVYRSLADPEPTGRDTMT YADLFKYIIIGDTGVGKTCFLLOFTD KRFQPVHDLVSLGVEFGGSLCSTLME NQFKLHIWD\TAGQESFRSITRSY\Y RGAAGVALLVYDITRALKPFNHLAS WLGGLPGQHFSFPTWVIHCFIGNKS DLESRRDVKREEGEAFARE\HGRIFR GTSAKTACN\VEEAFINTAKR\YRKI HQGLFDVHNEANGIKIGPQQSISTSV GPSASQRNSRDIGSNSGCC |
| 2042 | 7539 | A | 2202 | 20 | 222 | |
| 2043 | 7540 | A | 2203 | 1 | 458 | RSSLTSLSNSAAAMAPVKKPCGEG GAKKKKQVLKFTLADCTHPVEDGI MDAAQF*ASFCKERIKVKRKKLGT LSGGG/V*PIERSKISKITV\SEVPFS KRV/YLKYLTKKY\LKNNLRDLV CRVVAYQPKRELRNYSYFQINQ\DE GRREDED |
| 2044 | 7541 | A | 2204 | 2 | 321 | FIFFSFSFFSFFSETGSCSVAQAG VQCHDHGSPQS/PNLPGSSDLPTSAS \KVLGITGVRHHSPLPLGFQMGIFLL FSMLKFCFWVCSALLCTVLEFLRTN YFLS |
| 2045 | 7542 | C | 2205 | 46 | 234 | MTLRXWITWPFLFLSPSSKCLHLI ASILLDLQLGSTHSSLSTIFFVVLAF RKIGLVCP* |
| 2046 | 7543 | A | 2206 | 1 | 243 | |
| 2047 | 7544 | A | 2207 | 144 | 479 | RPLKPRRTF\CKK\CGKAPNPHKSDH STKKGKDSLYAPGKAAMVTRKQS GYGGQ\TKPIFRKKA\TTKKIVLKA LSALSPTCRSKRMLAFKRWQAFNL LGDKKKRKGPSASS |
| 2048 | 7545 | A | 2208 | 75 | 540 | GGSGSVRVLRSESPREEAVEEEVAA VAVVVAVAEAGTNQLRAETMANI AVQR\IKREFKEVLKSEETSKNQIKV DLVDENFTELRGEIAGPPDTPFERG RFP\LELKIP\ETYPFNPPK/VFRFYAL KLWHPNISSV\TGAICLDIL\KDQWG SWQWT |
| 2049 | 7546 | A | 2211 | 1 | 2640 | MYSGNRSGGHGYWDGGGAAGAE GPAPAGTLPAPLFPPTYERLALLL GSIGLLGVGNLLVLVLYYKFQRLR TPTHLLLVNISLSDLLVSLFGVTFTF VSCLRNGWVWDTVGCVWDGFGSGS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LFARPA\PLPARPRAPRPTPPRSPLAS STLPDPSRMAGAF\FLRPLPPHAVQ DSIPVVSHLPPTCHQTLLLPKMADN LPTEFDVVIIGTGLPESILAAACSRSG QRV\HIDSRSYYGGN\WASFSFSGLL SWLKEYQQNNDIGEESTVVWQDLI HETEEAITLRKKDETIQHT\EAFCYAS QDMEDNVEEIGALQKNPSLGVSNT FTEVLDSALPEESQLSYFNSDEMPA KHTQKSDTEISLEVT\DVESVEKEK YCGDKTCMHTVSDKDGDKDESKST VEDKADEPIRNRITYSQIVKEGRRFN IDLVSKLLYSQGLLIDLLIKSDVSRY VEFKNVTRILAFREGKVEQVPCSRA DVFNSKELTMVEKRM\LMKFLTFCFL EYEQHPDEYQAFRQCSFSEY\LKTKK LTPNLQHFVLH\SIAMTSESSCTTIDG LNATKNFLQCLGRFGNTPF\LFPLYG QGEIPQGF\CRMCAVFGGIYCLRHKV QCFVVDKESGRCKAIIDHFGQRINA KYFIVEDSYLSEETCSNVQYKQISR AVLITDQSILKTDLDQQT\SILVPPAE PGACAVRVTELCSSTMTCMKDTYL VHLT\CSSKTARE\DES\VVKKLFTP YTETEINEEELTKPRLLWALYFNMR DSSGISRSSYNGLPSNVYVCSGPDC GLGNEHAVKQAETL\FQE\IFPTEEFC PPPPNPEDIIFDGD\DKQPER\PLGTNN VVMAKLESSE\ESKN\AESPEKHPSK LEKSNLEMLFWTSFMASEF\SHLKD RFPI |
| 2050 | 7547 | A | 2212 | 328 | 583 | |
| 2051 | 7548 | A | 2213 | 1 | 416 | PSSGDMAGVKALVALSFSGAIGLTF LMLGCALEDYGVYWPLFVLIF\HAI SPIPHFIAKRVTYDS\DATSSACRELA YFFTTGIVVSCLWISP\ILARVALIK\ WGACGLVLAGNAVIFLTIQGFFLIF G\RGDDFSWIEQW |
| 2052 | 7549 | A | 2214 | 1 | 180 | AAATGAVGAAIYPCAAPNWK*\RND EKTAADYKILGGSVLHLVLALRGG GGLRQ |
| 2053 | 7550 | A | 2215 | 162 | 557 | VASEHSPKIGASQGLDYEP\LLVVAK VWYLTRPTGTKAGSVFSQYLPFLEP GILGPASLPWLRQTLTGKEIEIDIEP\ TDKVERNQRSVWEEKEGNPP\PPQQ RLHLQVAKQM\NDEKDSSLIYKILR WVQSFQT |
| 2054 | 7551 | A | 2216 | 684 | 1496 | LETSGLSENPLGQAVGFGQDEFFLE QTKKKGVKRPARLHTKPSQAPAVE EAPSGA\SYNPSFEDHQTL\LSAAHE VELQRQKEAEKLERQLRPCATEQ ARHPRSSTFQELCEGLLEESDGE PGQGEPEAGDAEVCSTPARLATT EK\KTEQQRREKAVHRLRVTARA ALRAA\RLRATQELVFRVRGIQRPQ V\ALRLA\ELARRRRRRQARREAEA \DKPRRLGT\RFKYQAPDIDVQLASSE LTD\SLRTLKPEGQHPSRPVQELPRG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GI |
| 2055 | 7552 | A | 2217 | 116 | 285 | KLRNQRIQERHTDGGGEPLKSL*CSP KTRVESRSASRRGPLFLNKGHARAR SSLTLA |
| 2056 | 7553 | A | 2218 | 3421 | 3698 | AGRGPLRLQSHRFGPSPQVDCLSPA APDQPGQHGKTPSPQK\QKLAGHG GAHLQSQPLGRLRREDPLSPGGGGC SEPRSHHCTPAWAREYGD |
| 2057 | 7554 | A | 2219 | 381 | 1772 | KMAESEN\RQELSES\SQEEAGNQIM VEGLGEHLERGEDAAAGLGDDGKC GEEAAAGLGEEGENGEDTAAGSGE DGKKGGDTDEDSEADRPKGLIGYV LDTDFVESLPVKVKYRVLALKKLQ TRAANLESKFLREFHDIERKFAEMY QPLLEKRRQIINAIYEPTEECEYKS DSEDC\DDEEMCHEEMYGNEEGMV HEYVDEDDGYEDYYYDYAVEEEEE EEEEDDIEATGEENKEEEDP\RGPID FWLTVLKNVDLTPLIKKYDEPILK LLTDIKVKLSDPGEPLSFTLEFHFKP NEYFKNELLTKTYVLKSKLAYYDP HPYRGTAIEYSTGCEIDWNEGKNVT LKTIKKKQKHRDL/WGTIRTVTEDF PKDSFFNFFSPHGITSNGRDGNDDFL LGHNLRTYIIPRSVLFFSGDALESQQ EGVVREVNDAIYDKIYDNWMAAI EEVKACCKNLEALVEDIDR |
| 2058 | 7555 | A | 2220 | 17 | 250 | |
| 2059 | 7556 | A | 2221 | 2 | 899 | GFSKKCVSSRSPELRVTRLRYLRIQ AFRGSLATADLLLLVSPLRHPEPA KVLVLFLLSFASCWAGPGRAGPPG RSLTMA SLF\KKKTVD DVIKEQNR ELRGTQRANRDRAALEKQEKQLEL EIKK\MAKIGNKEA\CKVLAKQLVH LR\KQKT\RTFAVSSKVTSMSTQTKV MDS\QMKMAGAMSTTAKTMQAVN K\KMDPQKTLQTMQEFFGRENMK M\EMTEEMINDTLDDIFDGSD\EEE SQ\DIVNQVLDEIGIEISGKMAKAPS A\ARSLPSA\T\SKATISDEEIERQLK ALGVD |
| 2060 | 7557 | A | 2222 | 3 | 586 | ARAMGISRDNLHKRRKTGGKRKPY HKKRKYELGRPAANTKIGPRRIHT VRVRGGNKKYRALRLDVGNFSWG SECCTRKTRIIDIVYNASNNELVRTK TLVKNCIVLIDSTPYRQ/WTPEEEEL NKKRSKKIQKKYDERKKNAKISSLL EEQFQQGKLLACIASRPGQCGRAD GYVLEGKELEFYLRKIKARKGK |
| 2061 | 7558 | A | 2223 | 2 | 727 | LFPASAEQMGISRDNW\HKPARKTG GPRESPTYQAEAKSM SLGRPAA\NTK ILAPRRJQHSPVCRGG*QVNTVPLRF D\VGNFWSWG/SKECCTRKTRIIDVV YNAI**PSWVRYRPLVERICIVLID EQHPYRQWVRSPTYALPLGPQRK GAKLDSL RKEEJFKPKTDLK*IQKK YD*/ERKKNCQNSASLPGRSSFQQG KASLRCIAFK/RPGQCGRADGYMT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RGHRVRSYYLRKIKARQSKINT |
| 2062 | 7559 | A | 2224 | 298 | 408 | CGII*ALNKKEHRGCDSPDPDTSYV LTPHTEEKYKKINEEFDNMMRNH KI APGLPPQNFSMSVTVPVTPSPNALS YTNP |
| 2063 | 7560 | A | 2225 | 1 | 1369 | |
| 2064 | 7561 | A | 2226 | 409 | 1944 | LKMGRKKIQITRIMDERNRQVTF TK RKFGMLMKAYELSVLCDCEIALIIF N SSNKLQYASTDMDKVLLKYTEYN EPHESRTNSDIVEALNKKEHRGCD S PDPDTSYVLTTPHTEEKYKKINEE FD NMMRNH KI APGLPPQNFSMSVTVPVTPSPNALS YTNP GSS LVSPSLAASS TLTDSSMLSPQTTLHR\NVS PGAP\ QRPPSTGNAGGMLSTTDLTV P NGA GSSPVGNGFVNSRASPNLIGAT GAN SLAGKVMPTKSPPPGGG NLGMNSR KPDLRVVIPSSKGMMP LSEEELE LNTQRISSSQATQPLATPVVSV TTPS LPPQGL\VYSAMPTA YNTDY\SLTS ADLSALQGFNSPGMLS LGQVSAWQ QHHLGQAALSSSLVAGG QLSQGISNL SINTNQNISIKSEPTSP PRDRMTPSGF QQQQQQQQQQQPPPP PQPQPQP QPRQEMGRSPVDSLSS F\SSSYDGS D REDPRGDFHSPIVLGR PPNTEDRESP SVKRM RMDAWVT |
| 2065 | 7562 | A | 2227 | 3 | 168 | PCPTHSRMLGSPQPKRQLPVAPVPT AQP\PPSPPKGRCQGQEPKPPRLSP AQGPW |
| 2066 | 7563 | A | 2228 | 272 | 416 | VGRCCFLSSGGFFSLTSALPPPS/PSA HPGVLVTPFGAPTKPDRGRSRG |
| 2067 | 7564 | A | 2229 | 109 | 866 | DTRVGYFSSGAFAFFFLWARAECRP LSKDSL VKPRATLPSIVGLGSVAVP RARRARRQRERSR PRTGPGACLP PS LAPYGFARV ERRARAMKAGFPVRR SGRKAPYGC GME LALRCLAEHG HSLGG\SAALGAS\AAAARCKAAEA AADEPALCLQCD MND CYSRLRLV PTIPP NKKVSKVEILQHVIDYILD LQ LALETHPALLRQPPPPAPPHHPAGT CPAAPPRTPLTALNTDPAGAR\NKQ GDSILCR |
| 2068 | 7565 | A | 2230 | 107 | 1073 | |
| 2069 | 7566 | A | 2231 | 23 | 538 | LPEVPHSLRPRVKPHLCCAQPAVRV MARLPKLA VFDLDYTLWPFWVDT HVDPPFHKS/KVR*GQ RGLGAR*DP ARAERTLALSSDGT VRDRRGQDVR LYPEVPEVLKRLQSLG VPGAAASRT SEIEGANQLLELFDL FRCYLHSHPE WNESSNSKSRVRDICE GPNWAFEV QP |
| 2070 | 7567 | A | 2232 | 685 | 1161 | TFPLLPLADYTLWPFWVDTHVDPPF HNSR*GRDREDW/PAR*DPARAERT LALSSDGTVRDRRGPDVRLYPEVPE VLKRLQSLGVP GAAASRTSEIEGAN QLLELFDLFRYFVHREIYPGSKITHF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ERLQQKTGIPFS\QMIL\FDDERRNIV DVSKLGTE |
| 2071 | 7568 | A | 2233 | 79 | 564 | SPTSAARSLRLRVMARLPKLAVFDL DYTLWPFWVDTHVDPPFHKSSDGT VRDRRGQDVRLYPEVPEVLKIDLQS LGVARCGCFQGQVRLGRGQPATGA LLTFFRYFVHRAEIYPGSKITHFERVA AE\TGISF\SQMIFFDDERREYCRRSA NWCVTCTSHPEW |
| 2072 | 7569 | B | 2234 | 48 | 209 | XKNQCETRTMQENGYSSHAVDGT GPAGGAGRPAGSTGAQVSVQPNFQ QDKFLGRX* |
| 2073 | 7570 | A | 2235 | 2 | 353 | |
| 2074 | 7571 | A | 2236 | 3 | 676 | SAVEFPPLSHTTGTRPRTPIILQQE NGYFIHTLWMGLALLGVLGDLGSGQ HRRRSPCQPNFQDKFLGRWFKR G\LASNSSWLREKKAALSMCKSVV APATDGG\FNL TSTFLQEKTSVETR TML\LQPRGVPSASLQLTGVPHWGQ A/HYSVSVVETDYDQYALLYTRAS KGPGEFRMATLYSRTQTPRAELK EKFTAFCKAQGFTEDTIVFLPQTDK CMTEQ |
| 2075 | 7572 | A | 2237 | 1 | 1165 | MGVTEVFLKDV TILLNLEELVQCRCQ TWGEARTRGKRVLGSLADEIVVRT QPPSLEHKAWNATCKHWLAEEA ALEKYYLSIFYGIEFVVGVLGNTIVV YGYIFSLKNWNSSNIYLFNLSVSDL AFLCTLPLIRSYANGNWIYGDVLC ISNRYVLHANLYTSILFLTFISIDRYL IIKYPFREHLLQKKEFAILISLAIWVL VTLELLPILPLINPVITDNGTTCNDF ASSGDPNYNLIYSMCLTLLGFS\IPLF VMCLFYKIALFLKQRNRQVATAL PLEKPLNLVIMAVVIFSVLFTPYHV MRNVRIASRLGSWKQYQCTQVVIN SFYIVTRPLAFLNSVINPVFYFLLGD HFRDMLMNQLRHNFKSLTSFSRWA HELLLSFREK |
| 2076 | 7573 | A | 2238 | 1 | 567 | |
| 2077 | 7574 | A | 2239 | 58 | 544 | GKKMGSKAKKRVLLPTRPAPPTVE QILEDVRGAPAEDEVFTILAPEDPP VFRMMEDAEAPGEQLYQQSRA YV AANQRLQQAGNVLRQRCELLQRA GEDLEREVAQMKQAALPGGEGWL LGLTLWGLGALGRAQGSATQAL PGGPSAPDWHSRGPSPRG |
| 2078 | 7575 | B | 2240 | 1 | 1551 | MCELDILHDSLYQFCPEHLKRLNS LTLACHALLDCKTLTLTELGRNLPT KARTKHNIKRIDRLLGNRHLHKERL AVYRWASFCSGNTMPIVLVDWS DIREQRLMVLRSVALHGRSVTL YEKAFPLSEQCSKKAHDQFLADLAS ILPSNTTPLIVSDAGFKVPWYKSVE KLGWYWLSRVRGKVQYADLGAEN WKPISNLHDMSSSHSKTLGYKRLTK SNPISCQILLYKSRSKGRKNQRSTR HCHHPSPKIYSASAKEPWVLTNLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VEIRTPKQLVNIYSKRMQIEETFRDL KSPAYGLGLRHSRTSSSERFDIMLLI ALMLQLTCWLAGVHAQKQAFPCD DSSAVHRLRYCKGRDYNRVRSSCV QRHAPVLNRKIGTGSDQHANEFGLS WILLGARTPTCKADLSRPYSCPH QPQQRFLGDSGITTTSVPRYRGQEH CLHPKLQSTKRFIKCTTAWNENRRK YQVMPIEAQRPKCQLLFPNRSPTWQ ISIDKGPRQDTFMLFPPIKI* |
| 2079 | 7576 | A | 2241 | 2 | 456 | GTRSTRTARRRWLSSPPRACPGTEV RSTACTPSCAPPVSMRLAAALLLL LLALYTARVDGSKCKC\SRKEPKIR YSDVKKL\EMKPK\YPHCEEKMMVIIT TKSVSRYRGQEHCPHPKLQSTKRFI KWYNA\WNEKAQRRVYEEAQGLR RRIG |
| 2080 | 7577 | A | 2242 | 308 | 615 | ETRVASWGTGAAEV*GMVRLDISE GRAAVAAVVGGVAVGTVLVALS AMGFTSVGIAASSIAAKMMSTAAIA NGGGVAAGSLVAILQSVGAAGLSV TSKVIG |
| 2081 | 7578 | A | 2243 | 332 | 484 | |
| 2082 | 7579 | A | 2244 | 240 | 610 | LWVEVQSEWRLTEAKGPTMGKES GWDSGRAAVA VVGGVAVGTV\ PWRSSAMGFTSVGIAASSIAAKMM STAAIANGGGVAAGSLVAILQSVGA AGLSVTSKVIGGFAGTALGAWLGS PPSS |
| 2083 | 7580 | B | 2245 | 158 | 2382 | MARGKAKEEGSWKKFIWNSEKKEF LGRTGGSWFKILLFYVIFYGCLAGIF IGTIQVMLLTISEFKPTYQDRVAPPG LTQIPQIQKTEISFSSMAIRDAGFEIS AMQMFNMDRVNVEQFYEVYKGV VTEYHDMVTEMYSGPCVAMEIQQ NNATKTFREFCGPADPEIARHLRPG TLRAIFGKTKIQNAVHCTDLPENGL LEVQYFFKILNN* |
| 2084 | 7581 | A | 2246 | 753 | 1007 | LAQGCSGPSQDTALGPPPPCTEP/ CPVPYVLRSTPEPPQHGTCHSPCLLP IPLCSSPSLGGGGNSEGEKALTFHV CGDHPVKN |
| 2085 | 7582 | A | 2254 | 188 | 833 | ALIMSFIFEWIYNGFSSVLQFLGLYK KSGKLVFL\GLDNAGKTTLLHWLK DDQIGPTLFPPLPPTSEELTIAG\MT\ FTTFD\LGGHGAKHVA VWKN\YLP QLMGFVFLVDCA\DHFPSWNPKEVE LNALMT\DETILPMCPIL\LGKN\IDR TDAISEEKLREIFGLYGQTTGKGNV TL\KELNA\RPMEVFHVAVLLKEGK VYGRGFSAGLLPVLF |
| 2086 | 7583 | A | 2256 | 333 | 621 | CRKNSCYQAQNFNLRIPFSTTKLINL FHF*NDSQKST*/SDSHLARSSQFCS LN*NY*I*TAKSHDVVCTRQHFP ESYIWHVKEKKYNPTAAAI |
| 2087 | 7584 | A | 2257 | 29 | 659 | LSVASFSFLSNASAEDTMSRLSRSL WAATCLGVLCVLSADKNTTQHPNV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TTLPPIVRETSAPVTPLPLVTTTPAPET CEGRNSCVSCFNVSVVNTT\CFWIE CK\DESYCSHNST\VSDCQVGNTTD FCSVST\ATPVPTANS\TAKTHSSSP LLQLPRQLLHQGTNNTVNS\TSQP VRKSTFDAASFIGGIVLVLEIRCHTR NYIPDLKK |
| 2088 | 7585 | C | 2258 | 101 | 411 | MEMKMQSERLSKEYDQLLKEHSEL QKQREILPHRRGESTVTXXXXXX XEPQQRNADXXXXXXXXXXXXXXXX XXSSSRSMALQIPIKXXXXXXXXXX XXXXXLF* |
| 2089 | 7586 | A | 2259 | 2 | 575 | |
| 2090 | 7587 | A | 2260 | 1 | 265 | SDALSKAQNDVMEMKMQSERLSK EYDQLLKEHSELQHSSFGFLSKRS HKNGSIGKQTGSRKGSFRKRQKEK TVNFIKDTLQYTVSK |
| 2091 | 7588 | A | 2261 | 47 | 906 | RKKLPLQWPAVPPFLYAEIGLILIFC LPFIPPQRWQKIF\SFNVWGKIATFW NKAFLTIIILLIVLFLDAVREVRKYSS VHTIEKSSTSRPDAYEHTQMKLFRS QKNLYIPGISLFFWLVLRLVTLITQ LAKEPVTQRCALYLQAENTNKA K\FMEEENEKLRILKSHGKDEECVL EAENKKLVEDQEKLTTELKTS LASKAQNDVMEMKMQSERLSKEYD QLLK\EHSELQVPLGSFYLAFA PGLHNPSPSSPRSGGGFSAIDNPR GALPPCLVCVLFHHL |
| 2092 | 7589 | A | 2262 | 669 | 995 | KVFFCFYRIYVCICVCVCVCVC/TLQ TL/CYSIANMLTSSQCLQSCGSQSW CQMHIKSSKAIMTIPCKFISRKPWEG DCSSLEPHGVSAFDIWVPLCIKKV LNHFSPRKN |
| 2093 | 7590 | A | 2263 | 3 | 379 | WPFLKLRLGTCGTCSSHEGRAAA WSAESSLQHSVVMTSLPLNPKPFL NGLTGKPMVKLKWGMEYKGYL\ VSVD\GYMNMQLANTEEYIDGALS GHLGEVLIRCNNVLYIRGVEEEED GEMRE |
| 2094 | 7591 | A | 2264 | 68 | 268 | QYLSLLLTQYSLVFICWLFICL\LYV YFLCMLLCKYGLQLFLCGILSFRIS CKLLESRIHVIPLFL |
| 2095 | 7592 | A | 2266 | 190 | 554 | HGVRSDLGRWPDHLCVCRHYHH LLHLLLLPLQDVPPTTSWLSPPHP PLWCM/PPYPQPPSVPPSYPGPSLPG LPHHAASARECQHPYPIAVPTHLT HAHAHGPTTRTPPLAGRSSRD |
| 2096 | 7593 | A | 2267 | 2 | 445 | |
| 2097 | 7594 | A | 2268 | 200 | 894 | TSPRARPHCSLCLPNLPPVTYMHY ETDGFSLGVFLKSGTISPLHDHPG MHGMLKVLYGTVRISCMDKLDAG GGQRPRALPPEQQFEPPLQPRREA VRPGVLRSAEYTEASGPCILTPHR DNLHQIDAVEGPAAFLDILAPPYDP DDGRDCHYYRVLEPVRPKEASSA CDLPREVWLL\ETPQADDFWCEGEP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YPGPKGLPLKPLAHQERWAEDVPY PTTRAVSLPP |
| 2098 | 7595 | A | 2269 | 257 | 781 | QELLSGLVNYFSLSWFLYVAQESIP SLPQSPMRETPSKAFHQYSNNISTLD VHCLPQLPEKASPPASPPIAFPFAFE AAQVEAKPDELKVTVKLKPRRLRAV HGGFEDWRPLNKKWTGMKWKKG KIYIGTPNGTLKTPLA/EDEID/EFSKE MGHFLKPDGPCKIIGKVWWHEKGM NDK |
| 2099 | 7596 | A | 2270 | 271 | 404 | |
| 2100 | 7597 | A | 2271 | 2 | 5684 | PTSPCGEGYGISLNLTFIISNMRVLR AHFIELQFPFMGQVVTGTQNSEQN LGPQAIPQDGSITHQISRPNPPNFGP GFVNDSSQRKQYE/EWPQETQQLLQ MQQKYLEEQIGAHRSKKKALSAKQ RTAKKAGREFPEEDAEQLKHVTEQ QSMVQKQLEQIRKQQKEHAELIED YRIKQQQQCAMAPPTMMPVSQPPQ PLIPGATPPTMSQPTTFPMVPQQLQH QQHTTVISGHTSPVRMPSLPGWQPN SAPAHPLPLNPPRIQPPIAQLPIKTCTP APGTVSNANPQSGPPRVEFDDNNP FSESFQERERKERLREQQERQRIQL MQEVDRQALQQRMEMEQHGM VGSEISSRTSVSQIPFYSSRLYLCDF \MQPLGFLQSQSPQHQQQMGQVLQ QQNIQQGSINSPSTQTFMQTNERRQ VGPPSFVPDPSIPVGSPPNFSSVKQG HGNLSGTSFQQSPVRPSFTPALPAAP PVANSSLPCGQDSTITHGHSYPGST QSLIQLYSDIPEEKGGKKRTRKKKR DDDAESTKAPSTPHSDITAPPTPGIS ETTSTPAVSTPSELPPQADQESVEPV GPSTPNMAAGQLCTELENKLPSNDF SQATPNQQTYANSEVDKLSMETPA KTEEIKLEKAETESCPGQEEPKEEQ NGSKVEGNAVACPVSSAQSPPHSA GAPAAKGDSGNELLKHLKKNKKSS SLLNQKPEGSCSEDCTKDNKLVE KQNPAEGLQTLGAQMGGFGCGN QLPKTDGGSETKKQRSKRTQRTGE KAAPRSKKRKKDEEEKQAMYSSTD TFTHLKQVRQLSLLPLMEPIIGVNFA HFLPYGSGQFNNGNRLGLTFGSATL EGVSDYYSQLIYKQNNLSNPPTPPA SLPPTPPMACQKMANGFATTEELA GKAGVLVSHEVTKTLGPKPFQLPFR PQDDLLARALAQQPKTVDPASLP TPPHNNQEELRIQDHCGDRDTPDSF VPSSSPESVVGVEVSRYPDLSLVKE EPPEVPSPPIIPSTAGKSSESRRND IKTEPGTLYFASPFGPSNPGPRSGLIS VAITLHPTAAENISSVVAAFSDLLH VRIPNSYEVSSAPDVPSMGLVSSHRI NPGLEYRQHLLLRGPPPGSANPPRL VSSYRLKQPNVPFPPTSNGLSGYKD SSHGIAESAALRPQWCCHKVVLG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SGVRKSFKDLTLLNKDSRESTKRVE KDIVFCSNNCFILYSSTAQAKNSEN KESIPSLPQSPMRETPSKAFHQYSNN ISTLDVHCLPQLPEKASPPASPIAFP PAFEAAQVEAKPDELKVTVKLKPR LRAVHGGFEDCRPLNKKWRGMKW KKWSIHIVIPKGTFFKPPCEDEIDFL KKLGTSLKPDVPVKDYRKCFCHEE GDGLTDGPALLNLDLDLWVHLNC ALWSTEVYETQAGALINVELARR GLQMKCVFCHKTGATSGCHFRCT NIYHFTCAIKAQCMFF\KDKTMLCP MHKPKGIHEQELSYFAVFRVYVQ RDEVRIASIVQRGERDHTFRVGLI FHTIGQLLPQQ\MQAFHSPK\ALFPV GYEA\SRLLGGTRYANRRCRYLC SIEGGRDG\RPVFVIR\IVGNKGHGR TGV\KVD\SPKGVWDKILEPVACV RKKSEMLQLFPAYLKGEDLFGLTVS AVARIAESLPGVEACENYTFRYGRN PLMEPP\AVNPTGCARSEP\KMSAH VKRFVLRPHTLNSTSTSKSFQSTVT GELNAPYSKQFVHSKSSQYRKMKTA EWKSNVYLARSRVSGGWGLLWL VRR\LEETHHGSFEYIGTNHFETKL GQQGKEKLYESQNRGVYMF\RMND DHVIDATLTGGPARYINHSCAPNCV AEVVTFERGHKIISSSRRIQKGEELC YDYKFDFEDDQHKIPCHCGAVNCR KWMN |
| 2101 | 7598 | A | 2272 | 1 | 2806 | |
| 2102 | 7599 | A | 2273 | 288 | 843 | AGSGVLQGLFICPKAPGPRPTGAEG KR\KLQIGVKKR\VD\HCPKSRK\GD VLHMHYTG\KLEDGT\EFDSKPAPR TSPFVFS\GTGQVIK\WDQG\LCL GMCEGE\KRKL\VIPSELGYGE\RGE LPPKIPRPVQPLVFEVELLKIRADEL SCNQTGEGQGEKAPHQGPDCSKKK NKKQKPIKKT\KSPK |
| 2103 | 7600 | A | 2274 | 80 | 308 | VLTHLGNWILGSTEGPMGGP*FCTN LSEGLRFGISPSWREALYGWHA |
| 2104 | 7601 | A | 2275 | 2 | 456 | RSFFFFFCEVGSWVGS\MRVVMARL LSEGEQGIPTACAFAQQPGGRPRR GLAGVGEGGPQCSWVNYRCTLEFL VSLLGTDLARGRGNSASGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCHVV QGWVSTSWGSSSPVPQFFPKLLEF TGK |
| 2105 | 7602 | A | 2276 | 2 | 81 | |
| 2106 | 7603 | A | 2277 | 325 | 485 | ELRVDPVNF\KL\LSHCLLVTLAAHL PAEF\TPAVHASLDKFLASVSTVLTS KYR |
| 2107 | 7604 | A | 2278 | 291 | 529 | LFL\CKVGTWHQGP\NHQKAPKAPG TPPTPSYPGT\PSRQLLWQWVQRP LPA\PLPAVGTSS\TPGRQCPGFSAQ HHLFP |
| 2108 | 7605 | A | 2279 | 52 | 109 | TVRLPR\HPGSRKNMASYCRIPACIA AERRYGTCMYQGR\WAFSS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2109 | 7606 | A | 2280 | 3 | 452 | |
| 2110 | 7607 | A | 2281 | 26 | 526 | NSTDSETHPWLLSPADKTTVK/AP AWGKVGHAHAGEYGSEALERMFLS FPTTKTYFPHFDLSHGFCPGLRATG KKVADALTKRRGAPLDDMPNALV RPLASDLHAHKL\RVGPGSTFKLLKP LACL\LTGPAHLPRPSFTPGGCKAS LGQSFLGFLKHRCLNLPNYR |
| 2111 | 7608 | A | 2282 | 447 | 539 | |
| 2112 | 7609 | B | 2283 | 8 | 694 | MQYNRRFVNVVPTFGKKKGTTFTK IFVGGLPYHTTDASLRKYFEGFGDIE EAVVITDRQTGKSRGYGFVTMADR AAAERACKDPNPIIDGRKANVNLA YLGAKPWCLQTGFAIGVQQLHPTLI QRTYGLTPHYIYPPAIVQPSVVI PVPSSLSPYIEYTPASPVYAQYPPAT YDQYPYAASPATADSFGYSYPAA VHQALSAAAPAGTTFVQYQAPQLQ PDRMQ* |
| 2113 | 7610 | A | 2284 | 3 | 191 | |
| 2114 | 7611 | A | 2285 | 101 | 444 | CSLFVPRPSRLQPLRRVTGQETGRP RSKAHVASTWRAFPPEQVVLLAG APLEDEATLGQCGVEALTTEVTG \RMLGGKSPWFPWPVLGKVMKVRL LKVAKQGERRKKKTGSG |
| 2115 | 7612 | A | 2286 | 2622 | 2881 | KKSKDNKTTTTFETESCSALQAGV QWCNLGSLQTL\PGSNDSSHASR VAGTKGMCHHARLIFVFLVETGLH HVGQACLGTPLK |
| 2116 | 7613 | A | 2287 | 41 | 655 | TKLVMMQKLLKCSRLVLALALILV LESSVQGY\TRKPRHQWVPCNPDS NSANCLEEKGPMFELLPAE\STKIPR L\RTDLFPKTRIQ\DLN\RIPLSEDYS GSGFGSGSGSG\SGS\GSWFPNGKW EQDYQL\VDE\SDAFHDNLR\SLARI LASASRDWQHGLAEFNVIKEDL PTLTTRQMVKQYFNVPMVNMINS WDKEFYRNF |
| 2117 | 7614 | A | 2291 | 163 | 703 | READMGTMKTQRDGHSLGRWSLV LLLGLVMPLAIIAQVLSYKEAVLR AIDGINQRSSDANLYRLDLDP MDGGP\DTTK\PVSFVTKETVCPRP TQQSPKDGDFKRDGLNRMGMGTV\ TLN\QARGSFDISCDKNRKFALLG DFFRKSKEKIGKEFKRIVQRIKDFLR NLVPTES |
| 2118 | 7615 | A | 2292 | 100 | 546 | PPRTGQRQPLHSARRHGSPVS\ELAC \YSALISARTDEVTV\EDKINAL\K A\AGVNVE\PFWPWLCLQRPLA\NV NIG\SL\CNVRGPVEPAPSSLVAAP AGRSLPPPLACCSKLKEERKLEAKK RKNPKEVLNDDIGLLVLFELKPLL |
| 2119 | 7616 | A | 2293 | 33 | 494 | |
| 2120 | 7617 | A | 2294 | 1 | 609 | PLKRS DGCNDGRPTRPPTRPDTTVF TSNLKQTRMVHLTPEEKSAVTALW GKVNVDVGGGALGRLLVVPWT QRFFESFGDLSTPDVVMGNPKVKA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HSKKGLRGAFSDGLAHL\DNLKGT FATLASEL\HCDKAAPWIPEELQAPW ATCLVCVAWPITFGKRISTPPVAGL PNQENWLAWCWLNALGPTSNHLS LAFLAGPISN |
| 2121 | 7618 | A | 2295 | 1 | 338 | AALAWAVSRLHFSRLSFPPWAFRG AFAAVPTTAAMISLTDQKIGMGLT GFGVFFLFFGMILFFDKALLAIGNG\ FFPVVDGFIIRVPVLGSLNLPGIRS FVDKVGESNNMV |
| 2122 | 7619 | A | 2296 | 67 | 283 | LPFPGCFFLF*VLFVAGLAFVIGLER TFRFFQKHKMKATGFFLGGVFVV LIGWPLIGMIFEIYGFFLLFR |
| 2123 | 7620 | A | 2297 | 3 | 209 | |
| 2124 | 7621 | A | 2298 | 3 | 544 | TRAALAVAVSRLHFSRLSFPPWAFR GAVAAVPTTAAMISLTDQKIGMG LTGFGVFFLFFGMILFFDKALLAIGN VLFVAGLAF\VIGLERTFRFFF\QKH KMKATGFFLGWVYLVVLIGL/WPLI GMIFEIYG\FLLFRGFFPCRCWTFI RKECPVLGIPSPNLPGIRSFVDKVG ESNNMV |
| 2125 | 7622 | B | 2299 | 54 | 1731 | XKLSRECEIKYTGFRDRPHEERQAR FQACRDRGRSEIAFVATGTNLSLQF FPASWQGEQRQTPSREYVDLREA GKVYLKAPMILNGVCVIWKGWIDL QRLDGMGCLEFDEERAQQEDALAQ QAFEEARRRTREFEDRDRSHREEME VHELEKSKRALETQMEEMKTQLEE LEDELQASEDAKLRLEVNMQALKG QFERDLQARDEQNEEKRRQLQRQL HEYETELEDERNERLAAAANKKL EGDLKDLELQADSAIKGREEAIKQL RKLQAQMKDFQRELEDARASRDEI FATAKENEKKAKSLEADLMQLQED LAAAERARKQADLEKEELAEELAS SLSGRNALQDEKRRLEARIAQLEEE LEEEQGNMEAMSDVRKATQQAE QLSNELATERSTAQKNESARQQLER QNKELRSKLHEMEGAVKSKFKSTIA ALEAKIAQLEEVEQEQAREKQAAT KSLKQKDKKLKEILLQVEDERKMA EQYKEQAEKGNARVKQLKRQLEEA EESQRINANRRKLQRELDEATESN EAMGREVNALKSKLRGPPQETSQ* |
| 2126 | 7623 | A | 2300 | 1 | 2448 | |
| 2127 | 7624 | A | 2301 | 1 | 2655 | |
| 2128 | 7625 | A | 2302 | 5 | 605 | VDPDSGQIQVPCTPRGLKWSPNMN PARKTDACGEDTHPSLLGVFFSRPP LGILRFALQNPRSPGKESEMLPPPA WVYLKAPMILNGV/CVIWKGWIDL QRLDG/MGCLEFDEERAQSWPW*A HPQC*EGRRPSCRELGNVALGADG DSPGSIYTRRWKLRSQVRPAPPQE PKMPSLCCRNTSTTFSGRPSQSPRTK KQRPR |
| 2129 | 7626 | A | 2303 | 1 | 588 | MGFCHVDQTGLELLTQPLLALIGAA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LEGGRAGGAADLAPDFGRLALQIK YTGFRDRPH/EERQARFQACRDGR SE/IFFPASWQGEQRQ/TPSREYVDL EREAGKLNIPKGPAGDETPSSLSSM MIVLSSDSGPAVLAIPNLVTPPRYTP MVPCGGHHQAQRKRPLCTPPPSIQ QGSMSVKSMPTPVAAHKSFTSALC |
| 2130 | 7627 | A | 2304 | 1 | 615 | GLKGGKMPRVVPDQSRKFENEFF RKLSRECEIKYTGFRDRPHEERQAR FQACRDGRSEIAFVATGTNLSLQF FPASWQG\DQRQTPIREYVDLREA GTVYLKAPMILNGVCAIWKGWIDL QRLHGMGCLEFDEERAQQEDALTQ QAFEEARRMTREFEDRDRSHRQEM EARVSQLLA VTGKK\QLDPRPGSNL GGDDLKLR |
| 2131 | 7628 | A | 2305 | 73 | 168 | |
| 2132 | 7629 | A | 2306 | 322 | 671 | RLWASPAAPGKKKEMGNSMKSTP APAERPLPNPEGLDSDFLAVLSDYP SPDINPPIFRERGEKLRVISDERGWW KA\SLSTGRESYIPACVARSYHGW LLRGPG\KNMAEELLQLPD |
| 2133 | 7630 | A | 2307 | 624 | 1581 | KAATSENKIICCEWRTSQAALMLHR LWASPAAPGKKKEMGNSMKSTPAP AERPLPNPEGLDSDFLAVLSDYSP DISPPIFRERGEKLRVISDEGGWWKAI SLSTGRESYIPG\ICVARV\YHGL/W LFEGLGRDKAEELLQLPDTKVGSF MIRESETKKGFYSLSVRHRQVKTY RIFRLPNNWYYISPRLTFQCLAE DLV NHYSEVADGLCCVLTTPCLATQSTA\ APAVRACSSPVTLRQKTVDWRRVS RLQEDPEGTENPLGVVESLFSYGLR ESIASYLSLTSEDISSFDRKKKSISLM YGGSKRKSSFFSSPPYFED |
| 2134 | 7631 | A | 2308 | 52 | 454 | SQTQREPTMVLSPADKTNVAAA/W GMFLSFPTTKTYFPHFDLSHGSAQV KGHGKKVADALTNVAHVDDMPN ALSALSDLHAHKL RVDPVNFKLLS HCLLVTLAAHLPAEFTPAVHASLDK FLASVSTVLTSKYR |
| 2135 | 7632 | A | 2309 | 3 | 452 | |
| 2136 | 7633 | A | 2310 | 26 | 502 | NSTDSETHHGARLLPDKTKAQRPP RLKLGANA\GEYGFGGPWKGMFLS FPNPPKTYFRQFRP*ANGFAQG*RG HGQRKVA\DAL TQSPCRNVD\MPQ TALSAP EATLHG\HKL\ RVDPVNFKL \LSH\CLLG*PWPAHLPRPSFTPCGCT PSLEQSSWAF C |
| 2137 | 7634 | A | 2313 | 43 | 595 | LRNMWQLERN\IET\INTFHQYSVK LGHP\DTL\NQGEFKELVRKDLGQN FLKKENKNEK VIEH\IHEDLDT\NAA Q\QLSFEEFIMLMARAKPGALPTRR MHEGDKGPWPPPHKPGLGEGTPPR PQWPRSPVATAHGHKSWWPRPQA TNHGGQATLPLPKPGPRGLLCQTVL AVGLGGWGQIKSLP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2138 | 7635 | A | 2314 | 3 | 419 | SLYHNSSQKRHWTFSSSEQLARLRA DANRKFRCCKAVANGKVLNDPVFL EPHEEMTLCKYYEKRLLEFCSVFKP AMPRSVVLTCAFLACKVDEFNVSN PQFVGNLRESPLGQEKALEQILEYE LLLIQQLNFHLIVHN |
| 2139 | 7636 | B | 2315 | 324 | 487 | MQRVRAGRIVITTAQRRLPDALG FREIFSSEQLARLRADANPNDAK PWPTGS* |
| 2140 | 7637 | A | 2316 | 1 | 1050 | |
| 2141 | 7638 | A | 2317 | 191 | 229 | |
| 2142 | 7639 | A | 2318 | 186 | 1232 | CVWVLVCRPSGPGHDSIMYHNSSQ KRHWTFSSSEQLARLRADANRKF CKTRAH\GKVFPNDPVFLEPHEVMT LCKYYEKRVIEFCSVFKPAMPRSV VG/SRACMYFKRFYLNNSVM\EYHP RL\IML\TCAFLACKVDEFNVSSPQF VG\NL\RESPLG\QEKALEQILEYELL PYTSNFNHFL\VHNPHY\RPFEGFLND LRTR\YPILNPEILRK\TA\DDFLNRI ALTDAYFLYTPSQ\IALTAILSSASRA GITMESYLSESLMLKENRTCLSQLL DIMKSVRN\LVKKYEP\PRSEEVAVL KQKLERCHSAELALNVITKKRKG EDDDYVSKKSKHEEEEWTD\DLV ESL |
| 2143 | 7640 | A | 2319 | 152 | 371 | DVLLATSSSEPSLFCPLCLTASTPKP LPPPG\PLPCPVWAMWGTGGFPLPG PPGQPRVRGPTAARGTPCCRPS |
| 2144 | 7641 | A | 2320 | 4 | 474 | PQYPAWHEGERAEWLCGRVSETGS ACSMADQL\TLKEQIAEFKEAFSL\F DKDGDGTITTK\ENLGTVNEILLGSN PTEAELQDM\NEVDADGNGTIDFP\ EFLTMMARKMK\DTDSEGRKL\EEA FRVFGLRVGNGLYL\ACRNFHRV DGQTLGGGSLPD |
| 2145 | 7642 | A | 2321 | 291 | 648 | LTQLKTHCPLIKSKTMNKKRAIREP AQEPGPQKEENPKKHRSPSFTSTSP GLEVPASYSPTKAEQPGQVRKAV QPAVRLEPRASHPAGPPVPPSGVLV SRRRPEPGQGKPPESDFDH |
| 2146 | 7643 | C | 2322 | 155 | 316 | MTGPVSGSFIHWVLFSGFSSMSSNA SNVFGLVVRPSCCTGLSRMAADSAG CCSL* |
| 2147 | 7644 | A | 2323 | 28 | 1323 | PSGARVAGAGPCGGGGMFVQEEKI FAGKVLRHLHICASDGAEWLEEATE DTSVEKLKERCLKHCAHGLSKDPK SITHHKLIIHAASERVLS\DARTILEENI QDQDVLLLIK\RAP\SPLPKMADVS AEEKKK\QDQKAPDKEGILG\ATAN LPSNKLDRAAVQTNMRDFQTELK ILVSLIEVA\QKLLAL\NPDA\VELFK EGECNCWDEDGGMSVWDEACPA FQREMGLFRENRA\TKALQLNHMS\ VPQAIGSWL\NEHA\EDPTIDTPL\PG QAPPEAQG\ATAAASEAAAGASAT DEEARDELTEIFKKIRRKREFRADA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RAVISLMEMGFDEKEVIDALRVNN NQQAACEWLLGDRKPSPEELDK GIDPD\SPL\FQAIWDTRWVQLGLTN PKTLAFEDMLENPLNSTQWMNDP ETG\PVMLQISRIFQTLNRT |
| 2148 | 7645 | A | 2326 | 307 | 412 | SVQTIVFQPQLASRTPTGQS*SSCPY PLFATINAE |
| 2149 | 7646 | A | 2327 | 50 | 247 | |
| 2150 | 7647 | B | 2328 | 276 | 779 | MRTLAILAAILLVALQAQAEPLQAR ADEVAAAPEQIAADIPEVVDSFAW DERAPLQVSGKSSPVCARLLLQET RDRGLLFALPLHSAYLEDLLRQSHF RQELMKLQPRSSLEQMIRKWLMP HGMKVPLFRFPDKIIVLSTLIPTGD YSPHNLKNLFMRMVTPSP* |
| 2151 | 7648 | A | 2329 | 3 | 333 | |
| 2152 | 7649 | A | 2330 | 35 | 717 | RRSSPSLLPLAERGGARARGRPERA PHPSTPATRTAPPPWARRMMKLKS NQTRTYDGDGYKKRAACLCFRSES EE\EVLLVS\SSR\HPDRWIVPWKEG MEARRKEAKCGKQVREVCEGRG VKGTLGRLVGIFENQERKHRTYV\ YVLIVTE\VLEDWEDSVNIGRKREW FKIEDAIKVLQYHKPVQASYFETLR QGYSANNGTP\VVAATTYSVSGFRA SMFRAFRWT |
| 2153 | 7650 | A | 2331 | 104 | 381 | IQGGSMTSSSFSTICQKILNKEKQS CCSN*SKWSRNVSSNGKPNWTGTS LPALTEMARTTIWKKHIFTKKFSSV SIFQVFKSF*I*GSVLS |
| 2154 | 7651 | B | 2332 | 228 | 445 | METSSRELQAAEYLEKHQIKEVVSY LTSALLFLRPALKTLGLCTEDEDLQ DDGHKITLDKFKEEVNKRMEIX* |
| 2155 | 7652 | A | 2333 | 3 | 1459 | GSKQVSEGTDNGLPSYVSFAFIEKE VGNDLKSLLKLDKLIEQRTVSKMQ LEEQVLTISSEIPKRIRSALKNAEESK QFLNQFLEQETHLFSAINSHLLTAQP WMDDLGTMISSQIEIERHLAYLKWI SQIEELSDNIQQYLMTNVPEAAST LVSMALDIKLQESSCTHLLGFMRA TVKFWHKILKDKLTSDFEILAQLH WPFIAAPPQSQTVGLSRPASAPIYSY LETLCQLLKLQTSHELLTEPKQLPE KYSLPASPSVILPIQVMLTFLQKRFR YHFRGNRQTNVLSKPEWYLAQVL MWIGNHTEFLDEKIQPILDKVGSV NARLEFSRGLMMLVLEKLATDIPW LLYDDNLFCHLVDEVLLFERELHSV HGYPGTFASCMHILSEETCFQRWLT VERKFALQK\MDSMLSSEAAWVSQ YKDITDVDEMKVDPDAETFMTHLL VITDRYKNLPTASRKLQFLELQKDL VDDFRILINTK |
| 2156 | 7653 | A | 2335 | 46 | 1146 | |
| 2157 | 7654 | C | 2336 | 17 | 196 | MTTLVTTTTMDMVIIATSRVVMGR YPGEVVIIKATNHTKLFHLQLIPNSG NFIAGPVS* |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2158 | 7655 | A | 2337 | 208 | 1504 | FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSAESEGA KIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEVESIELPMDNKTNRKR FCFITFKEEPPVKKIMEKKYHNVGL SKCEIKVAMSKEQYQQQQWWSR GGFAGRARGRGGGPSQNNWQGY NYWNQGYGNYGYSSPRLRWLWRI *LHWLPTTTYGYGDYSNSQSGYK VSRRGGHQNSYKPHLNY SICNL PTGGEAVFSNLKIQFESGS/CH*LLI AVQTKFLYQVPEWKYDVGSL |
| 2159 | 7656 | A | 2338 | 208 | 1466 | FRFAAGGCSLGGSGGDTSTMSEEQF GGDGAAAAATAAVGGSAGEQEGA MVAATQGAAAAAGSGAGTGGGTA SGGTEGGSAESEGA KIDASKNEEDE GHSNSSPRHSEAATAQREEWKMF GGLSWDTTKDLKDYFSKFGEVVD CTLKLD PITGRSRGFGFVLFKESES DKVMDQKEHKLNGKVIDPKRAKA MKTKEPVKKIFVGGLSPDTPEEKIR EYFGGFGEWDPIELPHGQTRPNKRR GFCFITF*G\EEPVKKIMEKKYHNVG LSKCELK\VA\MSKEQYQQ\Q\QQW DSRGGCAGRA\RGRGGDQ\QSGYG K\VSRRGH\HQ\NSYKPYLNY SICNL SPTAGTSLQALCRADFRFSQARSMR TG*RDAPRSRMLPFGGEAVFSNLKI HL\NGGSCHLLIAVQTKFLYQVPE WKYDVGSL |
| 2160 | 7657 | A | 2339 | 1070 | 1238 | PQRDFQFFLLWPPGGEA\VFSNLK\IP FERGSCHLLIAVQTKFLYQVPEWK YDVGSL |
| 2161 | 7658 | A | 2342 | 1 | 456 | RPRRPQREPTMVLSPADKTNVKAA WGKVG AHAGEYGAEALE/RMFL/SF PTTKTYFPHFDLSHGSSQVKGHGKK VADALTNAVGHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHAFLDKFLASVS TVLTSKYR |
| 2162 | 7659 | A | 2343 | 2 | 512 | GLEFGTSHRLRENPPWCLSPA\DKT NVKA\AWGKVG AHAGEYGAEALE RMFLSFPTTKTYFPHFDLSHGFAQ VKGATAKKVA\DALTKAVAHGRGT CPNALSALSGPATAHKL\RVGPGST FKLLKPLACLVDPGPAHLRPSFNP WRLQGFLGTFKFLGFLVEAPLLEPSK |
| 2163 | 7660 | A | 2344 | 265 | 426 | SFSISVFAACLALPMAQPQ*PCSQK V*QHCRVYMHAAHTWPLCLQDVLV ECCSQS |
| 2164 | 7661 | A | 2345 | 56 | 341 | IVTLDWSRNLKYNRCWSKCYILSSS DSSSFRDSFTNPAEF*FKSFILNFV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MYVYVNYFCNFFNDITAGHFFHLKL LYFRLCSLPGFADGTAPITV |
| 2165 | 7662 | A | 2346 | 333 | 534 | LMEDMKLFQKI*EKKQRNMLRNL* RKKMNQMM/YNM*HLLQHLLYFK FLL\HPM*LFSPGLYILSNFH |
| 2166 | 7663 | C | 2347 | 117 | 386 | MDILICTDFGSVNYFNVWRLPKSYL SLFYRSRIYIVHDEVKDKAFELELSW VGELTNGRHEIVPKDIREAEKYAK ESLKEEDESDDDNM* |
| 2167 | 7664 | A | 2348 | 2 | 359 | FEDGVLLCHPRLEGSVTISAHCNLS LPGFKRSSCLRLPSSWDYRNMPY PGYFCIFGFTNNTETGFHQASFKLL NSRDLP TLAPVKCWDYRHEHCTRP LKYIFYQRYSHCMLEQHLLN |
| 2168 | 7665 | A | 2349 | 648 | 887 | SWKLLLLLCLKNEHLPTK PATGHS NIADQTLKKSFCLEPFFHKV*KGLIF LTPRTTSLHLPIA VLLFSTAFIAYS T |
| 2169 | 7666 | A | 2350 | 306 | 449 | EIKKKYLLPGVVAHACKPSTLGGR GGQIISGQEFETSLTNMAKPCFF |
| 2170 | 7667 | A | 2351 | 1 | 625 | NFALEAKNSARAISYVQTPMGHFT RGGPRLTITSLWGK\VNVE\ DAGGE TPGKGS LVVYP\WT\QRFFDSFGNLS SAFCPSWPTPKVKAHGK\KVL\TSLG DAHKSTWDDLKGHLLPKPEVNLHC \DKPAMWDPENFKAPGEMCLVTRF GQSLFRQKNFTPEGCRASLGKKDG ELQLASCPGPSQITTEASWPMNSEA FKDKAFILASNYK |
| 2171 | 7668 | A | 2352 | 1324 | 1671 | IVQTLSTLSKSSCRSTEPCTSLPDL QVGTTCTRPHGTCC/NRCHVGGLMN PLKPNC/GCRKCNCGYLYIYLGQR LHPRGKFQPGNNHRFSCTQSVHMDI THGSGMFSLCFPGSTMF |
| 2172 | 7669 | A | 2356 | 8 | 564 | SAQMAVTTADPRVRPRVRTQLCSL ASLIQTLVHLTPEEKSAVTALWGK VNVDE\VGKALGRLLVVYPWTQR FL\ES\FGDLSTPNAV MANPKVKAHS \KKI\LGALLVVGLAHL\DNLKGTF HTEVSLHCDKLHV\DPENFQAPGAT CLVLCAWANHF\WQKNFTPPV\QAC LFRKLVAG\VANALAHK |
| 2173 | 7670 | A | 2357 | 23 | 679 | GLLTSGGAHLSPSRVTQGIYYMSAL SEMPKPPDYSELSDSLTAVGTGRF SGPLHRAWRM MNFRQRMGWIGV GLYLLASAAAFYVFEISETYNRLA L\EHQQHPEEPLEGTTWTHSLKAQ LLSLPFW\WVWDSYFFWVPLYLQMFF VSLYSCYKELDPQNSGGYCPSPIW LWAVYFGNRHHAF\VKASNSDSA DLQLIDTVKSVTRFFPLRJTGTQS |
| 2174 | 7671 | A | 2358 | 17 | 392 | SFKMADQDPAGMSPLQQMVASGT GAVVTSLSFMTPLDVVKVRLQSQR SMAS\DAFVKIVRHEGTRTLWSGLP ATLVMTVPATAIYFTAYDQLKAFL CGRALTS DLYAPMVAGALARREHR LGPLTS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2175 | 7672 | A | 2359 | 1 | 725 | RFTGTMDAFVKIVRHEGTRTLWSG LPATLVMTVPATAIYFTAYDQLKAF LCGRALTSDLYAPMVAGALARLSI VLGL*PPSVPTSAQTQSVAPSPNLC QPRDRGVF*VPRPGTAGR*CHVRPV ISLLPIVTPNPHTVGTVTVISPLELMR TKLQAQHVSYRELGACVRTAVAQGG GWRSLWLGWGPTALRDVPFSALD WFNYELVKS/WLNGLRPKDHTSVG M/SFVAGGISRTVAAELTLPY |
| 2176 | 7673 | A | 2360 | 102 | 1573 | SFKMADQDPAGISPLQQMVASGTG AVVTSLFMTPLDVGKVRQLQSQRPS MASELMPPSSRLWSLSYTKLPSSLQS TGKCLLYCNGVLAEPLYL\CPNGAR CATWF\QDPTRFTGTMDAFVKIGE ARGAPRTLWSGLPATLVMTVPATA IYFTAYDQLKAFLCGRALTSDLYAP MVAGALARLGPVELWISPLGALCS NKACRVQHVVNRNRELGIACVRTAV AQGGWRSLWLGWGPTALRDVPFS VHPPQAL\YWFNYELVRSWL\NG LRPK\DQTSVGMSFVAGGISRTVA AVLTLPF\DVVKTRQ\VALGALAE VKSEPPCNVDSTWLL\LRIRIAESG TKGTLLQASFPRNKGCPSCA\MIQ HLIEFRQKAFFPRGLNPGTGFLGGL EKGPKGKDPVSSQREWGRGQGGD PSQSAFSSALREGGLFSLPLPATKLP GQGCPSGRPSTSSRHNFLLLPVVG ITYPPPKFKTKSSELPFVFPCGLL |
| 2177 | 7674 | A | 2361 | 1 | 215 | QPMSEESDQYLAVLTFPRCVLV MIHTHAQVLNHVCIYVCVHMSVAV Y/ISACRATDPDTHTCVYMIQTY |
| 2178 | 7675 | A | 2362 | 3 | 543 | TRNTLGWEVSSFSPLLSSCLNMVRT KADSVPGTQEKVVAARAPRKGL\G SSTSAHLIRPSVSIEESLKNKYARRE PPFCVRP/TLPKWAKREIGEFFRLSP KDSEKENQ\PEE\AGSSGL\GKRQRR KSMFLLQPGFTQLMEKGLGTFLHFI FGLTSPLFYPGYSRKVKFTINGVWF QLGFG |
| 2179 | 7676 | C | 2363 | 69 | 290 | MCLWNCCRKTQLAADILWLTAPAS PRDLRLGCVAEVFLARWELFGEDSF REKFFGFFFRDGWQPFLLSAGER* |
| 2180 | 7677 | A | 2364 | 663 | 793 | DGDSVMVLPTIPEEEAKKLFPGGVF \TKELPFGKKYLRYTPQP |
| 2181 | 7678 | A | 2365 | 1 | 726 | MPGGLLLGDVAPNFEANTTVGRIRF HDFLGDSWGHSFSQ/RGGFTPWCA PRSFARAAKLAPDFAKR\NVKLIALS IAVFEDHLC/AESKDIHVYHCE/ESPT EKLPIIDDRNRELANPVGACWIP AEKDEKG/LCPVTASVWCFVFGP** RKLKAVYPSYPSYPLAGNFE*RFLR VVHLLSQLTA/EKKRVAHPQLIWKD GD\SVMVLNPNPSPEEEAKKLFPEKE SFTQKELPNLAKKYL\RYTPQP |
| 2182 | 7679 | A | 2366 | 3 | 452 | |
| 2183 | 7680 | A | 2367 | 1 | 627 | TLLVPQDSERTHPWLLSPADK\TNV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KA\AWGKVGAAHAVRSMCAEALER MFLSFPTTKTYFPFHDLSHGSAQV KGATGKKVADALTKRRGAPLDDM PNAL/SSALEATLHAHKL\RVGPGST SKLLKPLACLVDPGPAHLPRPSSTP GGCNVFPGTKFPGLFVEAPLLEPSK LPLKLGSLRLAIVFLPLWGFPAPPP LSCTRTPVVFEIKS |
| 2184 | 7681 | A | 2369 | 1 | 467 | GTSACGVASLSVDCVPAPFSQQQP LPEGERTLGGRHRLRTRARALHPAP ACFCHASLCVCM/CA/CVLVCGLLC EHQSDSIHCLCHLCLCKCNLYLCIRA ASSQHLKCHWVGGNKTCFGPDDL GGRSEPTFETLSGEPATPADGKTGS CTGPERYQM |
| 2185 | 7682 | A | 2370 | 131 | 406 | EAMGILKLQVFLIVLSVALNHLKAT PIESHQVEKRKCNTATCATQRLANF L\VHSSNNLGGILSSTNVGSNTY GK RNAVEVLKREPLNYLPL |
| 2186 | 7683 | C | 2371 | 257 | 422 | MQVCFRQGFTLPKGHHGLIATLGA POLYMFLVLRASLFLWLSXFXRSX KLXXXRN* |
| 2187 | 7684 | A | 2372 | 621 | 1202 | GVPEPRARPSTSGMNGDRIRLPCWR NDRQK\THML\DVMDHFSRASSIH RRALSRRDRFFREPQ\DTYHYL\PFQ PCPHRRPAHFFPKSRNRPA*\CPFSS \TKPLNFHAMFQPFLEMIHEGSAGP WDIHFHSPAFQHPPTEFIREGD\DDR DCCAGEN\RHNSTGLPCGLKDQVVT K\CREDLVLWDCFHQQPLPG |
| 2188 | 7685 | A | 2375 | 154 | 1702 | IGHRDPARGRSCRCSGYYSRMVCE KLAPQSEMASAG\VSLRATILCLLA WAGLAAGDRVYIHPFHLVIHNESTC EQLAEANAGKPKDPTFIPAPIQAKTS PVDEKALQDQLVLVAAKLDTEDKL RAAMV\GMLANFLGFPYMGMH ELWG\VHG\ATVLSPTAVFGTLAS LYLGALDHTADRLQAILGVPWKDK NCTSR\DAHKVLSAL\QAVTGLLVA PGRADKQA\QLL\STVVGVFTAPG LHLKQPFVQGLALYTPVVLPRSLDF TELDVAAETID\RLMQAVTGWKTG CSLTGAKADSTLAFNTYVHFQGM KGFSLLAEPQ\EFWVDNSTSVSVP LSG\MGTFQHWSDIQ\DNFSVTQVPF TD\SAFLLLIQPHYASDL\DKVEGLT FQQN\SFNWMRKLF\PRTIHLTMPQL VLQGSY\DLQDLLRPGSSCPFLHTE LNLGRISGN\DRIRVGEVLNSIFFEL EADEREPTTESTQQLNKP\EVLE\VPL TRPF\LFVY\DQGATALALSWGRV GKPA |
| 2189 | 7686 | A | 2376 | 181 | 353 | VGDRCEGNGNEARGHWKREVCCP GARSGASV*\GSSGRLGLCL*\VGTR AG*\PGYPASLVPT |
| 2190 | 7687 | A | 2377 | 1550 | 1823 | GRLLDEPQAAHKFLRGEMGGQSPG VRGTELLGAFSLPGES/GSPGRASPL PFPPNLEKTVTFQSLLGPLKIPKEG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LKEIKLTNVKKSCTLP |
| 2191 | 7688 | A | 2378 | 134 | 321 | GCF*KGRDLFADKMQEHSQ*FTAL FQPTNQKISSWVC GPKVNFKAIKTG SRSGKAIQNVES |
| 2192 | 7689 | A | 2379 | 1 | 602 | RTRASTRPSRDYGNVAVLWTRTSH RPLTEPEPRATMSHGKGTDMLEPIA APVGFLLSLLRTRGCVSEQRKLVFS GALQEA\TEHYNNHWFPEKPSRG SG\YRCIR\NHK\MTPHSRVASQ\VG LSQAQL\HQLP\SELTWVDPYEV SVYRIGEDGSICVLYEAPLAASCGA SFT/CARNQVACWGRSSPSK\NYVM AVSS |
| 2193 | 7690 | A | 2380 | 28 | 423 | SKPLKMADDLDFETGDAGASATFP MQCSALRKNGFVVLKGRPCKIV*M STSKTGKHGHAKVHLVGIDIFTGKK YEDICPSTHNMDVPNIKRNDFQLIGI QDGYLSLPQESGGGIRDPLNLQRPP PRAWPGSG |
| 2194 | 7691 | A | 2381 | 1 | 930 | |
| 2195 | 7692 | A | 2382 | 171 | 695 | NRQDDLDFETGDA\GASATFPMQC SALRKNGFVVLKGRPCKIVEMSTSK TG\KHGHAK\VHLVGIDIFTGK\KYE\ DICPSTHD\MDVP\NIKRNDFQLIGI QGWGTLSL\Q\DSGEVREDL\RVSP EGDL\GKEIEQKYDCGEEILIP\LSA\ MTEEAA\VAIKAHGKITGSPGVAVV ASK |
| 2196 | 7693 | A | 2383 | 789 | 1380 | IPYFLMVYGLQTLCKHITRRIRDH LHEAMNYFLIPSSPFLEANPPPPTPG TICPAC/YPPPPRAGQQLACFLSIPPL FPNLPIPPQKKDYWVLLSLGAPKFK GYLVLCMLQEPCRKQPGKSTGWI RNYPSWMHLATSTPQLRRGSKEVH NYKTMGSRPQKRYETGPGTQGGAE RILLSKPGRWRGSPGQEQVLGLQ |
| 2197 | 7694 | C | 2384 | 248 | 433 | MSGILVLNLFLLTGLSVGPSSSVTLV LSVHQLPACAKLEKGNLHPCPNSS FPPRDFCVHPP* |
| 2198 | 7695 | A | 2385 | 1 | 1108 | |
| 2199 | 7696 | A | 2386 | 1 | 1528 | MGTRAARPAGLPCGAENPARRRLA LGARQQIHSWSPRTPTSTRLTAPAGP ARGVARPAMAPDPVAAETAAGQPT PRYFTWDEVAQRSGCEERWLVIDR KVYN\INEFTRRHPPGSRVISHYAG QDATDPFVAFHINKGLVKKYMNSL LIGELSPEQPSFEPTKNKELTDFRE LRATVERMGLMKANHVFFLLYLLH ILLLDGAAWLTWVFGTSFLPFLLC AVLLSAVQ\AQAGWLQHDFG\HLS VFSTSK\WNHLL\HHFVIGHLKGA SWRNHMHFQHAKPNCFRKDPDIN MHPFFFALGKILSVELGK\RKKKF M PYNHQBKYFFLIGPPALLPLYFQWY IFYFVIQRKKWVDLAWMITFYVRFF LTYVPLLGLKAFGL\FFIVRFL\ESN WVFWVTQMNHMPMHIDHRNMD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WVSTQLQ\ATCNVHKSC/AFNDWV SVG\HFNQIEHHLFPTMPRHNYHK VA\PLVQSLCAKHGIEYQSKPLLSAF ADIIHSLKESG\QLWLDAYLHQ |
| 2200 | 7697 | A | 2387 | 45 | 949 | APWWYHPERLLGYPIAATLPSRL VLPGEVEPSTQWCSPLRLEPQFHLL PLQHLRRDSSSLSPPLPALGRTRGRR SSAPAHGDESCSLLPRPLSLAHGEP GGRRAEACSRLSRSRGRHSMTEPR STSASAAHAAAFCCFCCCRPPRPRP LAPPPP*PCR*SRRGCAGIDGAAAD VALGHPPE/HCPVPDVQMTSRRLMF IQLSQSPGVHCTSPHFSAPPTWCRR GPGSPATSPPLHTLPAVVAAPRAL RRAADRGRGRGLDRGVACAAERL QRQQLSRQSQSRSEAQPDAMEQ PRKRW |
| 2201 | 7698 | A | 2388 | 804 | 985 | VGGDSQDLRDPVPPQTAPPPNSLS PPALSPRCASPSYPQKCLP/PPVTHR SACLSSAHRTHKKGQELVTG |
| 2202 | 7699 | C | 2389 | 258 | 461 | MSVTFI\AVARGK\FFENLGHSELPL SLEWQTS\DGVEARGSRGGEALPR PGSMQPCPADVTRRPTRP* |
| 2203 | 7700 | A | 2390 | 1 | 370 | GTRVTSGGGSRRPGMAAWSPAAA APLLRGIRGLPLHHRMFATQTEGEL RVTQ\MLKRKVSPRLQLIKVTDISGG CGA\MYEIKIESEEFKEKRTVQQHQ MA\NQALKEEIKEMHGLRIFTSPVK R |
| 2204 | 7701 | A | 2391 | 1 | 1107 | |
| 2205 | 7702 | A | 2392 | 1 | 1230 | |
| 2206 | 7703 | A | 2393 | 1 | 908 | |
| 2207 | 7704 | A | 2394 | 177 | 934 | PGLSQEP\SGSMETVVIVAIGVLATIF LASFAALVLVCRQRYCRPRDL\Q RYDSKPIVDLIGAM\ETQSEPS\ELE L\DDVVITNPHIEAIL\ENEDWIEDAS GLMSH\CIAIL\KICHTL\TEKL\VCHD NGALGAKMKTSASVSDIIVVAKRIS PRVDDVVKSMYPPLDPKLL\DART TALLSV\SHLVLVTRNACHLVTG\G LDWIDQSL\AAEEHLEVLREAAL\ ASEPDKGLPGP\EAFLQEPVLQFSAY RPAA |
| 2208 | 7705 | A | 2395 | 1 | 333 | GTRGERKAGLARGQVCGLSPPFPKT NKESFPNSQLNPFWNY\CGASLSLV SFSCPATRLCGNALLPSLFFSMRGF GLAVRIRDND\SRLLSRMTSMCSISR VPEHVEFPNPK |
| 2209 | 7706 | C | 2396 | 7 | 279 | MXKGS\PRXNFLECEKKSGQNPWAG LLRPWWVGHP\SAKPLIPVFSSISFPL YNPHFP\IXILCNKLKSHVCKKASKY TNNPISQQWTL\SF* |
| 2210 | 7707 | A | 2397 | 35 | 416 | SRAVEFVRSCAGYGERKAGLARGQ VCGLSPPFPKTNKESFPNSQLNPFW NYVWGLGPCGASLSL\VSFSCPATR LCGNALLPSLFFSMRGFGLAVRIRD NDSRLLSR\MTSMCSISR\PEHVEFP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NPK |
| 2211 | 7708 | A | 2398 | 3 | 344 | |
| 2212 | 7709 | A | 2399 | 1 | 1359 | |
| 2213 | 7710 | A | 2400 | 1 | 463 | LAQAACGPAALQLCPAGHGAAMA ATFFGEVVKAPCRIAGTEDEEEEE GRRETPEDREVRLQLARKREVRLLR RQTKTSLEVSLEKYPCKFIIAIGN NAVAFLSSFVMNSGVWEEVGCACL WNEWCRTTDTTHLSSTEAFCVFYH LKSNPVFLCQCSCYVAEDQQYQW LEKVFGSCPRKNMQITILTCRHCT DIKTSESTGSLPSPFLRALKTQNFK DSACPLLEQPNIVHDLPAAVLSYC QVWKIPAILYLCYTDVIGLDFITVE AFKPILSYR\SLKGLV\KNIPQSTEIL KKLMTTNEIQSNIYT |
| 2214 | 7711 | A | 2407 | 160 | 441 | |
| 2215 | 7712 | A | 2408 | 107 | 691 | RTAILSRLMKIFLPVLLAALLGVERAS SL\MCFSCLNQKSNLY\CLKPTICSD Q\DNV\CVTVSASAGIG\NLVTFGH SL\SKTCFPCLAPFPEGRSMLGVAS MGHSAFCQSFLVAIFSCGPMAGLRG KRSPLLGARACCLSLAGRALL\RFG PLDRPEPCSPDPPAQEGKPSFWIPQ CMGAPDSSRALICALGPRSG |
| 2216 | 7713 | A | 2409 | 2 | 432 | GRPPPDVEVMTSLKVDNLTHTSP DVYIPRDYTKESRCFAFVRFHDKR DAEDAMDAMDGAVLD/GSELRLQ MARYGRTPDSHHSRRGPPRSYGC VGYGRRSRSPRLRRMP/RSRSRSRSR SRSRSRYSRSKRSRSTRSRSRSTS |
| 2217 | 7714 | B | 2410 | 1522 | 2003 | MAIIYGVFSASNLITPSVVAIVGPQL SMFASGLFYSMYIAVFIQPPWSFY TASVFIGIAAVALWTAQGNCLTINS DEHSIGRNSGIFWALLQSSLFFGNLY IYFAWQGKTOISESDRRTVFIALTVI SLVGTVLFFLIRKPDSENVLGEDESS DDQDMEVNESAQNNTKA VDAFK KSFKLCVTKEMLLLSITTAYTGLEL TFFSGVYGTICIGATNKFGAEKSLIG LSGIFIGIGEILGGSFLGLLSKNNRFG RNPVVLLGILVHFIAFYLIPLNMPGD APIAPVKGTDSSAYIKSSKEVAILCS FLLGLGDSCFNTQLLSILGFLYSEDS APAFAIKFVQSICAAVAFFYSNYLL LHWQLLVMVIFGFFGTIFFFTVEWE AAAFVARGSDYRSIMLKSFLDSGDI LAQLCRRQQPRAPLTIRTSPDTLRR VFEKYGRVGDVYIPRDYTKESRGF AFVRFHDKRDAEDAMDAMDGAVL DGREL RVQMARYGRPPDSHHSRRG PPPRS* |
| 2218 | 7715 | A | 2411 | 2 | 229 | |
| 2219 | 7716 | A | 2412 | 3 | 353 | FPLPFFTLVIWPGIRKFKLVHADGSL CEIFLIGPFKNMAGWNISVPYWFDQ SLSKYVPETETMCTLMEGKLNFFLF KPRCIGKQCKRRTWGKRTT*SIRRR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SPW NKQLGYLKRLFW |
| 2220 | 7717 | A | 2413 | 18 | 282 | DPLKSGPRNRS*TRWTPSPRS\ARRS KSKSLSVSRSSRSRSR\SRRESLPP VSKRESKIQVAMGEKREGSPSSP\EE EAGVLLRK |
| 2221 | 7718 | A | 2414 | 2 | 830 | LRSPSVLFCGKAFFVSPRGRQLPER RGVAPPRAEEAGASSRGSGPPLRA MSYGRPPPDVEGMTSLKVDNLT\Y\ RTSPDTLEGAVFEK\YGRVGDVVHP RGIRYTKGSSRGFAFVRFDKRD\AE DAMDAMDGA\LDGGELRVQMAR YGRPPDSHHSRRGPPPRRYGG\G\GY GRRSRSPRRRRRSRSRSRSRSRSR SRYSRSKSRSTRSRSRSTSKSR\AR RSKSKYSSVSRSSR\SRCRCGYRSP PPVSKRESKSRSRKSSPKSS\EEGA VSS |
| 2222 | 7719 | A | 2415 | 1 | 320 | RGRASKECSGLSAHLVIHCGEKPYK CNECTRTSGTN/SSLTQQRSH\AEKP YTRNECGKVFG/HIARHQIH\STKP YKCN/NTLKAFSKHSG\MAHLLIDR PEKLCHYS |
| 2223 | 7720 | A | 2416 | 733 | 1005 | NPQTPMKNCWP\LEKKAEP\PLGS SMPLGFCPHGPPCSCDFLETH\FLDE \EVKLIKMGDHLTN\HRLGDPEA GLGEYLFERLTLKHD |
| 2224 | 7721 | A | 2417 | 148 | 1057 | |
| 2225 | 7722 | A | 2418 | 87 | 241 | EGGLGNDPMTTDCSMAA*LFK**SP SS*ALGSFCEAQIIQSSKGLFSRGSC |
| 2226 | 7723 | A | 2419 | 1 | 924 | |
| 2227 | 7724 | A | 2420 | 1 | 1004 | MPVGAGRRRAKGDPATLGALAVFTV GAKRSKGHSPKHPAGRLPPLPLR QRSTPMIDTLRPVPFASEMAISKTV AWLNEQLELGNERLLLMDCRPQEL YESSHIESAINVAIPGIMLRRLQKGN LPVRALFTRGEDRDRFTRRCGTDTV VLYDESSSDWNENTGGESVLGLLL KKLKDEGCRAFYLEGGFSKFQAEFS LHCETNLDGSCSSSSPPLPVLGLGGL RISSDSSSDIESDLDRDPNSATDSG SPLSNSQSPFVEILPFLYLGC AKDS TNLDVLEEFRGSSPYMILFHYGEIG TSYVPITSHFRQKLAQGFPVSTGTP GFIYSAK |
| 2228 | 7725 | A | 2421 | 686 | 1812 | TCPVARASLTRGEDRDRFTRRCGTD TVVLYDESSSDWNENTGGESLLGL LLKKLKDEGCRAFYLEGGFSKFQA EFSLHCETNLDGSCSSSSPPLPVLGL GGLRISSDSSSDIESDLDRDPNSATD SDGSPLSNSQSPFVEALALPSYLG A\KDSTNLDVLEEFGIKYILNVT\nL PNLFENAGEFKYKQIPISDHWSQNL SQFFPEAISFIDEARGKNCGLVHCL AGISRSVTVTVA\YLMQKLNLSMND AYDIVK\KKKSNISP\NFMG\QLL GLSRRDAGDSAGPCGQQGSRHSRL YFYHPFPTRNVLPGWDFLQSTWKD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PTPFLAGMCLALQQFLLAASAGAA FFVCGPRCQNDTKLSVLRQGYQVR ELG |
| 2229 | 7726 | A | 2422 | 66 | 187 | WGGGGSAAAAMEANWTAFLFQAH EASHHQQQAQNSLLPLLSSAVEPP DQKPLLPIPIQKPGAPETLKDAIGI KKEKPKTSFVCTYCSKAFRDSYHLR RHESCHTGIKLVSRPKKTPTTVVPLI STIAGDSSRTSLVSTIAGILSTVTTSS SGTNPSSSASTTAMPVTQSVKKPISK ACKKNHACEMCGKAFRDVYHLNR HKLSHSDEKPFECPICNQRFKRKDR MTYHVRSHGGITKPYTCSVCGKG FSRPDHLSCVHKVHVSTERPFCQQT CTAAFATKDRLRTHMVRHEGKVSC NICGKLLSAAIYITSHLKTGHQSQSIN CNTCKQGISKTCMSEETSNQKQQQ QQQQQQQQQTHVTSWPGKQVET LRLWEEAVKARKKEAANLCQTST AATTPVTLTTPFSITSSVSGTMSNP VTVAAMSMRSPVNVSSAVNITSP MNIGHPTITSPLSMTSPLTLTTPVN LPTPVTAPVNIAHPVTITSPMNLPTP MTLAAPLNIAMRPVESMPFLPQALP TSP\PWRPTGPRCSRPMKLPITNSR QHRTACCP |
| 2230 | 7727 | A | 2423 | 3 | 777 | RTSLVYDYPLRRRWLRRQRGGGGF CFGCGGRSPGPGFLSPTVVTLAEL LVLLAALLATVSGYFVSIDAHAEEC FFERVTSGTKMGLIFEVAEGGFLDI DVEITGPDNIGILPTRLYNLSGKYTF AAHMDGTYKF\CFSNRMSTMTPKI VMFTIDIGEAPK\GQD\METEAHQN KL\EEMINELAVA\MTAVKH\QEQY MEVRERIHRAIQRRTQNSRVVLWSF FEALVACCHDIWGQIYYLEGDFFEV RRSCFKKPLPG |
| 2231 | 7728 | A | 2426 | 89 | 136 | |
| 2232 | 7729 | A | 2427 | 1 | 916 | MFYHLVPDGKKPGATLKATSAPKG KANGGRQAHAPPRWASAGDVTHS AISELRESATAAASASSESAGSGPR MKSVIYHALSQEANDSDVQPSGA QRAEAFVRAFLKRSTPRMSPOARE DQLQRKAVVLEFYFTRHKRKEKKK KAKGLSARQRRELRLFDIKPEQORY SLFLPLHELWKQYIRDLCSG\LPD TQPQMIQAKLLK\ADL\HGGLFISVT K\SKWPLLMLGITGNPFYQETK\HIF QNLSPKGRPALKVIPPSLNCRVPLW KPDGFIPPTFTGSKFPSLGQVNR\SA KKFQSEGNRLTL |
| 2233 | 7730 | A | 2428 | 2 | 484 | PDSSGPHRLRENPPWCLSPADKTNV KAAWGVKGAHAVRSMCAEALER MFLSFPTTKTYFPHFDLSHGFCPGL RATGKKVD\EALTKRRGAPLDDMP NAL/SSALEATLHAHKL\RVGPGSTS KLLKPLACLVDPGPGPPSPAEFHPL RCNVFPGDKVSVWSC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2234 | 7731 | A | 2432 | 197 | 332 | |
| 2235 | 7732 | A | 2433 | 1 | 1788 | |
| 2236 | 7733 | A | 2434 | 3 | 111 | |
| 2237 | 7734 | A | 2435 | 220 | 423 | HEELKSGPYLLTFRDCFLHFWALV SKR/LALNFM*TSAPT*KALSKRNIC LVNKNRNIPYPKKKKK |
| 2238 | 7735 | A | 2436 | 273 | 499 | RSGVRDQPGQHGKITSLKIQKLAR RGGACL*SQLLRRLRQENRLNPGG GGCSEPRSCHCTPAWETEQDSISKIK |
| 2239 | 7736 | A | 2437 | 1 | 1176 | |
| 2240 | 7737 | A | 2438 | 245 | 394 | |
| 2241 | 7738 | A | 2439 | 458 | 701 | GPAPTRRGPAHPGAHTR**PAGTAR AACGSA*SAGTASPAHKGKGHPG SRASGTGPGPCQRRRRSDHSSAGK WPLREASL |
| 2242 | 7739 | A | 2440 | 365 | 814 | AALRSSSENSRHRSLVKMSDKKAK DPVNVKSGGQGPKRKNWSKGKSSG TSFNNLVLFDKATYDKLCKEVPNY NLITPAVGSERLAKIRGSLGQGPFPQ ELLSKGFIPNWFSKHRASSYFTPGIT KGGDAPSLLEDGCMNRSNPPVHLE K |
| 2243 | 7740 | A | 2441 | 41 | 565 | APSPRRPWGHFTEEDKATIKNLWG KGEMWKDAGGKNPWERPWLSTYP MGQRFFDQLLANLSLCLPIMGNP PKVKGTWPRKVLTSLGSAHKSTW DDLKGHLLPKPEVNLHCDKPMW DPENFKAPGEMLLVTRFGQSHFRQ KNFTPGGCRASWGRKMGDLELASA LVPSRYH |
| 2244 | 7741 | A | 2442 | 3 | 284 | |
| 2245 | 7742 | A | 2443 | 1 | 3339 | VEGMTQCQSCVSSIEGKVRKLQGVV RVKVSLSNQEAIVITYQPYLIQPEDL RDHVNDMGFEAAIKSKVAPLSLGP DIERLQSTNPKRPLSSANQNFNNSET LGHQGS HVVTLQLRIDGMHCKSCV LNIEENIGQLLGVQSIQVSLENKTAQ VKYDPSCTSPVALQRAIEALPPGNF KVSLPDGAEGSGTDHRSSSSHSPGS PPRNQVQGTCTTLIAIAGMTCASC VHSIEGMISQLEGVQQISVSLAEGTA TVLYNPSVISPEELRAAIEDMGFEAS VVSESCSTNPLGNHSAGNSMVQTT DGTPTSVQEVAPHTGRLPANHAPD ILAKSPQSTRGSGHRRKCFFTDSKG MTCVASCVSNIERNLQKEAGVLSVL VALMAGKAEIKYDPEVIQPLEIAQFI QDLGFEAAVMEDYAGSDGNIETIT GMTCASCVHNIESKLTRTNGITYAS VALATSKALVKFDPEIIGPRDIKHIES KTSEALAKLMSLQATEATVVTLGE DNLIIEEEQVPMELVQRGDIVKVVP GGKFPVDGKVLEGNTMADESITG EAMPVTKKPGSTVIARSINAHGSVLI KATHVGNDTTLAQIVKLVEEAQMS KNPNKHISQTEVIIRFAFQTSITVLCI ACPCSLGLATPTAVMVGTVAAQN |

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|---|---|----------------|----------------------------------|---|--|--|
| | | | | | | GILIKGGKPLEMAHKIKTVMFDKTG TITHGVPRVMRVLLLGDVATLPLRK VLAVVGTAEEASSEHPLGVAVTKYC KEELGTETLGCTDFQAVPGCGIGC KVSNEGILAHSERPLSAPASHLNE AGSLPAEKDAVPQTFSVLIGNREWL RRNGLTISSDVSDAMTDHEMKGQT AILVAIDGVLCGMIAIADAVKQEEA LAVHTLQSMGVDVVLITGDNRKTA RAIATQVGINKVFAEVLPSHKVAKV QELQNKGGKVAMVGDGVNDSPA AQADMGVAIGTGTDAIEAADVVL IRNDLLDVVASIHLKRTVRRIRINL VLALIYNLVGPIAAGVFMPIGIVLQ PWMGSAAMAASSVS VVLSLQLKC YKKPDLERYEAQAHGHMKPLTASQ VSVHIGMDDRWRDSPRATPWDQVS YVSQVSLSSLTSDKPSRHSAADDD GDKWSLLLNGRDEEQYI |
| 2246 | 7743 | A | 2445 | 14 | 503 | NNDFIVIGTGTEFGIPGPTHAYEKT IYDDYNCL*QCELETENQNLQRQF YDKRKLEAMLQGMVTETTMKWEK ECERRVAAKQLEMQNKLWVKDEK LKQLKAIVTEPKTEKPERPSRERDR DKVTQRSVSPSPVPLLFQPV*NAPPI RLRHRRSRVSGDRWV |
| 2247 | 7744 | B | 2446 | 226 | 347 | XGKIIVASCFFPSSRRKRSSTVAPA QPDGAESEWTDVETR* |
| 2248 | 7745 | A | 2447 | 8 | 2985 | WIQYSSTTLPNWDNKRKKKEKKA MLSARAKTPRKPTVKKGPKRTLKT QLG/Y YCRVRPLGFPDQECCIEVINN TTVQLHTPEGYRLNRNGDYKETQY SFKQVFGTHTTQKELFDVVANPLV NDLIHGKNGLLFTYGVGTSGKTHT MTGSPGEGGLPRCLDMIFNSIGSF QAKRYVFKSNDNRNSMDIQCEVDAL LERQKREAMPNPKTSSSKRQVDPEF ADMITVQEFCKAEVDEDSVYGVF VSYIEIYNNYIYDLLEEVPFDPINPNL HNLNCFVKIKHNHMYVAGCTEVEV KSTEEAFEFVWRGQKKRRRIANTHL NRESSRSHSVFNIKL VQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAIC\GLTPRRRYRNQPRGP\IGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLEALEKRHNLRQMMIDEFN KQSNAFKALLQEFDNAVLSKENHM QGKLEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLOQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFQPDQNAPPRLRHRRSRAG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAES\EWDRCR\NKVFCGL WEMR\AGSQLGTWISASRHNPSAKS HETDSPSTERTFSFVWMISRKPCQK QSSRSSCRTPALVENHEPQLHHTLT PEQSFPYGSQKTTSIQ\QNVYSVCFA \SNINSRGRRLRVSSL\YEF\FIMFFLK YISCILIN |
| 2249 | 7746 | A | 2448 | 20 | 349 | SFCLEFPCTPGEALLQDSAQNSTF DKTALPLCLAPCPPPLGPQS\THIQP CFPHTGPCAPFFTTDLLQGQRLSL HTPLHPVPAHWALPARRALARLTD RPNARLTP |
| 2250 | 7747 | A | 2449 | 3 | 384 | PFLSVVSSQVAGHGRIFQCTYLMND CQTKQPCWSGATWPHPWMQVKGT PALRAHPQTLSESRLPEGTRGSRPE DCPKPQPADPPSLGT\QCPPPWQLSP TQQKMSPTFAAAKGASQGLMWAH AVLSRA |
| 2251 | 7748 | A | 2450 | 1 | 1503 | |
| 2252 | 7749 | A | 2451 | 1 | 855 | NPRRRLRGRCRASASSPRRVRRRGQ RPRHPAPRRPQAARPSAAPRARRFL SQRPAAAAAAQRAALMQAIKCAG GWKAEAVGKTCLLISYT\TNA\FPGE YIPTVFDN\YSA\NVMVDGK\PV\NL GLWDT\SGQKDYDRVTPPYPPYA/Q ADVFL\CFPFVSPAS\FENVRAK WY PE\VR\HHCPN\TP\IILVGT\KLDLRD DKD/TRIEKLKEKLT\PIITYPQGLA\ MAKEIGAVKYL\ECSALTQRGLKTV FDEAIRA\VLCPVPVKERGRENCLPV VNVSAPSFLGPVPLEPL |
| 2253 | 7750 | A | 2452 | 41 | 556 | APSPRRPWGHFTEEDQGLLSTSLWG KV\NVEK CWKEKTPGKGS LVVP\ WT\QRFFD\SFGN\LSSAFAHHGQTP KVKAHGK\KVL TFLGRCQOSTLDD LKGHLLPKPEVNCTVDK PAMWDPE NFKAPGEMLLVTRFGQSHFRQKNS PPEGCRASWAERWVT\GV\ASALVP SRYH |
| 2254 | 7751 | A | 2453 | 2 | 454 | RSFFFFCEVGSWVGS MRVVMARL LSEGEQCIPTACAAFAQQPGGRPRR GLAGVGE GGPQCSWVNYRCTLEFL VSL LGTDLARGRNSATGP\TAPAD SKQLSCKTFIAVLSLSKEAGFCNVV QGWVSTSWGSSSPSV PQFFPKLLEF TGK |
| 2255 | 7752 | A | 2454 | 94 | 218 | |
| 2256 | 7753 | A | 2455 | 266 | 547 | |
| 2257 | 7754 | A | 2456 | 2 | 494 | RGPVMAESWSGQ/SFLQALPATVLG ALGSEFLREWEAQDMRVTLFKLLL LWL VLSLLGIQLAWGFYGNVTGL YHRPGLGGQNGSTPDGSTHFP SWE MAA\NEPLKNPTENKGRQQRVSKGI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HWVCWLLHWVLLLPRPQQGPAGG SGLVAGSTQLPTGLGLILPS |
| 2258 | 7755 | C | 2457 | 12 | 356 | MGDSFMDEVAPRLASVDSRFFSFSQ GAHIKXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX X* |
| 2259 | 7756 | A | 2458 | 764 | 1135 | LLQTTSRNFKNLNQCTKSPICKKK GSVFFFFFFFETESCPVAQAGVQWR DLRSLQAPPPG\SRHSPTSASRVART TGAHHYTRLIFVCLVETGFHHVSQ DGLDLQDQFLESFLCCLLVRLRT |
| 2260 | 7757 | A | 2459 | 1414 | 1761 | SAINFFFLFETESRSVAQAGVQWH DLRSLQAPPPG\SRHSPAPASRVAGT TGTRHHARLIFFFFFFFFFLVETGF HRVSEDDLDLFTSGDLPTLTSQSAGI PGMSHCAWRIDGI |
| 2261 | 7758 | A | 2460 | 63 | 542 | TALPNQLHGGRHLCPSHAFGSQGA ARPKRPQPGPGVASEPWVQLQSHH PLPPPTPQSPEGGEFLREQRPKPLSF KPLLHPRGPLCPAAPKLPPWPCPLR VPQFPHPLPPSGRKRDRERGMEEGE GGWAAGERRGGKEETLGRGPFTQR ERPRNQEGEGG |
| 2262 | 7759 | A | 2461 | 2341 | 2443 | GRVWWLTPVIPALWEAEVGRSLT ARSLRPAWPTL |
| 2263 | 7760 | A | 2462 | 28 | 403 | NTTTCVKGLQTQSYKTSPDGNTTK QTNKVKHTHTII*II*NAPPAVSTTAIR NKFSKNGEQRFIEPYTNRPNIHSLK *RTIQQYASSSKNLEIKDFSWKKLQ* FLENRNKHECFQFPKVNVGAS |
| 2264 | 7761 | A | 2463 | 727 | 1156 | ETTLSEARRGRSAAASCRGSALRRG RFPESRRGREAAPVCPRHVLL*GAQ SKQAAVAGKRSGRHASRWPKSLF TPRRRRLSLKRALHFWQQSADSPS VSRAPGSTWVGPKAPTEVTSVAPSR MMWQNEKKKVGGGERQDWRK |
| 2265 | 7762 | A | 2464 | 10 | 302 | MERFEAGLSHISPWLC*CCSHCGD CCLGSRSWGLVGGGSCGALGPWG RCVCAGGEFPDRASLPVDPALAKLE CSHKFPTPKDFHPRDRSPSRFL |
| 2266 | 7763 | A | 2465 | 303 | 531 | VLRickVSEENSLFPLSDITYLASIPN KTQTHCPEPAQKPSCKAQ*FWPKC KPHPPCCHWALPPGCCWACHRW D |
| 2267 | 7764 | A | 2466 | 6 | 100 | |
| 2268 | 7765 | A | 2467 | 2998 | 3570 | QDRKQGSSAPATPSRA*AAAAARAP RRPAGRWRG*DAPQSPAEPAPRSPP WRRAAD |
| 2269 | 7766 | C | 2468 | 125 | 404 | MMARPPPWLESHCTRVVRADGQV RXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXXX ADAW* |
| 2270 | 7767 | A | 2469 | 1348 | 1807 | CPTVDPLLQKNCNDGSATALARVP LHACREGRWASPSGFFCCCCCFLR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WSLALLPRLKCKGPISTHCNLRPG SKDSPVSAS*VAGITGARHHAQLIFF VFLVETGFHQVVGQAGLELLTSGDPP ASASQSAGITGVSHRARPVSWFNSQ SMNP |
| 2271 | 7768 | A | 2470 | 538 | 676 | VKRNPEAGAVAHTCNPSTLGGRGG WIS*AHEFDTSMTGNMT*PHLYK |
| 2272 | 7769 | A | 2471 | 40 | 336 | EYLYRHFKNKLFLYANILCSSGIWR HYVLILRTVSELDD***GCRWGLSR FDYLSNTGWV*VLLDISSFAFVTGP LIHGTGGLSAFDLHCEALSFYRD |
| 2273 | 7770 | A | 2472 | 2063 | 2406 | SQKKKIQWYLRMFRQFDIYVCFLLF SVVLLMIGGLLSHRLIPVKQYIKLHL ALLRTGAGAHACNSSTSGGQGG*II RGQEFETSLGSSNPSASASQSAGTT GVSHHAQPIFFF |
| 2274 | 7771 | A | 2473 | 22 | 273 | LTQKMDHNQVKFKSTTFYSILGKSV LSLSRPEYISGKSDTYSENIYPLSIKS EIEPIETRCLNRSNASLVQK*YGHKT GLWWLP |
| 2275 | 7772 | A | 2475 | 1269 | 1511 | INFFFF*IIDRFLCHPGWTA VAQSR LTATLLPSRFKRFLCLSLPSSWEYRP LPPYPANFCSKLLICLSTFYKDCG NSA |
| 2276 | 7773 | A | 2476 | 1411 | 1827 | LHTCCLRRRPSGRGRSQQGHCSQSG SSPPRRRPSAPEGPGFHAP*LCIPDL GHGSRKRGCWPPCGPRTGWADLV ASAQAACGCQPPPPSGSCSL*GRG PVGGSGHGSPCWQLVELCGRCWSW PGVAGSTWQWRRHPH |
| 2277 | 7774 | A | 2477 | 1345 | 1642 | WQQFTGAVIHLAYVVLVCVLVAFS SVSLGLNFFHKNFSFDFQRERCWLF SPFKGCC*RCFFTQSLYCYQVCEFT KTLIILLIQDVPEIFWSLFCFFHGP |
| 2278 | 7775 | A | 2478 | 113 | 584 | WQDYIYKEVRVTASEKNEYKGWV LTDPV SANIVLVNFLEDGSM SVTG IMGHAVQTVETMNEGDHVRREKL MHLFTSGDCKAYSPEDSVREKEQP* INGFRRTHIPITEQGDAPRTLCVAGV LTIDPPYGPENCSSSNEILSRVQDLI EGHLTASQ |
| 2279 | 7776 | A | 2479 | 658 | 785 | KTHGWVQWLTPVIPAL*KAETGGW LEPRSSRPATWATQRDLIS |
| 2280 | 7777 | A | 2480 | 2 | 598 | PLGKGKFTGQSAQLTTGTGRGLILA KGSHATLQKHRINHTLTHKNPFL FWESPPSLNLALIKGLNGFCLGTEK LFEQMTYGGKVKVCPIGYFALQS WEFHPPPPTLFLSLPLAILWPGGENR GPRVSTKTGIKTRWPAPFLGPLSNR LGNPQPNNPAPAAVPSLGLSPW*RG RGLPWGWAKPRCALWTPVSLPST |
| 2281 | 7778 | A | 2481 | 253 | 286 | NDDDP*LPCLGQPPRSSCQPSSLP*S LLWSKMTTTPAQRSG |
| 2282 | 7779 | A | 2482 | 407 | 587 | QAGRGRARGVSEEARNKPVPPTET PQPTLSPQ*MGPAQDPAPQQDYRG KKSLNAWCGRS |
| 2283 | 7780 | A | 2486 | 246 | 519 | FQFGIHNTNYQRQGA KVFFKNKGV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WGGPRSLPYSC*EGLPLGESYQFEP QSLRDA*DIP*GSVGKNPVGSHWW VSGVIGGFIITGDYSQH |
| 2284 | 7781 | A | 2487 | 470 | 977 | TPPPAGLRQRGYPPPGNRLEARNW ARAKGGKTSAGRVFTQP*FPEQQLP PGRPWWPRPGCPHGLPTRACKWSG GVLAPESPEPPSLPEGSHSWLGDG LLASRKLKLAGGSVATFTSPQLCPLG PHEDREAREGEGRLAPAQPVSSPSA PAGHSLSHPSRTGKLALVPGH |
| 2285 | 7782 | A | 2488 | 393 | 618 | IREWVNIFWNIHTEEYYTVIKKN*V CQTWLTTVIPELWEADVGGSLP RSSKLR*AMILPLYTSLDHKARLSL |
| 2286 | 7783 | A | 2489 | 308 | 626 | IRGTSNMNRKNVEKAYYAEA*LSL |
| 2287 | 7784 | A | 2490 | 1222 | 1374 | AQQVKRLEGQRGWKLGRGRRWL TPVIPAL*EAEAGGSLEARSSRP AWAKK |
| 2288 | 7785 | B | 2491 | 60 | 378 | NAVLEADFAKRGYKLPKVRKTGTT IAGVVYKDGIVLGADTRATEGMVV ADKNCISKIHFISPNIYCCGAGTAAD TDMTTQLISSLAAMAVFEDKFRPD MEEEEAKNLX* |
| 2289 | 7786 | A | 2492 | 1 | 437 | DPRATEGMVVADKTCQKSTGRLPE LVTAIRMLKQMLFRYQGYIGAALV LGGVDVTGP/HLYSIYPHGSTDIAAG IFNDLGSGSNIDLCVISKNKLDLFRP YTPVNKKGTRLGRYRCEKGTAVL TEKITPLEIEVLEETVQTMDS |
| 2290 | 7787 | A | 2493 | 2288 | 2668 | FGRGHYCRRSVSQEEEAKNLVSEAI AAGIFNDLGSGSNIDLCVISKNKLDF LRPYTPVNKKGTR*VKETKFFLGPL ASWPPLVSPWHLDGVLVLSTLSTS SVPKSTSHDLRLVTCFMTVGCCQ V |
| 2291 | 7788 | A | 2494 | 3 | 861 | FLGKMAAVSVYAPPVGGFSFDNCR RNAVLEADFAKRGYKLPRPRKTGT TIAGVVYKDGIVLGADTRATEGMV VADKNCISKIHFISPNIYCCGAGTAA DTAMTTQLISS\NLKLHSL\STGR/LP RV\VTANRMLKQMLFRYQGYIGAA LVLGGVDVTGPHLYSIYPHGSTDK VP\YVTHGFLAPLA\AMAVFEDKFR PD\MEEEEAKNLVSEDSPPQFPFPS WRIFNGPGLPEANIDLCVISK\NKL GSPNTQLPNKKGTRLGWRYRCEK G\TTAVLTEKIPLWST |
| 2292 | 7789 | A | 2495 | 466 | 607 | KKKERSCLWCPS*SLKNYGLSCR KKKKGAVKKIILVQAWWLMPVITV LWEAEVGGLEARGLRPTRATW |
| 2293 | 7790 | A | 2496 | 449 | 694 | ILRILGTPISFPVNKISFLPFKCLFPDS YIENLMNIYQPIKKNEIHVPLQ*PW MHLETHLSELIQEQTKKHKFSLIR GS |
| 2294 | 7791 | A | 2497 | 52 | 298 | YNIEEQQNKRTQRSNRHRPTPPPEPP NPEW/TPKPTPPTK/PSSPQGE/P GW TGGPAPHAGAAPPFAPSPANPTL FPS LTTGGKV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2295 | 7792 | A | 2498 | 112 | 485 | YNIEEQQEQTYSKTE*SAQTHPSPGT AESRMEPKPTPTKRLPPTGGGGRG GTWGDPPGPCWGGHPPVFPSPCPTP TLFPIFDPLGGQSLAQLGWSMVET LQRATTLSTFLKMGKKETVAPPQI |
| 2296 | 7793 | A | 2499 | 32 | 392 | RPTFGIWFYPPQVFPELLELKAKYIG KHCFSIHSLPDTGPLPGCP/SPPGRA ALGIIPGNLPAPEQKPCWDP/SPSSTL VWRMLNSASTSPSPAPSYISPPFPGQ SYFPAHPPTSSLSLGGIY |
| 2297 | 7794 | A | 2500 | 914 | 1417 | PQCLLPNRGGSVQVRLWGATASLS GWGFLASFHPIHPFGKFSSLPDTPW GLCLGCPFPQAERPWA*YPGTLPAP ELETLLGSLPSSTLVWRMLNSASTS PSPAPSYISPPFPGQSYFPAHPPTSSL SLGGIYHQLLPL*PLPSTDPPCAPLL TSPPLTFLKSPRP |
| 2298 | 7795 | A | 2501 | 1120 | 1159 | ERAVCGC*CIFVM |
| 2299 | 7796 | A | 2502 | 1145 | 1367 | IFFSFLHIYIHNTHMYIYYTLCVC VCCVYGMVCVACVYSSSKPKQVC VWIEGNLNY*LQVVCLWYLDFFHS |
| 2300 | 7797 | A | 2503 | 155 | 454 | GGFSVWHTETPPRMRLMHQVQFNL EYLTTPESTQKGGPTLCIYGYVFFK SDYLYSLSLFFRFLYFSSLL*YLML VNFLFRMLFSLFMSFCYLFHIL |
| 2301 | 7798 | A | 2504 | 901 | 969 | RWPGMVAHACNPSTLGG*VGDP |
| 2302 | 7799 | A | 2505 | 903 | 1339 | DKTVQSIRSMGGWKMDASDSKFV DLWIAEGIGTSWRNPGYQAPRPFLH HGCWGDGKSPPLPKPVSHITDVG WLRMMVSTGLSHLW*VPSQGQSSQ GPHPPAPGVQPPQTPPPASLKGKSL HLQGACSEGGAPFSIELFAGRS |
| 2303 | 7800 | A | 2506 | 433 | 548 | PSEYTLGFKNPBKIKLTFNGGNSMSG VHF*TGFTFLFL |
| 2304 | 7801 | A | 2507 | 637 | 906 | RIKKLSDGSYFLPGVSQIA*GSNYF* SKLGPDGGASRLQSHHLGRPKVGV FHHVGQDGLDLLTLVIHPPSAFPEV LGFTGREPPRPSLHL |
| 2305 | 7802 | A | 2508 | 211 | 575 | RENHDLESQCKRGAPVPAGVPSSAL PQGPVSLLPGAGALCPFERSQQASP QVSPQGVDPKICSLQTTSLCSFCDR CTGMGSL/C/SSCPPCSSS/CHGRSHS SPC/CL*SRTSSVVGDEVCNTL |
| 2306 | 7803 | A | 2509 | 274 | 488 | SGDKTMQLRGPCGGWGSPAGLGT CTAGSP*LCHHKGHCSIHSTSCFCLA TVSPCAIFNSTSKAGRGAQP |
| 2307 | 7804 | A | 2510 | 83 | 442 | NFTMVMYTDHILRNAHLMYTSGR RLSVPKIACHITDHSHTCYMPYL RD*Y*TMFSQGFHYAPYLHLHT*EH PFECLLAGRTFTDALFEPTYPTLTL LTPSHWQDGPPLTGSQMPG |
| 2308 | 7805 | A | 2511 | 2 | 270 | ARLGLPKCFFCVFVKTASRSVSQA GVQRCDHNSLQP*PPGLKRSSLASR VAWTTGSHHHAQLIWLKCFKQYFV SSGFYLLLVALLWWGG |
| 2309 | 7806 | A | 2512 | 234 | 409 | KGFYAHEKNARTWWLTPIIPTLSEA *GGKMA*ARSLRPAWATIRDPISAK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SKKKKKKS |
| 2310 | 7807 | A | 2513 | 78 | 460 | NVCRKMPPSDRLAGAYILQCNPVE VVGPEREDAPQNRVQVRHGCVAW PLLAPPPRHLOGEGLTSARKRVL LGVTSGL*RTDSHNPPGPPQREQTE PRARPPALEHRAQQ*PGPGLGGHRG AGCHQ |
| 2311 | 7808 | A | 2514 | 67 | 279 | SHRVSERDAACGAAPAAARLAGGQR NGRAISGRPLSS*GAGGGNVFKVC LLLKNKRTGGGRGHGYLYSLQR |
| 2312 | 7809 | A | 2515 | 683 | 933 | YTSELIGKIISGQEVVVGAWCEDLG *GPRKSRGREGKG*G*EGSGNAGRI VGFKQGRRGEDAHSWSQRGRQEFV FYLKSTRNW |
| 2313 | 7810 | A | 2516 | 2 | 208 | SKIALLVHLK*ENRHQLFFELIPTVF FLFIFETGSHSVTLQECSGVIMVHCT LTSWAQASSPLSLPTA |
| 2314 | 7811 | A | 2517 | 426 | 601 | PSFRIFTQYSSFLKNSLKRLGAVAH VCNLSTMGG*GGRTA*AQEFETSLV NVVRPPSL |
| 2315 | 7812 | A | 2518 | 55 | 489 | HSALIQASVWFRYKYPGGLGASLP TN*GKKGSQVGSSAHFATTFTIPNG DNA*GAKSGSGCPGGECHPG*GPIS SCPLSEGQTCALNPLSCGSPGPDWLI LGKLGPLGCSKPKGSHFAFPLVPIF HPCSKTKLFPREELFVVR |
| 2316 | 7813 | A | 2519 | 52 | 286 | MMPCLRQRQREREREREREREH MRTQRKQLK*WITRFKNSSKRQR TEKNSKKPPVPHRGAGHSNGKLC FRPAAS |
| 2317 | 7814 | A | 2520 | 3 | 296 | TNTTRYTIGDPALQDMNSRRAHSH TYGHTLLWEGICDLTRPPKLGSCRE KECPRPHPSLDR*SSGFWDPAGRGE LMQWEMPQPCSPQPLPKPCRSSI |
| 2318 | 7815 | B | 2521 | 83 | 241 | SEWQKKLTPEQFYVTREKGTEPPFS GIYLNKEAGMYHCVCCDSPLFSV KLI* |
| 2319 | 7816 | A | 2522 | 19 | 629 | YFVLISPLLTFTSTHGFDLCYLICNTV HKTPCVFRSLWDIQKEVFSIKGSRSP SPSKGNFGDSEGPVRTIPGGTLVE*L GMGSGRGEWDRILLPGTTHRGTSW HVNDVSSCSIVYVFHSSEKKYCSG TGWPSFSEAHGTSGSDESHTGILRR LDTSLGSARTEVVCKQCEAHLGHV FHDGPGPNGQRFICINSVALKFKPRK H |
| 2320 | 7817 | A | 2523 | 1 | 707 | MGAGAETGRGQRAAAPERRHGRL LWLLRGLTLGTAPRAVRGQAGGG GPGTGPGLGEAGSLATCELPLAK/SE WQKKLTPEQFYVTREKGTEPPFSG IYLNKEAGMYHCVCCDSP/LFSSE KKIYCSGVTGWPSFSEAHGTSGSDE SHTGILRLRLDTS/LGSARTEVVCKA /QCESSILGHVFPADGP/PNGQRF/CI NQCWLWKFKPKGNHWTIFQESAFP CHPFHVAPSIFHNSLE |
| 2321 | 7818 | A | 2524 | 303 | 743 | TGAQWGRGLGHVCWSMGFVSWE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CSGNGLSQAGLVKLKLLIHLHSTVQK GLTPRWGGMNLTQLPGGVGGP*FP KMPGATL*PFEGKSPAPQLFPCQPW AGAAHGGAGGPPSSGSPVPGPPQCPV KALPVL RAGWATQPPGSFLWPTPS D |
| 2322 | 7819 | A | 2525 | 102 | 421 | VQYGSNWNKPYWNRVGP*SHTTG ELKKRWPHPRSCCPHGAAGQGAER CGRERGPEDTSDLLNK*QW*RRFPS GPAECGA AVAGL*GAAGCRGRSRP LKSRDAGLKS |
| 2323 | 7820 | A | 2526 | 225 | 448 | TQEGRGIDFGPWWPQLLPSSPSPG L*SPATPPQAWVPPLSSSSSPALILS GPNRKPEPPPGIPPQFYLTSL |
| 2324 | 7821 | A | 2527 | 43 | 390 | GDVPTVTGECPPSYRAMSPSYR*MS PQL*GKSPQL*GDVHQL*GNVPPVT GLCPPITGQCPLIVSPSYTVLSPHYK VVSPTVR*CPPVTG*CPPIAGQCPL *CPQAISWSPPVTG |
| 2325 | 7822 | A | 2528 | 525 | 635 | HIQQQLWWMPVISALWEA*EGGL LDPRSLRPAWAT |
| 2326 | 7823 | A | 2529 | 66 | 432 | TRGSWHKHALAPT VHRAGLWGGK AGTQASPGAADNVPPPY*TSGFCG WKAGTDFPTSKKPCPFLPHNPPLP PCKWQKGLSLFVISHSLICKVGMQL PRGSQVRLLLTKIQIHRSLGRAE |
| 2327 | 7824 | A | 2530 | 5 | 95 | |
| 2328 | 7825 | A | 2531 | 1 | 123 | |
| 2329 | 7826 | A | 2532 | 118 | 363 | |
| 2330 | 7827 | A | 2533 | 23 | 250 | YLIVVWICISIGLYTY*LIIRALYILR KLT LFKYIPISH*SLSFIVFCSLVYIY MYIYIYVYIYIYIYIYIYIY |
| 2331 | 7828 | A | 2534 | 346 | 611 | TSVEAQDATDRLWPDSCCPAHGAC TRTVWPKPPYFPVKKMESCSVAQ AGVQ*CVLSSLQPPSPRFK*SPASAS GVAGITDFQKLFCQ |
| 2332 | 7829 | A | 2535 | 267 | 682 | HFSSLRMQARPPSFRPYLVLPKNC WIFILINDSWMVLFEEASLPTVPSLV QTTIFLLGILQQPLTDLPSSTSTPF*S LHLSAV*VVFRKFLSWPGMVAHTC NLNTWGG*GGRTA*AQEFDTSLGNI VRPCLQKKKS |
| 2333 | 7830 | A | 2536 | 45 | 280 | |
| 2334 | 7831 | A | 2537 | 1560 | 1885 | QLGVLLAGPFTSSPYGGVSPGLKRP WPAPRSYPLPAL*PLPAPYGVQRS LPNPKLGKNPLGPPISSQKPPCGGPV KTSIVAHNYSALSLSLTPQPGSA PQALSL |
| 2335 | 7832 | A | 2538 | 60 | 341 | VTLSLVILFSAHICRIKLNITINLQM YSVVHPNFHLDVTIPKIVVALCFRK KYAFFCFMQQKYRM*SEIHYYIFILS VVLNVNEINSIIQMY |
| 2336 | 7833 | A | 2539 | 442 | 686 | TSYNNLLNNLKNITFRKELSSLSHL CNRGQGILKSLIAWLGAAGHAGNP STLGGRRRIA*AQEFKTS LGNLRP VSPKK |
| 2337 | 7834 | A | 2540 | 459 | 603 | GFLLEIIDKAEGGAHACNP S AFGGQ |

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|-----------------------------------|--------------------------------|--------|---------------------------------|---|---|--|
| | | | | | | DGRTT*GQEFKTSLSNVTRPHLY |
| 2338 | 7835 | A | 2541 | 1 | 188 | PEQVLWQTKVTYSGKKKKKATKRP GAVAHTCSPSTLGG*GGWIT*GQEF KTS LANMVKPCLY |
| 2339 | 7836 | A | 2542 | 582 | 825 | GLSNMVHLWIEHHPAARSRDCHSG RLRREACLG YRKIS*HWP G MVAHA CNP GTLGG*GRRIT*GQEFKTS LAN MVKLCLY |
| 2340 | 7837 | A | 2543 | 775 | 1019 | DRSSPKKPPDDLPEFTEPQWFTLKHI KQCFSDISRLRVGPGMVAHAYGVA YLSTLGG*GRRIT*GQEFETSLANM VKLCLY |
| 2341 | 7838 | A | 2544 | 303 | 429 | AACVLPSPPSAHSSTHTTGSTHLG* GPPCSGPAPT WGSWKT |
| 2342 | 7839 | A | 2545 | 853 | 867 | NP*NLACFCV LLEFPSSF*RGFRRLG AVANICNPNTLGGQDGWITSGREFE TSLGNMVKPCIY |
| 2343 | 7840 | A | 2546 | 357 | 560 | KGSLVGLSLEERIFVVA VQPSLFHK KCLWQGTVAHTSNPSTLGGQG RSV A*PQEFKTS LGNIVRCL |
| 2344 | 7841 | C | 2547 | 486 | 728 | MWVG VWEV FSGVVLGWGVPV ML QSDG SWKLPVHLHELLPFHMSWYP PQDDPN IWSLQ LGLPGCP LLSLC DVS YMVSSA* |
| 2345 | 7842 | C | 2548 | 240 | 332 | MACFSFTSAQLKDRLRSPATH TPL LNAPL* |
| 2346 | 7843 | A | 2549 | 2 | 603 | SLPYLPQHPLEFGPLNLHRDQRAG AQTLTQ PMSLCCSKSLQLPNALTDK RPCWVLFPA GLSSLLRND SAKLPFR NKSGFPPAQGLCPGGSRLTTWHLSF HGLFLLHQ RSAQRSTSQIPSNHTLT *CPTVTTETVPCLK*PRLSVVSVCF SGSP*RALQCTPPGKSPFLSQLSLT DPLPSTNLLFHPVGTPRAPGWA |
| 2347 | 7844 | A | 2550 | 132 | 419 | |
| 2348 | 7845 | A | 2551 | 1083 | 1563 | PENQSSLYFLPANLLKMPFCFFVFF* DGVSLCCPGSAVAQLQPPAS*VQSD SPA FSLTSRWDCRRVPPRANFCIFS SDRGFSMLVRLVSNSRPQVIHLSQP PKVLGLQVETGPQKREWVPRELTA SGQWK GQEPDQGEDSGTEGRWLPL LPSAGHSGED |
| 2349 | 7846 | C | 2552 | 173 | 501 | MPSPSAPSIVPVLHGCWVHICQADV YHTLLKGFLFLRQSPTLSPRLECS GTILTHSNLRLQGSSDPAALASQEA GLKLLVSSDPPTSASXXXSAXLXCQ TGV SXXRP* |
| 2350 | 7847 | A | 2553 | 174 | 364 | YDAEFPRCSFGLIYPRLSVKEASRLS AVAHTCNPSTLGGQGRWIT*GQEFE ISLANMVKLHLY |
| 2351 | 7848 | A | 2554 | 61 | 283 | GGRIA* TQHSILDNRVRLHLKKKKK KKQYLKKVHLPGAVAH/TYNPSTL GGQGGWIT*GQEFETSLANMAKLC LY |
| 2352 | 7849 | A | 2555 | 1140 | 1313 | HVENSEGASGERKLTQRLGVVAL ACNPSTLGGQGRIT*GQEFETSLA NMAKPHLY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2353 | 7850 | A | 2556 | 99 | 296 | WVLIVHVISSKCLVLEICVYRLGAV AHACNPSTLGGQGRWIT*GQEFETS LTNMVKSSLYLKYKN |
| 2354 | 7851 | A | 2557 | 175 | 332 | RNPIFSLRKWPLRPGGVAHACNPST LGGQGWIT*GQEFETSLANTVKP RLY |
| 2355 | 7852 | A | 2558 | 667 | 772 | ARCTNPSTLGGQGRWIT*GQEFENS LANMAKNRLY |
| 2356 | 7853 | A | 2559 | 7155 | 7302 | IMKLKMYIWPAGAVAPACNPSTLGG RGGWIT*GQEFETSLANMVKLRLY |
| 2357 | 7854 | A | 2560 | 227 | 410 | FQVDPDTWLFIEVTLFIFMAIFYLW QVLLVFHFTAVR*CSLFQGSYGIFGI EGRIPYSEL |
| 2358 | 7855 | A | 2561 | 275 | 685 | LKPLFTPSPGPA GVPRGLCWKEAPT PGSLLGEEETELNVY*GPPPGSLRPA SHWAPPEGLRPTSPLFVAATSTIGPL PVLVTLGPHLSPLFGQFINKGRDDT VLLPPQSPGCRESLACQGEETSRLCF VSHTSPSSL |
| 2359 | 7856 | A | 2562 | 20 | 354 | PLYSQSFPIIYPFITLLPE*SF*NNNYC SFVNIPSLTPSHQLYKVHSPHPHPVF HTWAHPAPALCSSWVAMLTVYQG AVLYQCLSTAVSVQGPLRLLGFSNR DTLPSKGLS |
| 2360 | 7857 | A | 2563 | 374 | 585 | GNLINC*LHTHTHTHTHTHTHTHTH NLTNYPDFLYLLVTFPGDIVIQESAF IFFTKSPKHCGLGAIRNA |
| 2361 | 7858 | A | 2565 | 918 | 1096 | HCHSNSEFDTE TLGMVAHTCNPSTS GDCGKQII*TQEFGTSLGNMVKPHL YQKKKKKSR |
| 2362 | 7859 | A | 2566 | 101 | 327 | LVKNQQSTQKLAKHGWACL*SQLL ERLREENHLNAGGGGCSELR*RPCT PAWATETVDSL PIMCLVLQPFSLSL R |
| 2363 | 7860 | A | 2567 | 347 | 478 | RDHCRLGTVAHAYNPSILGGQGRRI A*DQQLSIGNTVRPLY |
| 2364 | 7861 | A | 2568 | 622 | 761 | KSVEVFYLSIGQEECLPHIQFIFHAT IFIIGRAQWLTPGIPAFWETEAQEFK CIHICMQVWWHTSV*SVRNKSLYE ELLQARDPGKFVILHYHYWLFHGK A |
| 2365 | 7862 | A | 2569 | 70 | 316 | ISHPSPSTRWEAVT WALG*LFPCPC HLQGGGRQAPLPLPYPLPIVAPPLI SRLNPDGDL SAKTILDVTLYISSTTV GGSWG |
| 2366 | 7863 | A | 2571 | 145 | 331 | IFHSMKPISEWKLV*TLWQFFKELKI ELPFDPAIPLLGI*PKFQRLKNTNGIC HYFYM |
| 2367 | 7864 | A | 2572 | 918 | 1135 | GFISASLCNWILTHLKFFKEMGSRG VAQAGVQWLLTGAVMAHCNLKLL GSSNPLASAH*VAGAICMYDHWHA |
| 2368 | 7865 | A | 2573 | 590 | 936 | QLAACGGGCL*SQHFERPR*EDCLN PGVQDQPEQNRETPISTKIILKSWA WWHIPVVPGTWRADVGGLPEPSRP KATVSCDCATALQPGRRRARLCLK NKYIKYSVQKCVIFFLF |
| 2369 | 7866 | C | 2574 | 34 | 670 | MXVFLSSAGNMPVTCWCWEAPRC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NQKCTDPAARRPDPQTCASQDRLR CAPCTCHQPLXSRYTQHPGLVPLPH HDRQSVPPQGPRVVQTDAAAXMVE VSXVVLLEGWGXPTTRMKLSLLG IKMLRRGGTVRGAPGAGSALRCGW RWRPPAWRPQMSTSRVSGVQARS TSSSPXPXXSGXLWVHVLLXLAQL DSQQGFDLLLAGRRXSGSNLI* |
| 2370 | 7867 | B | 2575 | 70 | 165 | EQIEALLESLRQAQQNMDPKAAEE QEEKEE* |
| 2371 | 7868 | A | 2576 | 1 | 390 | FFFFFFGVLPVLFDFHVCVFCWK HAGYMLVLGSAAVQPEMHRPSRPP PRPI*RRQTQK*LWFEVDVSWLQGR WVENQHFINRVLTCLERV*NRIYYG TSSSSPLRSGSEGVGPGAFSRPLYPC LGPPN |
| 2372 | 7869 | A | 2577 | 435 | 861 | RASLITVCVPGHLQAADQKNLHPLR AHVVGPCLAGSSCARRPSRA/RGPP RPTPPEHGSRLPQPS/CAAASV*TTR GP*GTLCLS*WGKGTSPGCCVIERP KAGGKCTGHSVCVPVTRKSNHSLC ARSPTSCRPKFAPAAAGPRGGALPG RVILCSKAISGTGPPRPTPEHGSRLP QPSWLRLSEPRGGLEGRFVCRDG ARAQVLDVVCIERPKAGGKCTGHS GVCVPVTRKSEGLGGGRLGLCISGCT AALPSTNM |
| 2373 | 7870 | A | 2578 | 38 | 398 | PVLFLDFHVWLVFVCWKHAGYML VLGSAAVQPEMHRPSRPPNYIAK MCKLSILSLSFLKEGAGDKNSSEPN LG*VP*FSLHPCLSNQMTLGNKQA ESMSLCGFFLPDCFFLTYSKRIYL |
| 2374 | 7871 | C | 2579 | 42 | 443 | MKPAHSAVCPGHLASCETKEFAPR CGPTWLGPCPGRVILCSEAXSGTGP PRPTPEHGSRLPQPSWXRRLSEPR GGLEGRFVCRDGARAQVLDVVCIE RPKAGGKCTGHSVCVPVTRKSEGL PAEDKKTNMKV* |
| 2375 | 7872 | A | 2580 | 871 | 1253 | PRLPPGLPGADRSPAGSQACA\GPA EHGPQGRRGGRGGGGGGGPGPLPHP PTCGTWTSEGA\SRRAPPPAAKGG AGPRCSPDSPSPEHFDQKQGLHS PCCWLFPPLLFPPSISDLSKRKRLPK NCL |
| 2376 | 7873 | A | 2581 | 222 | 754 | YPP*HVAPHPAPLPWQVQGPDPW PRYLWKVPPASLWPRGTEKSPCWA WLVGAGLGLPPFSLPNLSDLGTS FPLPQTLPLCPAQGDLLKPKLGPK KGGSVLSTSPSSFPRGLVGGEAPPN LSPSHTHLGSNVCWTKKQEHTLLV PTFSQSSQNPPLPSPSPIGAVKALFAS TMG |
| 2377 | 7874 | A | 2582 | 2 | 431 | PEGAAPAAMAVTALAARTWLGWV GVRTMQA\RGFGSDQS\ENV\RG G\SIREA\GGAFGKREQAEEERYFR/ ALQVML*DLFGVKD*N*TLSHRVL VEAQSREQLAALKKHHEEEI\VHHK \KEIERLQKRNLNRHK\QKDSKLLKH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2378 | 7875 | A | 2583 | 1 | 232 | RETACCGRDARGAAPAAVMTAL AARTWLGWVGVRTMQARGFGSDQ SENVDRGAGSIREAGGAFGKREQA EEERYFR*GSDQSENVDRGAGSIRE AGGAFGKREQAEEERYFR |
| 2379 | 7876 | A | 2584 | 3 | 399 | LARNERLLAGGRDARGAAPASQWP VTAVGRRGTWLG RV/WGVRTMQA \RGFGSDQSENFPTGPRAPHP/RKAG GALGKREQAEEERYFRAQSREQLA ALKKHHEEEIVHHKKEIERLAEKK FERHKQKIKMLKH |
| 2380 | 7877 | A | 2585 | 3 | 316 | LLQILGTEPQKAVIVLVENFY*YVS KYSLVKNKMSKSSFREMLQKELNH MLSDTGNRKAADKLIQNLDAHNDG RISFDEYWTLIGGITGPIAKLIHEQE QSSS |
| 2381 | 7878 | A | 2586 | 3 | 469 | |
| 2382 | 7879 | A | 2587 | 434 | 815 | TQVDWTQRRARPGPWRHPPFPDD DSLGCCTSHLPPHGD*L*NPSSNGA NPRLSPAPHPPPREAQTPPGAGHR TPLSRACLGLAPPAQPVRLRRDTR DGRKEQRETVPPTFPDARGTRLIL RHK |
| 2383 | 7880 | C | 2588 | 204 | 354 | MWLQMTRAVLSSNLDPYVCRRRA RGRSSPSGSLXXKGEESWGPRHCY SP* |
| 2384 | 7881 | A | 2589 | 390 | 681 | RERGRRAGRRETA VRSREKERER EGLDRSSRKR*PELVKGSRAH*PQ SGRWSHRPRPAIVPTS FQPCDVRAG QPNGPSDLPDHLPTRRRKACDRR |
| 2385 | 7882 | A | 2590 | 598 | 769 | YPQCPTPCQAARVWWD SHLAIPAL LGGRGRWII*QGEFETSLANMAKPH FYQKKKKK |
| 2386 | 7883 | A | 2591 | 359 | 775 | KKTQPLHQGYPKINFRSPSPPIVPV PLLALPK*GHSPFVSPPLQKIPPKG SPHDPTRQRPSIAEGRAGTQLSSPL WMAGTLTEALHHKNRQYPLGSHN QLNLGSTGRTFSKRKGKDGPFDAAQ LQHLKGTFFFF |
| 2387 | 7884 | A | 2592 | 585 | 780 | TFSLPRLDFFFLKARKPRIKNTKNRP GVVAHACNPSTLRGQGRIT*VQEF ETSLANMVKHHL |
| 2388 | 7885 | A | 2593 | 436 | 1645 | GMSALVQSRVSHLHRVSLTRLTA RAQETSSPNTVTPPNQTLSTAQNK RTIPGPARE*VTLTRLSKEPLL VFK AAPT PHPQ*GPAPRPLQASALPLYE QHRRAPSSSEDPWRPLTPPSH*GVS TWT |
| 2389 | 7886 | A | 2594 | 1 | 373 | TCSCPWLAPLTLQKNCPPHCHILSL LRKTKQNDAPKKS PRGSLPAVSGM KQDTVTLGRMEKPPRSIPQRQWD GEATRSIPRRPRVPPVEPNPGHWQ NSPPG/EDQSILSTSNPRGPTPFKSGS |
| 2390 | 7887 | A | 2595 | 502 | 798 | SPKVQRHSSQAALRQAGGALSLWG CLPSQRRPPRTVSSREGPHPGKGV* GGVQRSGPHPLPTCPQGLTCLTPT DPGSAWNPPTPT*NEKGNSEIIRH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2391 | 7888 | A | 2596 | 1 | 136 | HPCVHEPMSFEWPWQYRFPFFFT*G SDPKKHGWASLPSPGPWAQP |
| 2392 | 7889 | A | 2597 | 429 | 1003 | VAYVIGFKSNMPAKHMIKNTSVRV FICPPSMEGKHG*SQPR*NNSPLSPQ NNLSPTLCPLFLPQLKQESMC*SFFN FYQPALAFSLYSIIPSDVDLPSSPFE TRVSWEQFAYLLLESAYLLVQAIE *ASSFLLKHSTSLWIPLHCLFYITFD ICWSLYMNIIFFRGSHCSLQYDPGFL TLSNAPSITI |
| 2393 | 7890 | A | 2598 | 367 | 463 | SGHGAHAYNPNTLGGRGRRIA*SQE FNTRLDN |
| 2394 | 7891 | A | 2599 | 436 | 833 | CLTSALLGCVYVYFFSPHPALFFLRI RTSAYNLLKQLFFRYWNSAKSDLS GHSKTLMCPKSGGGKACAVEPSC SLDTYLCPEIICQALFFICLFVHLL FYCYWRGHEL*YSYCP*FNVKLIM MNSIACY |
| 2395 | 7892 | A | 2600 | 53 | 95 | DSILLTQAGMQWCELGSLQP*TRP PIVCFFCLFIYLLRQHLAPHPSWNAV V |
| 2396 | 7893 | A | 2601 | 432 | 825 | NFKDTAKGFLHFDHQKILDPCPLPG SRARFGTYPECPHVPSVTEAQETGL SVPSFGFHFHFLTYFLLLEYFYFH*G TLYLHLDLHQB*HCQAMRNFLYKS RIQRHHIYHSLDAYANLGHDAKDPF FSLDF |
| 2397 | 7894 | A | 2602 | 83 | 111 | |
| 2398 | 7895 | A | 2603 | 1 | 71 | |
| 2399 | 7896 | A | 2604 | 215 | 758 | LPLQYHRKNIHANTVALADARAPR TASRNRLGVRASGLASSPRLGLQ GSISSASRGRPAQHVPGRPATLSPP AGAGPSR*ERSRAGARGRWVLLDH AGERPAVRELSRPDPRQVSFGPRNIS EIGQVLSPETSSCELPGIGDLLWQL EVYDARKHSLVGPESLSHRELGSPA GRRP |
| 2400 | 7897 | A | 2605 | 211 | 323 | LDSLIQHSASTLAQHSASKPWKPD FHTQFFHTVWKLQWCRAVVPATQ EGDAGGSLEPRSLRL*CVAGTTALH HCDSFHTVWKNVCVWKLSGFHGFE AECCASVEAEC |
| 2401 | 7898 | A | 2606 | 75 | 232 | TQPGHKGETPFFPKTPKISPERWWG PIPASWGVKAGKLF*PRGERFPLIW F |
| 2402 | 7899 | A | 2607 | 325 | 566 | FNDKYFYYPRGQIQCHITLFLNLKI TSDFFFCFKKTG*VAHTCNPSTLGD *GGIA*AQEFKTS LGT**DPIYKN |
| 2403 | 7900 | A | 2608 | 1114 | 1367 | AIARTLIIMINLTVNFSAINENCTTT *RYFDLL*YTTGMFRKIVRKLKVTH LKWNN*RYTKFCIRKFNNLSEPF NHVCKVF |
| 2404 | 7901 | A | 2609 | 100 | 450 | FLEENYKVKFSCFSPFEELKKKGRL N**NFIS*I*IGPKIFSQTNS*NSNFYQ YLCILSGLIQDK*NFKILS*FYYK*V GNFDILYIHTCVCVCVCVCVCVCVF VCLWSTLRMTDTV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | Sequence NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|---------------------------------|---|---|---|
| 2405 | 7902 | B | 2610 | 50 | 382 | XGEQLVRQDL DAGVSEHSGDWLD QDSVSDQFSVEFEVESLDESDYSLS EEGQELSEDEDEVYQVTVYQAGES DTDSFEEDPEISLADYWKCTSCNEM NPPLPSHCNRCWAHX* |
| 2406 | 7903 | A | 2611 | 1665 | 1787 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2407 | 7904 | A | 2612 | 1431 | 1553 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2408 | 7905 | A | 2613 | 1 | 752 | DL DAGVSEHSGDWLDQDSVSDQFS VEFEVESLDESDYSPSEGGQELSDE DDEVYQVTVYQAGESDTDSFEEDP EISLADYWKCTSCNEMNPPLPSHCN RCWALRENWLPEDTGDKDKEISEK AKLENSTQAEFGDVPDCKKTIVND SRESCVEENDDKITQASQSQESDY SQPSTSSSIYSSQEDVKEFEREETQD KEESVESSLPLNAIEPCVICQ/GST*K WLHCPWQNRTSYGLLYMCKEAKE KE |
| 2409 | 7906 | A | 2614 | 426 | 813 | SSRRFVWRAKLLCERAQSGTVYEI* QCAHRHPRHRHPGCCRRHLGYAGT AGPLAGYRPFROHRQSLWRAASAI CVD AISMRTSRSTVRPLWPPPSPA RFATWSHYRLRDHGDHTRPVDLPT SQFTILL |
| 2410 | 7907 | A | 2615 | 1740 | 1862 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2411 | 7908 | A | 2616 | 1174 | 1354 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPLRPAGLFKH SPGLYSQPILT |
| 2412 | 7909 | A | 2617 | 2271 | 2393 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 2413 | 7910 | A | 2618 | 1029 | 1197 | FFFFFFFFFGLVETGFHRVSQDGLD LLTS*SSRLGLPKCWDYRHEPPRPA EEGI |
| 2414 | 7911 | A | 2619 | 402 | 990 | |
| 2415 | 7912 | A | 2620 | 1326 | 1716 | KAKKKKRLFFFCIFLCFLWGLPASL LEPGNVWKHLVWNSLHWSTARVL SSPHLTSCNSWQKHPEHPKGAPKN HLKAGCSGSCL*SQHFGRLRQEDGL RQGV*GCSKP*LHHCTPAWDKHL KNSNNSNH |
| 2416 | 7913 | A | 2621 | 148 | 420 | LSLSLCRFLGRFCSGSSFSSIFVLFHF SFL*FMFSFSLETQKFHTSCVCVC VCVCVCVT*RILSFGIK*SSIQI*AQH LINFILSEKWR |
| 2417 | 7914 | A | 2622 | 565 | 916 | VPRARTQHSREKGRAGAWFGLHY QGSII CGSNSTW*NPPQRGPKLLVRL MS*GHCPPSSTQSGSTTTGKEEVKS SSGSDVALALYNDYFSLFCSSSVSKI KREPQLYKQTERETGHT |
| 2418 | 7915 | A | 2623 | 1132 | 1245 | KWHLGKIQNYSTGKCNRIYIYIYI*I YLF*CHLSIGNC |
| 2419 | 7916 | A | 2624 | 209 | 326 | |
| 2420 | 7917 | A | 2625 | 808 | 1010 | EETEGRARWLTVPNPNTLGGRGRW IT*GREFETSLTNKEKPPSLLKNAKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KKKRKKEIKPGMVATCL |
| 2421 | 7918 | A | 2626 | 1602 | 1940 | PSGNTSETSKGLNIRSHTRLFEDIKG VNHRSSQLFQKKPKNRDRIFQERYV RSLLSK*VHPCDICKRPTSFLTTL*Q QKHHHF*QKALENIKEEQTDKLILS CKRVLPFVKK |
| 2422 | 7919 | A | 2627 | 2565 | 2748 | KSLKLGMSLKIKFIFLIKGH LGFPHF LKICPKTNSIFNTHVS*YIYVCVYIY VYTYTHIY |
| 2423 | 7920 | A | 2628 | 1032 | 1292 | MYIPLNNGTVGVDSQMHLVDVQIDY RVLFSYDDWCRNV*FGWAFTSCLP LHGNIGGFFKMCVSYFFWEGELFSS VYFLESSYRKPNL |
| 2424 | 7921 | A | 2629 | 1640 | 1815 | NSKGESSAPLFLPD SHLEKRKSYGT HPLYISLLKNYEK*NNSNLKAVIFK ALLKNKQT |
| 2425 | 7922 | A | 2630 | 1089 | 1226 | IQIQNKLLKKECP SWVW*HMPVISAT QEGEVGRSLQPRSLRSAWAT |
| 2426 | 7923 | A | 2631 | 197 | 430 | SSFLLVYFFIFYFILFFETESRSVSRLE YSGAISAHCCRLFLGSSDSSCLSYSE G*GGSIDRAQEVKAAASCRITL |
| 2427 | 7924 | A | 2632 | 343 | 596 | GYSLLYIQKQPTPLKTKARIGCSYY VNCIFLWNFWKAHTSCFPLCSFVGD FMYICCLERNPEVGSAQ*DN GKQM PCYYRAASEG |
| 2428 | 7925 | A | 2633 | 1143 | 1553 | QCRRVPRGKRLELGVHSSSTG*QAPL LPSASATSSGFLADRRVGTGLRTPL RSRRSAGPYLARPASSAARGPPVGR RGPPWGWAAASAAISARSSPPSAAGS GPDWRRPGKRHSPRPTAAASAHTS PSQSPAIPAGGR |
| 2429 | 7926 | A | 2634 | 158 | 585 | ALTWVHLSSVSFFFPDLKLTSPSRSP ANPSTQQPPHPPHPAPKP*WEAGRI AAS*LPSKAGSWKPLL VNP KAKLW SHVGRMEGDLQCPLCLWLHLPILW FFGGSCFPQTEHSPVQSPDGLIIAWN CPASDAGIKDCLPKYFC |
| 2430 | 7927 | A | 2635 | 1348 | 1540 | SCCWACE*QCNWYVYISVCACVYT YICISTHIYIYTYIHVHLMGYVKIKQ LFNACDSMEHLQAH |
| 2431 | 7928 | A | 2636 | 263 | 615 | LVNSEGNIWVKLCHELQHGPLNSSP FLILLSHSEKINRASIMLKRYKLIN NYILSAFNPPPGKIHTHTHTHTHT HTHTESQKVKST*EIT*IFPQQYTNL CQREEHCYFLSHSE |
| 2432 | 7929 | A | 2637 | 270 | 665 | KLKGVAVHPYCQPARTLAPRLALS EGSFRATCPG*ELSGLRCSPICCPPRS PPALPLCPLKTKLPKC*KTQTYPGS GF*PSHPSCSGPKPLMGCP TPGGG QVDEWIVIYNKIYGRNTGLRRLHRP LYQFK |
| 2433 | 7930 | A | 2638 | 54 | 311 | SQHFRPRQVHHLRSGVRDQPGQH GEMPSLLKIQKL AGHGATHL*SQLL GRLRQENHLNLGGRGCSEPIVPLH FSLGKQSEALS |
| 2434 | 7931 | A | 2639 | 26 | 229 | CRMTMSRLVTMGVAVFLVVCERC DAVCPSGQSPSP\PWASPECCRDH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ICPHPVGPPGPPSLALPAW |
| 2435 | 7932 | A | 2640 | 133 | 586 | THVMLCAQVGSHHPALPWASPEEC CRDHICPHPVGPPGPPSLALPAWDT HTHTHTHTHTHARTRATHAHILPS HAVFYFPFDVQSGSLAGSPYPRGGG GGWFLGGAKKGRECPGG*MGPP MTPSSFQKQLLLPPSQGPTPKPEGG PCLQ |
| 2436 | 7933 | A | 2641 | 186 | 609 | RVGHHPPSVRHPHQGHGWLDPV QLHLWSSCVAFPPGGAPAGLPPSDQ DPGPPLAISPTHWPPCGQPKTIAA HGNGHTRTGGR*RPRRL*SRPAEWP SAPKGRSGGLPGSFQEPADSYPGCG TWCSSACKGRQPSYS |
| 2437 | 7934 | A | 2642 | 989 | 1790 | NYTPFLPCSASAEFCELWGRPLVV FCYFYFQPPLAVEPFFNVIVICCWVR VKVGPGAFPRGLRRDVQRADFSRS SEGLLMGWVRDFDNHQSTCALDPF SGGIGSLLVPGGSDLQIGCFQKSFOA LIEN*CLNRHNSLG*TPKRSIKILWA E*ISRAGLCNSSPEHPACGHPPPR*G QWEAGPTAARTCFSPPTSNNPPNSG PQAHEAQVSGDHSIHIGGS*GSPSPPL AYNLSTRKAQPKCGKKCMVLPSTC KNCTYCKPFALWNCMP |
| 2438 | 7935 | A | 2643 | 92 | 330 | RQVCLPPSERNVASLRTPHPRRGAQ KSQEGPPGRQSPSELKSRYWCVENS TWVSRAPQGTGWPGWALPFPHQ* GWLGP |
| 2439 | 7936 | A | 2644 | 1137 | 1290 | HGQINQMEVNLPMDRKV*THHTHT THHTHTHTHTSSTSCPYTLKRNVK S |
| 2440 | 7937 | A | 2645 | 96 | 357 | |
| 2441 | 7938 | A | 2646 | 2648 | 2953 | DWGYLPFKTLTYPGMVCHCLPLKS FPLFFPPLFSK*WMGPKLYPPKPHL YQNISPQYLCQKTPQTKMPILKKG VFFFRM*APQESGTNVFCMFLCPS TL |
| 2442 | 7939 | A | 2647 | 201 | 377 | QTVFVKLCVYTHIYN*VYMLIHI*A PLSVY*YIYAI*AHILSYIYVHLVIYI TEKYDF |
| 2443 | 7940 | A | 2648 | 1917 | 2056 | QSHAKEWIFLLTCFIF*KLLRNIIYI YIYTHTHAYIYIYIYIFQ |
| 2444 | 7941 | A | 2649 | 246 | 717 | KRQSEEGVFSCCQGWNESLLKSK VLEYP*FLHFPFSFDLYLFNYVFIY LFIYFCSIQSQTQSKAERAYIYIYLY MCCRQNTVNFTTTTKQLFCHLNIH LRRRNEKRWGCHFLVYAFEARSMF IYFFSLCINENDPEWRLAERSMYWS KHHKSC |
| 2445 | 7942 | A | 2650 | 191 | 657 | SGGERRNSSAPSAMSPSGSATTSPG T*PRIIDSERTPAFHARASTVKPPAGI NTREHPPLPCTPKPCTKTHTFTAPPP PQRCTHTSSPPRNLIQIFTRDTHPPPT HTHRHTHTQEPGWWSFDWVGCLR GFSFECTHFHFPQNKGTFFKMSYIA TY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2446 | 7943 | A | 2651 | 1108 | 1282 | PPLWAPAPAILFLQERKRGNDPNW DARRGN*TKNKNKNKNKNKKTETL LRRPVFGAAN |
| 2447 | 7944 | A | 2652 | 2 | 479 | FIIAHPD TVLGELSYFVTEKMISIHLE CSCNVWRVLYYGFNLYIIRYIICN YIS*YILYIK*YT*VFF*TMGVYYKIN NNMQTVVPVYLN YIQVCCY*QIYL TFIYYGSHFLIELRNY*TRMHMLLYI DLLPVFTLPLPFMLSMMLNMGGIFN GPNF |
| 2448 | 7945 | A | 2653 | 341 | 622 | YQNR LFPNQCFTCLLVWLWDSPAP PPRPWQPPPPQGAHT*DRKEEGDPI GIWAPEGKSCTPKPPPSLPTSPGW KRALQKGD TGCPGPSTAST |
| 2449 | 7946 | A | 2654 | 597 | 785 | NNSPSQ*CHFGTDSIICILKQRLGAV AYACTLSTLGG*GGRIA*AQFEAS LGNIVRPCLYI |
| 2450 | 7947 | A | 2655 | 237 | 656 | RGQGWVGDSSQGRGGAKEGLLP SH GLPTPNPIHPTSPIPPENYVQRNTEK SWSWREGGRWKEIGRGRMRGKPS VLP PP GDRVMEGGPPTLLQHRSPH PGGERHGF S*SKFPPPPGSRPQKERR KGQRGMCVRVGQIN |
| 2451 | 7948 | A | 2656 | 109 | 290 | NKLLNIYMD**IICQILLKLYLVPIKL MDTVYMSIYLSLELCFVISPFLLTGI YLNLYIY |
| 2452 | 7949 | A | 2657 | 122 | 359 | |
| 2453 | 7950 | C | 2658 | 133 | 315 | MQWLYIATLIPFFWTQRKGTFS GK SQLLDLFLQGALAILSPDPHPGILHR SLWAHLPA* |
| 2454 | 7951 | A | 2659 | 1399 | 1644 | CERGLPGPFSPMAHQG*TRAGDTG QPASSLPLGLTAGPYFPPSGCLGPFT LDGCGLSPPPLYLPVFFPGLLKSSR PLSCLN |
| 2455 | 7952 | A | 2660 | 592 | 943 | RTGCGQTLTVSHPDQARHWPGPGF ALILLYPAQGFHLLPEAGPEGRG SLLTEEGSREANSRSSLISAAQLPPA APPQGLGV*MQESSRWGGKGRSKG SLPINLGLNSKLKKTTPP |
| 2456 | 7953 | A | 2661 | 181 | 401 | |
| 2457 | 7954 | A | 2662 | 1163 | 1457 | HPRICWHHSDLHTITKTSHT*SESQ NPHSESPGPRGCEPPGPRGSEPPSL *LSLPPPLPFAFCSSCPGLMAGFPPK QALSITGPFSPSVALWLGH C |
| 2458 | 7955 | C | 2663 | 275 | 327 | MPFRLSQDCHHSAGAQQ* |
| 2459 | 7956 | A | 2664 | 70 | 191 | DLLQKPQV*DPSRTECVSM*CFLSPP *AETTSILPCFPRI |
| 2460 | 7957 | A | 2665 | 40 | 142 | THIHILGFLI*G*GLAMLPSLVNSW AQVILLPQH PKVLQLQAGSTVNQPA HRC |
| 2461 | 7958 | A | 2666 | 479 | 722 | YCIIFLG GFFCCCSQHILNVFLCLAS FFE*MISQL*KILLGLGAVAYACNPS TLGV*GGRIT*GKKFKTSLGNIVRA HLC |
| 2462 | 7959 | A | 2667 | 265 | 518 | VKTVFLSGLDPLSLNENNMVLIMTS IVIFSHPLHFRFETLIGEWPFNLILG QV*WLTP LIPGLWEAKVGG SLEPRS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LRTAWET |
| 2463 | 7960 | A | 2668 | 626 | 695 | GPAARARPGKGIRPFRL**HHFGCS LWMGWKMGSQCRSPVESIPLGRAR WLTIVIPVLREAEEAGGSLEPRGSIPG WATRVPRPLYIEKKKKK |
| 2464 | 7961 | A | 2669 | 66 | 610 | TNNGSKSFCLKEHRGSCGCCSSKDF GVPQRLVLGLVLEDLILGELQVLA FGALSGSISIFPSIPPHSAIIKKNSHLR KIPPVPPRQPFRRVWTSGPPAPRAS PSFCFSPPLAPRPPGLRTRPPPS*APA APQSRRTGGPARCPRGVPSPRSQPE *TPCKKNFLMEKISYDFHSQRSSD |
| 2465 | 7962 | A | 2670 | 1077 | 1598 | YVCHTSLYTSKSAHSSPWKFSWDV NPTPLAIHVTTSTKTVSFHTEEVVW SVHSTLKRFGFGAGGGE*GISEKGG HMAQTGTSRRPIAGRDPGPGRPGL LAEYRRPGEEAEVAPEPEDPH*CH HQHTGGPQAPSAQVKVQSSPRRPH QLPVSVSPWIPGGCRGPITTVGTS |
| 2466 | 7963 | C | 2671 | 40 | 180 | MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILSTISFHQLLH* |
| 2467 | 7964 | A | 2672 | 1818 | 2154 | PTPVFVPSLFPSHKHLPQALCGLCG LMSMATKGLSPYTSPLNLWRDTH QRLDFSSSYIIFKTNRLGAVAHTCDP STLGG*AGKIV*G*EFETSPCKKRD VSKIIFFKKEQK |
| 2468 | 7965 | A | 2673 | 137 | 1610 | EENIKSYKEYKCHNLVIRKELLGG GAVAHACNPSTLGLQV*AIPQKIKK YLNFKL |
| 2469 | 7966 | A | 2674 | 1 | 490 | GNRSRARRLASSPGSAAAAYRRPLP AGPSVYPQHERPCASTARRATGFRE IKVPSKSEVTRILDGKRIQYQLVDIS QDNALRDEMRALEQPQGHPTPDL STGDQYCGDYELLSWRLWKQNNNA AGVS*KLGLKSSPVPEFPLAGTPITN TPPQPFNLANERTF |
| 2470 | 7967 | A | 2677 | 2 | 215 | |
| 2471 | 7968 | B | 2678 | 63 | 203 | SFRRPMASASTHPAALSAEQAKVV LAEVIQAFSAPENAVRMDEAPG* |
| 2472 | 7969 | A | 2679 | 433 | 895 | VFHLPSEPRASDALMASASTPNRR PLSAEQAK\VVLAEVIQGVSPRRJA VAHGTRKAR\DNAC\ND\MGKMLQF\ VLP\VA\TPRSQQEVIK\AYGFQLPTG EGVP*SFAPWSSSYEA\QD\PEIRQA LSGKLEGACFCRP*TLTPWGLLVG GSVAAS |
| 2473 | 7970 | A | 2680 | 235 | 442 | RPTFFYIPFKISKIKPSKIST*RPPSLL VG*KSKEKASTQKCLTKIPVPSANL KDPLPKHDEKRELRH |
| 2474 | 7971 | A | 2681 | 199 | 1061 | RRSEPKGWNRAAFPPKVGCGCVW EKTGMGDQNPEETALPSSLHVSISQ RSPRSTQASPPTRGHPVQPRRVYTP FKAGRPRRQKQVTHGQTAATLQVE *ATLPTNT*TSTTRAPCENQRGGKQ RSGWLRATKPHTAERRPSLNRPLTP TEPNCKTTELKSYSLQSKTWRNKS* VKTCRSGK**VMER*WSGKHSVKI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VSTFPPSPRGSSSRLKPEARVARKY GPSPQLKPRRWREKHHGKPREMGR SEKSESLEWDRSLPVLRLMVDGFSFG KQNRNGQGRGAQSMW |
| 2475 | 7972 | A | 2682 | 415 | 575 | ISGWGVGGSC*SQHFGRTREQEDHL NLGVRDQPGQHSENKVSIIKKKRN VISI |
| 2476 | 7973 | A | 2683 | 457 | 549 | VSTGNKVVPQGKVKACI**KVLLK MQIAFTFCPGTTLLPVD*TKVTHL NECNILASLWWLKHDLVFQLLATW LHFNLRSSISSENASAPSYCPTGCVAT LSKPIFNYPHFIPFLHFSHMTLS*PY LAFFLPSPCNSKRNLDSHMVAIEAN RCLAN*NKNYDL*TAADVSSFQNILQ FIVNHKIKLPT |
| 2477 | 7974 | A | 2684 | 291 | 364 | RLKL*SPHLRSYFEKSKEQLASRTF TGQS |
| 2478 | 7975 | A | 2685 | 2 | 361 | TETLARPPSPLVTNMKLLAETVLLL TICLEGALVRRQAKEPCVESLVSQ YFQTVTDYGDLMKVKSPQLQAE AKSYFEKSKEQLTPLIQEGLGTGT WFNFFELFSVGTGLTTAWPPS |
| 2479 | 7976 | A | 2686 | 425 | 678 | LLGAISWELWGTQPCHPVEGVPGPF GLSNPQAGAFREQTPGPV*SSSFEK SKEQLTPLIKKAGTELVNFLSYFVEL GTQPATQ |
| 2480 | 7977 | A | 2687 | 64 | 287 | RQMA LLKANKDLISAGLKEFSVLL NQQVFNDPLVSEEDMATVVEHSMN *YMSYYSLQATGEPQDLRCCSCAL L |
| 2481 | 7978 | A | 2688 | 983 | 1386 | QEVRYRKVETLRCLLFSSCLVPVCA ASPVSRRPGCRFLRSSLHWPTGRLVF RQRGETFLVPEKTVLRGVASAPAQ KAAGRTPVPGRPDARLRADARS*S C*RAARPRRGASGAVGARGCGRPG FPFLRSGGIFV |
| 2482 | 7979 | A | 2689 | 473 | 706 | NLTLASKISLKYCKQYLWILFRKRL WPGVVAHVCPNRTLGGRRGGQT*T QEFETILGNMVKPISTKYQKKKKKK RAAA |
| 2483 | 7980 | A | 2690 | 1400 | 1600 | VGGGSGRSSKFPPLP*CPPPSCCSLPI SSPPPCSLTPGPSLLHVS KGTRRISRL LDKRISKRFTNH |
| 2484 | 7981 | A | 2691 | 6133 | 7646 | YMLFLFLSTKGWTVIQNRQDGSVD FGRKWDYPYKQGFNVATNTDGKN YCGLPQNEQACKIKSFYKWDFF*L KNIHCWKPVLS*EEFPDKNVEAK DKGRKAVFSFPKFYFW*EILFCFSFR VEYWLGNDKISQLTRMGPTTELLIEM EDWKGDVKKAHYGGFTVQNEANK YQISVNKYRGTAAGNALMDGASH LMG\ENRDHDPFHNGHGSFQPPYD\ RD\NDGWYV\WHSLLL*KSH*YHY SESLTIFLIATTSWALTVSHCPKLFM HHSKAFQL*GRHSYSHFTDEI*RDY VICPM SHNYPEIKLEFEHSYFLNNEH LDKYL\LYILKCV*KLSFSFPGFSDT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | Sequence NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|---------------------------------|---|---|---|
| | | | | | | KGCKSYYSIK*QTQSLDGLPQRPS YLSFLL*GTGGLWCISVTLCIAPKKG TTVHTSVAVFYG*SAKRNLTTVVLF LITPNTFSFRLTSDPRKQCSKEDGGG WWYNRCHAANPNGRYYWGGQYT WDMAKHGTDDGVVWMNWKGSW YSMRKMSMKIRPFFPQQ |
| 2485 | 7982 | A | 2692 | 711 | 865 | VTMKTFSLRHKACGQVKNTLTI*Q PNSSIQPTSHYYPHCQPNTGMLIRK G |
| 2486 | 7983 | A | 2693 | 26 | 351 | ASLPDVTNMKLRAATVLLLTICSLE GALNRTQATDPCSENLCQYFQTVT DYGKDLMEKDMSPQLAEAKSYFE NSKEQLTPLITKAVT*LGNFLSYFV* LGIQPASQ |
| 2487 | 7984 | C | 2694 | 10 | 123 | MSTDRHQGQRRWLGRPPHCYQHE AARSNCATPHHLQP* |
| 2488 | 7985 | A | 2695 | 6 | 409 | FCPALSSSTALFFLRGLWFRGKRLG STDLT LHKPFNLTPQFLHWYEMG ESHIDPKMLKPESGRSKSLFPSAAFL DLQSSFLPSFLVVFPPPLSGSCRSLSL PSGTNPLLQLVPLPPSILLPLSTVLF* RATKG |
| 2489 | 7986 | A | 2696 | 736 | 927 | SVAHSSCVSHTHMHTLLGRRATINC LFRNGRGQVQWLTSAPALRKADV GG*LEPRSSRPWAT |
| 2490 | 7987 | A | 2697 | 2 | 251 | FFLKPCLTQVATSGGCNFWPQAIPL SWPPNSISYRTQPTIFFQYNINILQAL A*FTLFACNPSSLGG*G*WIMWPRS RHCTPV |
| 2491 | 7988 | A | 2698 | 1278 | 1515 | SMVIRIMKVNHPMGLLTKRAKRS LNEMLNVDGKSGGYILGAVAHTCN PSALGGRGGWIT*GQEFKTSLSNME KPLLY |
| 2492 | 7989 | A | 2699 | 139 | 260 | |
| 2493 | 7990 | A | 2700 | 268 | 388 | |
| 2494 | 7991 | A | 2701 | 233 | 400 | HFLRAKVSVTQARVQWLDNGSLQP PTSMK*SSYLSLSKCWDYRHVPM APRHFNK |
| 2495 | 7992 | A | 2702 | 602 | 758 | IICLSVI*NPRYTLGTVAHTCNPSTFG G*GTWNS*GQKFETSLTNMAKLCF Y |
| 2496 | 7993 | A | 2703 | 379 | 1160 | LVDMQLWPPVFHENKCCLGPPPQT TH*RPAPAVPTPQAGPGTQGLATAS SVSMLCSDKLPSSDQPRV*PGDAE LSVLGVGRSSRKESPDQAPPLPVIC ELSFARVGGAPGEPLQRPVLS*TP GTLWSKEIA*LQAVLGQY*HEGCAT IMPADP*GRGPGENSGSVTAQGQPL PGRP*NRTHLFFVPHPGQAASQSQS SSSP*QSERRA*IVSPNSGQRYFFPE TEARRQ*GEPRGEGGDLPPFPQPV LLAALVHI |
| 2497 | 7994 | A | 2704 | 178 | 412 | LLHSSLGHVARLPTLQNMKTLARD GSVCFQSHLLGRLRQEDHGCSKP*L HHCTPAWVTEQDPILLKTEIGIPVCS FKR |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| 2498 | 7995 | A | 2705 | 67 | 398 | ISLTLGRHHGKINVYFLYLKMQG*Y FCCTFVSVVNCSDCLSGHSRRKTEG DKVRKEKQEA*AWCKTCETTLKTF PILLFTKKQAGHITPLMLPFLILHTV VTPYFNLEAD |
| 2499 | 7996 | A | 2706 | 264 | 612 | KHFSYNFFSFSFFLEGGGRVLLCPSG WSLAQCSLQLLGSSNPPTLAS*VAG TTGVCQRAWLILKFFCRDRVSLCCP GWSGNS*LQMILSPRPPKILGFQASA TALGPLTPFCLIV |
| 2500 | 7997 | A | 2707 | 179 | 472 | |
| 2501 | 7998 | A | 2708 | 498 | 849 | GSLLSRAPIPYPLNWVSFFIPEVRTTP DIHTIGSEFPRFLKYLKPTREKILVPA LSPPVQPGPSVPFPLPLSQDSSGQAK APWPSSLMH*PGALPLRTTSTQKCD SPSEQTSDASG |
| 2502 | 7999 | A | 2709 | 768 | 1073 | GVETGFDLIAFEDLHAVPRDSGISLF LQATSAPPPPGTARPHQESPLASHK* QARQAPEPLGYA*ARQAQRMEATK ARPRPKSSGARVGREPTCSKPAPRR |
| 2503 | 8000 | A | 2710 | 5451 | 5678 | |
| 2504 | 8001 | A | 2711 | 396 | 687 | TFCPRCGCPSGLAMRLFLSLPVLVV VLSIVLEGPA*GAPEVSNPFDGLE ELGKTLEDYTREFINRITQSELPKAM WDFSETFRKVKEKLKTD |
| 2505 | 8002 | A | 2712 | 1 | 93 | LPKRWNSCHEPLVPLFSPLLVNAVL GVLGSK*GKKIKDNEIGEEIKLSLFA YEMILFVVLL*NPYS*PKNFTVKLL YQSLRK*SDTRLKSTIYLYTSNKLK LRELYSE*PKRWNSCHEPLVPLFSP LVNAVLGVLGSK |
| 2506 | 8003 | A | 2713 | 376 | 469 | NQLPGERWLTPVIPTLWEARA*GL FEPRSL |
| 2507 | 8004 | A | 2714 | 715 | 1050 | |
| 2508 | 8005 | A | 2715 | 404 | 559 | VNIFHFKTFYLGPGAVAHTCNPSTL GG*GGQIT*GQEFKTSANMMEPHL Y |
| 2509 | 8006 | A | 2716 | 3 | 180 | FFFIGVLTLLPRLECSGAITAHCSLD LLGPGVYTT*TLQVLGITGVCHHGQ LIYFYFL |
| 2510 | 8007 | A | 2717 | 1825 | 1958 | LWTISVFWKAGVPLPC*QSPRWTKS ECLSFTPMFLNKS NFKKRI |
| 2511 | 8008 | C | 2718 | 23 | 349 | MPGRGSTAQRGFSKRYSRSGARSL CSLFLFLAKSLSRAMTSFSNISGAGL ASKKNAVFQHSPLSALIEQAGSFGF YGFISLLPWRQRDFNHVLLGICWA VTSVEASE* |
| 2512 | 8009 | A | 2719 | 41 | 298 | ASKVICQQRWHAGFAWLLSLEASL PREGTAGEAVVLAHCLSPSVLKEKR QPAVRAVRKASRPP*ILQRHSRQNE GHRQEWCHTA |
| 2513 | 8010 | A | 2720 | 277 | 651 | KPSRARLLYESKKEGEMLENCQFFL CLFAKEHLQAH*QKSS*TSMDRLIN EPSNDWDIYYWGHRS*TSPRNIWK MKSWALLERLCLKTKTKRQRLRGP SFWSTSLEKPRWSCAPRPGHGG SVC GW |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2514 | 8011 | A | 2721 | 76 | 185 | VWQCLPLYPLPNTLRAVAFRFLAIG YAFPLSCLCALWIFPQNLTSLVTDY *FGWSK*DPQ*FVICLCVCVCVCVC VCVISKLCSSSTDSSR |
| 2515 | 8012 | A | 2722 | 1685 | 2124 | |
| 2516 | 8013 | C | 2723 | 299 | 577 | MFCFDQSSLGSIVLESWITVKPLTLI SSTLMRRDDNFICCHAGRLFLLTVP YRWHTLSGVALFPGPCCGIFFCHSG FQCGRLLPYRVHAPQG* |
| 2517 | 8014 | A | 2724 | 14 | 213 | VDMGSHRVSQDGLELMT*P*SARLS LPKCWDYRRDTPRLALLVLLNLPV PLGASHVGHCLLRSYFCS |
| 2518 | 8015 | A | 2725 | 1169 | 1404 | SFLYFNGLMNFPRPGQAFEDSHEFKY KY*K*ARL*IAHTCNPSILENQGGQI P*AQVFETSLDHTPRPCIYPPKKKKK K |
| 2519 | 8016 | A | 2726 | 44 | 417 | CGCGLGEICLSHGVAQHNRRGNSNCQ KALFNAEPKCASSSSSGKGG/TILVP PAGGKGPNLI*WNP GPPGARGFPGL TPPRGGKKGRAQPPENLV*EKTG FPIVQRGGLKPPPGPPKGGE*RGPP |
| 2520 | 8017 | A | 2727 | 624 | 1023 | CWLWSRGILPAPWSCAAQPWLQLP EGSF*C*TKMCSSSSSPKREFPFGPP AGRQGPQSNKREPPAPRVKGIPPPPP PKTGEKEDGPTTPINLGFSSSRVPP VTGGGYKPPRPPKGGKEKTGGTPGT HHRAL |
| 2521 | 8018 | A | 2728 | 36 | 211 | KTKNISQL*WHTPIVAATWEARAR GSPEPRSLRPAVSLQTAPTALQPSRL EMFVRRYP |
| 2522 | 8019 | A | 2729 | 640 | 898 | VLLTCLVCLVSSKTKPNITKQHTKI KFPOSSRARWLTPVIPKFWEA*AGG SPEVRSLRPAAGLEFLVSHLGRKC WDYRHKPPCLA |
| 2523 | 8020 | A | 2730 | 707 | 1164 | SCIFLNQVFNKNLYFLFFKIKNNLYF LCCMRILICAYNG*RFYLCGMK*GL *SWF*CFSLSLFTAVKFIKCFSVVF CSLSFTGYFFMYTFRIFCLLYPVVQ MISYILQMPFQFLFSFIKLPSCP NVQ FVSVCVCVCVCVNLIFKSARLPI |
| 2524 | 8021 | C | 2731 | 270 | 371 | MQNLQCFRAFELLTHNSASELPLSA PVTYTEDD* |
| 2525 | 8022 | A | 2732 | 2553 | 2764 | GIGPGWGIRPKRTRPRQVNSNVLKA QEWQAEYPGIFQRPYSYEQSFPP* TPPNPIKTSFPPRNCNSP |
| 2526 | 8023 | C | 2733 | 25 | 288 | MSKVQTWGRQKTSHTRLSLHTWK VAQRPGRGAPHLPDGVAARQRCSS LSTRVCCHHVSPQPNLGWAASVG DHSQLACSHGPLQSPS* |
| 2527 | 8024 | A | 2734 | 1043 | 1207 | NMMTTHTLKKVGTGGRARWAHTC NASTLGG*GWWIT*GQEFETSLAN MVKLHLY |
| 2528 | 8025 | A | 2735 | 74 | 233 | MVTFNCFNLH*TVTKGFTRLIV |
| 2529 | 8026 | A | 2736 | 11 | 151 | ICHDAVDRPR/CCRSAMTPWIDRDL PGRPTRPEPAVQRMISYDDKNRMG SDDVCIFLILE |
| 2530 | 8027 | A | 2737 | 214 | 369 | QKDSPD*SCDCVLKENEISNLRCPIQ |

MISSING AT THE TIME OF PUBLICATION

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2554 | 8051 | A | 2767 | 108 | 279 | |
| 2555 | 8052 | A | 2768 | 3 | 314 | LLALVKEGPVPLFLLMKEREGVSSV RSLDTHGILSSTPPVHLPKTG/TEAS GSSWGPADPQDAEKSCRPTSPTLGG GVPACVRCACVLLCCHGALSRLAA SLFFL |
| 2556 | 8053 | A | 2769 | 1 | 465 | |
| 2557 | 8054 | A | 2770 | 192 | 400 | |
| 2558 | 8055 | A | 2771 | 1414 | 1597 | SGVYKRCKGGGRFVFLECATSGLSL ISS\GLSWG/RLWGHGGCRLAGGWG GGGGGSGGMALL |
| 2559 | 8056 | A | 2772 | 673 | 988 | |
| 2560 | 8057 | A | 2773 | 749 | 1169 | |
| 2561 | 8058 | A | 2774 | 2 | 290 | |
| 2562 | 8059 | A | 2775 | 3 | 520 | HERRVVAWAGRGFVCCARSSRSRV IFCSAPAGMAHKQI*YSDKYFEEH YEYRFVMLPRELSKQVPKTHLMSE EEWRR/LGVQQK/SLGWVHYMIHE PEPHILLFRIRPLPKSSTKMKFISGIV KSCFKFNVVVYKVVFWQNTWRN GYKSFHPYLCMSCILHSNRARVKC NCK |
| 2563 | 8060 | A | 2776 | 1134 | 1312 | |
| 2564 | 8061 | C | 2777 | 49 | 282 | MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAARRPDPQTXESQDRLR CAPCTXHQPLPLDTHNRTL VHNRL NIPQKL* |
| 2565 | 8062 | A | 2778 | 1 | 306 | |
| 2566 | 8063 | C | 2779 | 54 | 212 | MFVFLSSAGNMPVTCWCWEAPRC NQKCTDPAALIFLAMPVQSDDSGK RQTG* |
| 2567 | 8064 | A | 2780 | 34 | 308 | |
| 2568 | 8065 | A | 2781 | 35 | 407 | |
| 2569 | 8066 | A | 2782 | 41 | 360 | |
| 2570 | 8067 | C | 2783 | 105 | 302 | MXNLKRLQISMKPAHSGVCPVTRX SEGLGGGRLGLCIXWLQRGASQHQ HVTGMFPAEDKKTNMKV* |
| 2571 | 8068 | A | 2784 | 3007 | 3541 | KRVDYWGIKSSIICSTLLPHRSLC KYYFFFLSLSFKDSFWVIFFFCLSQR WKGERAKEKTTNNKENEAFPSGYQ NAPGEEGTVRGAPGAGSALRCGWR WRPP/SRCGWRWRPPAWRLRCPRP ARRWVCKPGPPPPPLPPRRPWGP CSAGPGAGLTPSRASICSWQARRQS GSHLITLERKRVRR |
| 2572 | 8069 | A | 2785 | 272 | 801 | |
| 2573 | 8070 | A | 2786 | 659 | 842 | |
| 2574 | 8071 | A | 2787 | 156 | 203 | |
| 2575 | 8072 | A | 2788 | 441 | 785 | |
| 2576 | 8073 | A | 2789 | 2 | 28 | |
| 2577 | 8074 | A | 2790 | 5 | 1049 | LRVAVLVAFKMSTKNFRVSDGDWI CPDKKCGNVNFARRTSCNRCGREK TTEAKMMKAGGTEIGKTLAEKSRG LFSANDWQCKTCSNVNWARRSEC NMCNTPKYAKLEERTGYGGGFNER ENVEYIEREESDGEYDEFGRKKKKY RGKAVGPASILKEVEDKESEGEED |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | EDEDLSKYKLDEDEDEDADLSKY NLDASEEEDSNKKKSNRRSRSKSRS SHSRSSSRSSSPSSSRSRSRSSSS SSQSRSRSSSRERSRSGSKSRSSRS VTGALLPHEKDLIQVHLLLRGTERE VVLDDLHLVIAKKDEQDHGHPKDA TGHHLDPILVPVQVQKRNNVLKFTS |
| 2578 | 8075 | A | 2791 | 971 | 1106 | |
| 2579 | 8076 | C | 2792 | 291 | 444 | MGCFFPNSWVRAGVLIPVPVICLSV RLTWGREARQGWVCRCSQNWVIFAP* |
| 2580 | 8077 | A | 2793 | 1 | 672 | |
| 2581 | 8078 | A | 2794 | 1 | 691 | MDFLLSWVHWSLALLLYLHHA KWSQAAPMAEGGGQNHHEVVKFMDV YQRSYCHPIETLVDFQYEPDEIEYIF KPSCVPLMRCCGCGCCNDEGLECVPT EESNITMQIMRIKPHQGGHIGEMSFL QHNKCECRPKKDRARQENGSA LAQRKDNVRSRQLPTSSRP*SRRWRSW STSRPAPVTPRASPLRATSSRPSRT SASRSREASRPAAWWATTSWARS RAAAARTCC |
| 2582 | 8079 | A | 2795 | 312 | 394 | |
| 2583 | 8080 | A | 2796 | 490 | 2890 | PVALTDRQTDAPSPSYHLLPGRRR TVDAAASRGQGPEPAPGGGVEGVG ARGVALKLFVQLLGCSTRFGGAVVR AGEAEPGAARSASSGREEPQPEG EEEEKEEERGPQWRLGARKPGSW TGEAAVCADSAPAAPALQALAS GRGGRVARRGAEESGPPHSPSRGS ASRAGPGRASETMNFLLSWVHWSL ALLLYLHHAWSQAAPMAEGGGQ NHHEVVKFMDVYQRSYCHPIETLV DFQYEPDEIEYIFKPSCVPLMRCCG CCNDEGLEC/VVPTEESNIPMQIMRI KPHQGGHIGEMSFLQPNKCECRPK KDRARQEKSVRGKGGKQKRKRK KSRYKSWVPCGPCSERRKHLFVQ DPQTCCKSCKNTDSRCKARQLELN ERTCRCDGSALAQKRDNVLFQAAT DEQPAVIKTLEKLVNIETGTGDAEGI AAAGNFLEAELKNLGFTVTRSKSA GLVVGDNIVGKIKGRGGKNLLMS HMDTVYLKILAKAPFRVEGDKAY GPGIADDKGGNAVILHTLKLKEYG VRDYGTITVLFNTDEEKSGFSRDLI QEEAKLADYVLSFEPTSAGDEKLSL GTSGIAYVQVQITGKASHAGAAPEL GVNALVEASDLVLRMTNIDDKAKN LRFQWTIAKAGQVSNIPASATLNA DVR YARNEDFDAAMKTLEERAQQ KKLPEADV KIVVTRGRPAFNAGEG GKKLVDAVAYYKEAGGTGLGVEE RTGGGTDAAYAAALSGKPVIESGLP GFGYHSDKA EYVDISAIPRLYMAA RLIMDLGAGKEFH HHHHHAS |
| 2584 | 8081 | A | 2797 | 326 | 1280 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2585 | 8082 | A | 2798 | 356 | 518 | |
| 2586 | 8083 | A | 2799 | 27 | 225 | |
| 2587 | 8084 | A | 2800 | 470 | 754 | |
| 2588 | 8085 | A | 2801 | 707 | 907 | |
| 2589 | 8086 | A | 2802 | 2 | 502 | VLSPEEDKATITSLWAKVNVEINAG RKKPLGKAPLVVLPWPTRGFLWN SFGKTL/ASALLAPSMGKTPQKSK ATLAKKGA*TSLGEDA\IKAPLDDSP RATFCPSLSEL\HCDKL\HVDPENFK A/LLGNVLVTVLA\IHFGKEFTPEV\Q ASWQKMVTGVA\SALA\SRYP |
| 2590 | 8087 | A | 2803 | 921 | 1146 | |
| 2591 | 8088 | A | 2804 | 1170 | 1482 | |
| 2592 | 8089 | A | 2805 | 1492 | 1853 | |
| 2593 | 8090 | A | 2806 | 909 | 1180 | |
| 2594 | 8091 | A | 2807 | 105 | 248 | CTCSRVSHNAPRNSLVSMVFRMHH PPPLDTFRQ/PQPSFNL*YP*PNYP |
| 2595 | 8092 | A | 2808 | 662 | 843 | |
| 2596 | 8093 | A | 2809 | 263 | 408 | |
| 2597 | 8094 | A | 2810 | 701 | 950 | |
| 2598 | 8095 | A | 2812 | 1426 | 1525 | |
| 2599 | 8096 | A | 2813 | 1 | 1416 | |
| 2600 | 8097 | A | 2814 | 108 | 520 | |
| 2601 | 8098 | A | 2815 | 3 | 201 | GRGLRSPDVTQQRGRSPSAAER *PTRPGVLRALPAPA*GKHCPWPRP GARRRPSSPAARPCP |
| 2602 | 8099 | A | 2816 | 318 | 428 | |
| 2603 | 8100 | A | 2817 | 448 | 647 | |
| 2604 | 8101 | A | 2818 | 42 | 191 | |
| 2605 | 8102 | A | 2819 | 3 | 452 | |
| 2606 | 8103 | A | 2820 | 25 | 519 | EFHRLRENPPMVAVSCPTKTNVKA\ AWGKVGAHAVRSMCAEALERMF LSFPT\TKTYFPFHDLSHGFAQV*G ATGKKVADALTNVAHVDDMPN\ ALSALSDLHAHKLRV\DPVNF\KLLS HCLLG*PWAAHLPRPSSTPGGCTPS LGTNFLGFLKHRCLNLPNNL |
| 2607 | 8104 | A | 2821 | 270 | 453 | |
| 2608 | 8105 | A | 2822 | 115 | 427 | |
| 2609 | 8106 | A | 2823 | 1 | 1656 | |
| 2610 | 8107 | A | 2824 | 1 | 1188 | |
| 2611 | 8108 | A | 2825 | 1091 | 1764 | SIAYQPKRVQDQTDSPILPELISNF SKVSGYKIN/AKKSQAFLYTNNRQT ESQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTKKWK NIPCSWVGRINIVKMAILPKVIYRFN AIPIKLPMPFFTELEKTTLKFIWNQK RVRIAKSILSQKNKAGGVTLPDFKL YYKATVTKTAWYWYQNSMVLVPK QRYRSMEQNRALRNNAAYLQLSDL |
| 2612 | 8109 | A | 2826 | 1 | 1449 | |
| 2613 | 8110 | A | 2827 | 2 | 1675 | |
| 2614 | 8111 | A | 2828 | 301 | 453 | |
| 2615 | 8112 | A | 2829 | 1 | 2139 | |
| 2616 | 8113 | A | 2830 | 83 | 1257 | WQQTAVVDGGLKRLSLLNCRDGD CPSPQEPGPNSGRFQPAATDWLEFQ ARRRMKLKAILSKLTQEQTCKHH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MFSLISGS*KMRIHGHK/VGEHHSPG PVEGVSMPTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENYKPLLNE IKEDTNKWKNIPCSWVGRINIVKMA ILPKGIYRFNAIPIKLPMTFFTELEKT TLKFIWNQKRARIAKSILSQKNKAG GITLPNFKLYYKATVTKTAWYWYQ NRDIDQWKRTEPSEIMPHIYNLIFD KPEKDKQWGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRFKTIKLEENLGITMRDIGMG KDFMSKTPKAMATKAKIDK WDLIK LKCFC TAKETTIRVNRQPTK |
| 2617 | 8114 | A | 2831 | 1 | 1383 | |
| 2618 | 8115 | A | 2832 | 2 | 153 | |
| 2619 | 8116 | A | 2833 | 1 | 2436 | |
| 2620 | 8117 | A | 2834 | 1569 | 1835 | |
| 2621 | 8118 | A | 2835 | 933 | 2812 | |
| 2622 | 8119 | A | 2836 | 56 | 1692 | KSKSKQHASKASRRQEITKIRAEKEI EIQKTLQKINESRSWFFERINKIDRP LARLIKKKREKNLIDAIKTDKGDIIT NPTEIQTIREYYKHL YANKLENRE EMDKFLD TYTL PRLNEEEVESLNT ITGSEIVAINSLPTKKSPGPDGFTAE LYQRYKEELVPFLLKLFQSIEKEGIL PNSFYEASIIIPKPRDRTTKENFRP ISLMNIDAKILNKILAKGIQHIKKLI HHDQVGFIPGMQGRFNIRKSINVIQ HINRTKDKNHMIISIDAEKAFDKIQQ PFMLKTLNKL GIDGTYFKIIRAIYDK PTASII L NGQKLEAFRLKTGTRQGCP LSPLL FNIVFEILARAI RQEKEIKGIQ LGKEEVKLS\LFADD MIVYVENPLP SQPQNLL*GWLSNFSK/MSSGYKIY KIDVQKS\QAFLYTNNRQTESQIMSE LPF\TIASKRIKYLGIHLTRDVKDLAF KETYKPLLNEIK\EDTNK WKNIPCS WVGRINIVK\MAILPKV\NYRFNAIPI KLPMTVFTLEKKNYFKVHMEPKKE PALPSQS |
| 2623 | 8120 | A | 2837 | 2 | 433 | |
| 2624 | 8121 | A | 2838 | 371 | 452 | |
| 2625 | 8122 | A | 2839 | 307 | 497 | |
| 2626 | 8123 | A | 2840 | 95 | 314 | |
| 2627 | 8124 | A | 2842 | 2 | 311 | |
| 2628 | 8125 | A | 2843 | 1 | 602 | |
| 2629 | 8126 | A | 2845 | 571 | 690 | CQQGFSFLQAYGPAQHAIS\MRKFK AKYPDYEVTWANDGY |
| 2630 | 8127 | A | 2846 | 130 | 943 | |
| 2631 | 8128 | A | 2847 | 45 | 405 | GIPGRRNMAVADLDLIPDVADIDSD GVFKYVLIPSPLGIPAPGIRPAESKEI VRGYKWA\GHHADIYDKSVGATCR KQGLRTVSILGGGRIS/HTKSPGQER FTVY\GYSMGLWSCPRTPIST |
| 2632 | 8129 | A | 2848 | 1340 | 1504 | |
| 2633 | 8130 | A | 2849 | 3 | 200 | GSCACAGSCKCKCKCTSCCKSEC GAISRNGLWLR\CCSCCPLGCAKC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AQGCICKGASEKCSCCA |
| 2634 | 8131 | B | 2850 | 1 | 384 | MWESVELPRDLLSGFAQNADSDMD NKVQVSDGDKELVGNWSKEKELPT VALHHALHVFWLWFSSRLGTPVSPR VAMEPKWSCEAGCCSCCPVGCACK AQVLRRLQRGIGEVQLLCLMWEQLF SQNCNT* |
| 2635 | 8132 | A | 2851 | 1 | 2880 | |
| 2636 | 8133 | A | 2852 | 584 | 1253 | |
| 2637 | 8134 | A | 2853 | 1 | 2736 | QSRARADQRITESRQVVELAVKEH KAEILALQQALKEQKLKAESLSDKL NDLEKKHAMLEMNARSLQOKLETE RELKQRLLEEQAQLQQMDLQKN HIFRLTQGLQEALDRADLLKTERSD LEYQLENIQVLYSHEKVKMEGTISQ QTKLIDFLQAKMDQPAKKKKVPLQ YNELKLALKEKEKARCALEEALQK TRIELRSAREEAAHRKATDHPHPST PATARQQIAMSIVRSPEHQPSAMS LLAPPSSRRKESSTPEEFSRRLKERM HHNIPHRFNVGLNMRATKCAVCLD TVHFGRQASKCLECQVMCHPKCST CLPATCGLPAEYATHFTEAFCRDK MNSPGLQTKEPSSSLHLEGWMKVP RNNKRGQQGWDRKYIVLEGSKVLI YDNEAREAGQRPVEEFELCLPDGD VSIHGAVGASELANTAKADVPIYLK MESHPTTCWPGRITLYLLAPSPDK QRWVTALESVAGGRVSREKAEA DAKLLGNSLLKLEGDDRLDMNCTL PFSDQVVLVGTEEGLYALNVLKNS LTHVPGIGAVFQIYIHKDLEKLLMIA GEERALCLVDVKKVKQSLAQSHLP AQPDISPNIKEAVKGCFLFGAGKIEN GLCICAAMPSKVILRYNENLSKYC IRKEIETSEPCSCIHFTNYSILIGTNKF YEIDMKQYTL EEFLDKNDHSLAPA VFAASSNSFPVSIVQVNSAGQREEY LLCFHEFGVFVDSYGRRSRTDDLK WSRLPLAFAYREPYLFVTHFNSLEV IEIQARSSAGTPARAYLDIPNPRYL PAISSGAIYLASSYQDKLRVICCKGN LVKESGTEHHRGPSTSRSSPNKRG PTYNEHITKRVASSPAPPEGSPHRE PSHPTATARGGPSCAGTSPWPDPG AREVPRPDAQHAERAVPREAV |
| 2638 | 8135 | A | 2864 | 426 | 539 | |
| 2639 | 8136 | A | 2865 | 1 | 1134 | |
| 2640 | 8137 | A | 2866 | 766 | 1115 | SARQIATFFNNGIKHLAIMGGDILH VAHIFVTPFNLEGAYTSINQRAEVG SLIVIFHRQQMFFIGNHPPLIV/YSMC MANGTPASNRHGWRYAPDR*RSVR RCDGDPLHPDVRRRSG |
| 2641 | 8138 | A | 2867 | 61 | 390 | |
| 2642 | 8139 | A | 2868 | 627 | 1324 | |
| 2643 | 8140 | A | 2869 | 343 | 452 | |
| 2644 | 8141 | A | 2870 | 589 | 672 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2645 | 8142 | A | 2871 | 1 | 3000 | |
| 2646 | 8143 | A | 2872 | 2 | 191 | |
| 2647 | 8144 | A | 2873 | 251 | 505 | GSSSRLGQRTD*ATASRRHFKNKV PGEAKNCSPEDDEIPLYLKGGV\AD ALLYRATH\MILTVG\GTSICPYTEL AVASFPKKAGS |
| 2648 | 8145 | A | 2874 | 1780 | 1914 | |
| 2649 | 8146 | A | 2875 | 1154 | 1256 | |
| 2650 | 8147 | A | 2876 | 1 | 2629 | |
| 2651 | 8148 | A | 2877 | 334 | 468 | YEEEEEDYD*EEEESEPPLDENDL EEDVVFQPPQIEGEAVYDA |
| 2652 | 8149 | A | 2878 | 2 | 416 | |
| 2653 | 8150 | A | 2879 | 1 | 4116 | |
| 2654 | 8151 | A | 2880 | 3 | 3080 | EEELEASKSFGPGNEEEEEKEEKEYE EEEEEDYDEEEEESEAGNQRLQQV MHAADPLEIQADVHWHIREEEEE ERMAPASESSASGAPLDENDLEEDV DSEPAEIEGEEAAENGHPGDTGAELD DNQHWYDSPSDADRELRLPCPAEG EAELELRVSEDEEKLPA SPKHQERG PSQATSPIRSPQESALLFIPVHSPSTE GPQLPPVPAATQEKSPERLFPPELL PKEKPKADAPSDLKAVHSPIRSQPV TLPEARTPVSPGSPQPRPPVAASTPP PSPLPICSQPQPSTEATVPSTQSPIRF QPAPAKTSTPLAPLPVQSQSDTKDR LGSPLAVDEALRRSDLVEEFWMKS AEIRRLGLTPVDRSKGPEPSFPTPA FRPVSLKSYSVEKSPQDEGLHLLKP LSIPKRLGLPKPEGEPLSLPTPRSPSD RELRSAQEERRELSSSSGLGLHGSSS NMKTLGSQSFNTSDSAMLTPPSSPP PPPPPGEEPATLRRKLREAPNASV VPPPLPATWMRPPREPAQPPREEVR KSFVESVEEIPFADDVEDTYDDKTE DSSLQEKFFTPPSCWPRPEKPRHPPL AKENGRLEPALEGLTPQKRGPLVLS AEAKELAEERMAREKSVKSQALR DAMARQLSRMQMELASGAPRPR KASSAPSQGKERRPDSPTPTLRGS EEPTLKHEATSEEVLSPPSDSGGPDG SFTSSEGSSGSKKRSSLFSPRRNKK EKSKSGEGRPPEKPSSNLLEAAAK PKSLWKS VFSGYKKDKKKKADDK\ SCPSTPFSGATVDSGKHRVLPV\VR AELQLRRQLSFSEDSDLSSDDVLEK SSQKSRRPRPTYTEELNAKLTRRV QKAARRQAKQEELKRLHRAQIIQR QLQQVEERQRRLEERGVAVEKALR GEAGMGKKDDPKLMQEWFKLVQE KNAMVRYESELMIFAELELEDQRS RLQQELRRMAVEDHLKTEELSEE KQILNEMLEVVEQRDSLVALLEEQR LREREEDKDLEAAMLSKGFSLNWS |
| 2655 | 8152 | A | 2881 | 1 | 4132 | |
| 2656 | 8153 | A | 2885 | 1898 | 2056 | |
| 2657 | 8154 | A | 2886 | 1 | 233 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2658 | 8155 | A | 2887 | 1092 | 1339 | |
| 2659 | 8156 | A | 2888 | 363 | 512 | EPLEGLLCLEGKGVEIVTILQAETPG EPLPP*KPHS*PGLCLRYRGHTL |
| 2660 | 8157 | A | 2889 | 1 | 136 | |
| 2661 | 8158 | C | 2890 | 12 | 236 | MTPGGLFLPYHSLPQPDFLASCPT HLSTPFLVADNELRLPKGQICPLHV FVLANRVVLKLCANSVWEHSGKIT * |
| 2662 | 8159 | A | 2891 | 1548 | 1849 | |
| 2663 | 8160 | A | 2893 | 1 | 1441 | |
| 2664 | 8161 | A | 2894 | 954 | 1194 | |
| 2665 | 8162 | A | 2895 | 2039 | 2207 | |
| 2666 | 8163 | A | 2896 | 680 | 757 | |
| 2667 | 8164 | A | 2897 | 361 | 476 | |
| 2668 | 8165 | A | 2898 | 226 | 293 | |
| 2669 | 8166 | A | 2905 | 265 | 396 | |
| 2670 | 8167 | A | 2906 | 250 | 447 | |
| 2671 | 8168 | A | 2907 | 632 | 1038 | |
| 2672 | 8169 | A | 2908 | 3 | 363 | VKDDPNDHEQKGRGHKPFRLRELPR ATIFFLINL*VIAEVEVQDSCIDQAES EMLLRSGAPDPGVPL*GCFALVIT HTHSSRAAMAFVPTGKKASCYSQE PS*WQNSPNDTQDHSNDLSE |
| 2673 | 8170 | A | 2909 | 57 | 448 | |
| 2674 | 8171 | A | 2910 | 62 | 371 | |
| 2675 | 8172 | A | 2911 | 398 | 789 | VTGAPLMLPVLPKPGMPLAALVTG LSGLLWPPCAELVGTEFKLPALVHL PHCFFASLLESPVSPRLAMEPNCSC AAGVSTCAGSCKCKECKCTSCCK SECCSCCPVGC\SKCAQGCVCCKG ASEKCSCCD |
| 2676 | 8173 | A | 2912 | 577 | 896 | |
| 2677 | 8174 | A | 2913 | 2 | 184 | |
| 2678 | 8175 | A | 2914 | 1 | 459 | SSNTMNGWFWIDKCSLWLSQSLPY TRATQVTIKIPPNPATGV/SSGFVD*F WIDKCSLWLSQSLPYTRATQVTIKIP PNPATGVRRALWIDSDLRCAPLGLS TGGGKSRIKLG LGVPKFRGSDRNR VLIGAFYNPLAGYRALIGAFYNPLP PHLLLQLLLSVLLQPLLCCGKCKL KAPEGEETEFYVSPKAAV |
| 2679 | 8176 | A | 2915 | 440 | 620 | |
| 2680 | 8177 | A | 2916 | 2 | 987 | FGLRWPRGAVRRWQLWEEAAWK AEGAQARTNPHVSWAATVTRCSVP GKRNPAGWAAEPESGTWSPPGAE IRMFRMRDVEPEDPMFLMDPFAI HRQHMSRMFASGGFWILAPFLSITD WQHCQGTRPASRRIMQAGSCSPL FG/MCLGIFGWFSWDMFWGLME*H DLGNMEHMTAGGNCQTFSSSTVIS YSNTGDGAPKVYQETSEMRAPGG IRETRRTVRDSDSGLEQMSIGHHIRD RAHILQRSNRHRTGDQEERQDYINL DESEAAAFDDEWRRETSRFRQQR LEFRRLESSGAGGRRRAEGPPRLAIQ GPEDSPSRQSRRYDW |
| 2681 | 8178 | A | 2917 | 121 | 329 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2682 | 8179 | A | 2918 | 323 | 457 | |
| 2683 | 8180 | A | 2919 | 1 | 243 | |
| 2684 | 8181 | A | 2920 | 147 | 321 | |
| 2685 | 8182 | A | 2921 | 1 | 2310 | |
| 2686 | 8183 | A | 2922 | 319 | 773 | |
| 2687 | 8184 | A | 2923 | 85 | 369 | |
| 2688 | 8185 | A | 2924 | 1 | 681 | |
| 2689 | 8186 | A | 2925 | 1556 | 1953 | HGVAAASLPSSAGRLSRARGPGSEE PAAAPAPRWRWQHPRGGGPVSR RRPPHGGTPGTVRRGGGGDPAAPG SGCPSPAVVPPRCPGAPLRRATLPP ACCGSLACSPLTL*PAPS/TPPL*ADD SCSVGLPT |
| 2690 | 8187 | A | 2926 | 322 | 376 | |
| 2691 | 8188 | A | 2927 | 365 | 666 | |
| 2692 | 8189 | A | 2928 | 310 | 448 | |
| 2693 | 8190 | A | 2929 | 908 | 1189 | |
| 2694 | 8191 | A | 2930 | 761 | 913 | |
| 2695 | 8192 | A | 2931 | 1188 | 1373 | EPHLKKKKKISRWWCIPVVPVTW KAEVGGSLPRRWRLQ*AEITPAHS SLGNGLTLLKKKK |
| 2696 | 8193 | A | 2932 | 240 | 475 | |
| 2697 | 8194 | A | 2933 | 1212 | 1424 | |
| 2698 | 8195 | A | 2934 | 403 | 539 | |
| 2699 | 8196 | A | 2935 | 436 | 594 | |
| 2700 | 8197 | A | 2936 | 1 | 570 | |
| 2701 | 8198 | A | 2937 | 1086 | 1359 | |
| 2702 | 8199 | A | 2939 | 40 | 361 | |
| 2703 | 8200 | A | 2940 | 12 | 337 | |
| 2704 | 8201 | A | 2941 | 232 | 339 | |
| 2705 | 8202 | A | 2942 | 951 | 1069 | |
| 2706 | 8203 | A | 2943 | 286 | 621 | |
| 2707 | 8204 | A | 2944 | 299 | 513 | HKCYFTLAHVHLIISFCAATLE*A*P SWGTCNCSTPNFVNTTPLTAYYLGL WRLRPFDSDVSFSFCGIL |
| 2708 | 8205 | A | 2945 | 97 | 258 | |
| 2709 | 8206 | A | 2946 | 5 | 464 | |
| 2710 | 8207 | A | 2947 | 1 | 522 | |
| 2711 | 8208 | A | 2948 | 76 | 488 | |
| 2712 | 8209 | A | 2949 | 619 | 746 | |
| 2713 | 8210 | A | 2950 | 125 | 279 | |
| 2714 | 8211 | A | 2951 | 1300 | 1410 | |
| 2715 | 8212 | A | 2952 | 1867 | 1947 | |
| 2716 | 8213 | A | 2953 | 2 | 52 | |
| 2717 | 8214 | A | 2954 | 352 | 538 | |
| 2718 | 8215 | A | 2955 | 3 | 313 | QFEGTRICPAACFPLESGTPGFSLAS KWTPNCSCSPVGS\CACAGSICK\CN RVANRTVLTQTSCCSC\CPVGCABA LPRGCICKGTS\DKCRSRCLDARDSC ALQM |
| 2719 | 8216 | A | 2956 | 1172 | 1914 | HFSAQPWASPCS/LLLLGLEGGQIV GSLPEVLQAPVGSSILVQCHYRLQD VKAQKVWCRFLPEGCQPLVSSAVD RRAPAGRRTFLTDLGGGLLQVEMV TLQEEDAGEYGCMVDGARGPQILH RVSLNILPPGAVEDDVQAGRWRVA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SRDDVACGSEEEETHKIGSLAENA FSDPAGSANPLEPSQDEKSIPLIWGA VLLVGLLVAAVVLFAVMAKRKQV TIQLLQGNPTALAKSKEELSMPKS YQY |
| 2720 | 8217 | A | 2957 | 3 | 632 | |
| 2721 | 8218 | A | 2958 | 3 | 728 | |
| 2722 | 8219 | A | 2959 | 194 | 451 | |
| 2723 | 8220 | A | 2960 | 2 | 484 | NVLTSHQTQPNQRGKAATVTPALWR LTDVRLVTKYKIHFERNVGSFENS KGNSIYF*GPGHDP LLNMNIVY*KS LTINNHMHKIT*ESL TEVLFSQGIFS VTNPHPEIFLVARIEKVLQGNITHCA EPYIKNSDPVKTAQKVHRTAKQVC SRLGQYRMPFA |
| 2724 | 8221 | B | 2961 | 65 | 391 | MAEVRKFTKRLSKPGTAAELRQSV SEAVRGSVVLEKAKVVEPLDYENVI AQRKTQIYSDPLRDLLMFPMEDISIS VIGRQRRTVQSTVPEDA EKRAQSLF VKECIKTY* |
| 2725 | 8222 | A | 2962 | 1 | 2148 | |
| 2726 | 8223 | A | 2963 | 816 | 1014 | |
| 2727 | 8224 | A | 2964 | 2 | 358 | |
| 2728 | 8225 | A | 2965 | 84 | 176 | |
| 2729 | 8226 | A | 2966 | 137 | 426 | QACIMREYK\LVVLGSGGVGKSALT VQFVQGIFVEKYD\PTIEDSYRKQV EVDAQQCML EILGYLPGTEQFTSNE GFIHEKWTRICISLFHHSTVHI |
| 2730 | 8227 | A | 2967 | 449 | 602 | |
| 2731 | 8228 | A | 2968 | 203 | 535 | |
| 2732 | 8229 | A | 2969 | 2 | 446 | |
| 2733 | 8230 | A | 2970 | 3 | 240 | |
| 2734 | 8231 | A | 2971 | 914 | 1291 | |
| 2735 | 8232 | A | 2972 | 188 | 266 | |
| 2736 | 8233 | A | 2973 | 191 | 306 | |
| 2737 | 8234 | A | 2978 | 1 | 440 | |
| 2738 | 8235 | A | 2979 | 3 | 670 | TSRGRVGTQAGEPRDLRPPPCPSSPL RV\AVV\CLEQPERGAWEAHNIPQ NGDSAVRSFG\TGTHVKLP GPAPD\ NPNVY\DFKTTYDQMYNDLLRKDK \ELFTQNGILHIAGRNKRIP\GPERF QNCKDLFDLILTCEERVYDRVGWK I*ISR\EQGDLPSVHVVNLDIQDNH EEATLG\ARFLICEVCQCIQHT EYM HNEIDELLQEFEEKSGRTFLHTVCF Y |
| 2739 | 8236 | A | 2987 | 367 | 492 | |
| 2740 | 8237 | A | 2988 | 49 | 332 | |
| 2741 | 8238 | A | 2989 | 582 | 923 | |
| 2742 | 8239 | A | 2990 | 523 | 668 | |
| 2743 | 8240 | A | 2991 | 942 | 1513 | |
| 2744 | 8241 | A | 2992 | 176 | 362 | |
| 2745 | 8242 | A | 2993 | 4937 | 5137 | |
| 2746 | 8243 | A | 2994 | 651 | 836 | |
| 2747 | 8244 | A | 2995 | 1686 | 1883 | |
| 2748 | 8245 | A | 2996 | 415 | 635 | |
| 2749 | 8246 | A | 2997 | 2 | 308 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2750 | 8247 | A | 2998 | 57 | 598 | |
| 2751 | 8248 | A | 2999 | 802 | 923 | |
| 2752 | 8249 | A | 3002 | 119 | 297 | |
| 2753 | 8250 | A | 3003 | 950 | 1314 | |
| 2754 | 8251 | A | 3004 | 1 | 579 | |
| 2755 | 8252 | A | 3005 | 27 | 483 | RDAEDAIYGRNGYDYGGCRLRVEF PRTYGGRGGWPRGGRNGPPTRRSD FRVLVS/GWQ/DLKDHMREAGDVC YADVQKDGVMVEYLRKEDMEYA LRKLDDTKFRSHEGETSYIRVYPER STSYGYSRSRSGSRGRDSPYQSRGS PHYFSPFRPY |
| 2756 | 8253 | C | 3006 | 34 | 171 | MPKSFRVIAERSMHSWYVCFLICFIL HISITLHSLVMVFVTWREY* |
| 2757 | 8254 | A | 3007 | 1688 | 1871 | |
| 2758 | 8255 | A | 3008 | 1 | 688 | MSGWADERGGEGDGRIYVGNLPTD VREKDLEDLFYKYGRIEIELKNRH GLVPFAFVRFEPRDAEDAIYGRNG YDYGGCRLRVEFPRTYGGRGGWPR GGRNGPPTRRSDFRVLVSGPSPSG SWQDLKDHMREAGDVCYADVHK DGVGMVEYLRKEDMEYALRKLK *PPKFRSHGETSLHRRFIPERSNQL MATSPVSGLGSRGRDLSIPKARGSP HYFSSFPGPPT |
| 2759 | 8256 | A | 3009 | 428 | 579 | |
| 2760 | 8257 | A | 3010 | 1924 | 2043 | |
| 2761 | 8258 | A | 3011 | 131 | 395 | |
| 2762 | 8259 | A | 3012 | 910 | 1173 | |
| 2763 | 8260 | A | 3013 | 1295 | 1489 | |
| 2764 | 8261 | A | 3014 | 1477 | 1604 | |
| 2765 | 8262 | A | 3015 | 443 | 805 | |
| 2766 | 8263 | A | 3016 | 1 | 2109 | |
| 2767 | 8264 | A | 3017 | 1297 | 1408 | |
| 2768 | 8265 | A | 3018 | 3 | 314 | |
| 2769 | 8266 | A | 3019 | 5 | 340 | GSGTSAKAFRSIWGPLPPVHRHGSP RSSVQR/DGPGLGTGEPRVYIRNKV ANTGVPGAPGPSIGGVTA PATDYCH RIAPILAARRRRRRRRRRRRRRRG GGGGVAGGGGGGG |
| 2770 | 8267 | A | 3020 | 1 | 1973 | DGGARARGRAAARRRRRPRRRRRR RRRRRRRRRRRRRRRRLGLERP QPTSRGRAPGASRAEEKMEELVVE VRGSNGAFYKAFVKDVHEDSITVA FENNWQPDRQIPFHDVRFPPPVGYN KDINESDEVEVYSRANEKEPCCWW LAKVRMIKGEFYVIEYAACDATYN EIVTIERLSVNPKNPATKDTFHKIK LDVPEDLRQMCAKEAAHKDFKKA VGAFSVTYDPENYQLVILSINEVTS KRAHMLIDMHFRSLRTKLSLIMRNE EASKQLESSRQLASRFHEQFIVREDL MGLAIGTHGANIQQARKVPGVTAI DLDEDTCTFHIGEDQDAVKKARS FLEFAEDVIQVPRNLVVGKNGKLI QEIVDKSGVVVRVRIEAENEKNVPQE EEIMPPNSLPSNNSRVGPNAPEKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HLDIKENSTHFSQPNSTKVQRGMVP FVFVGTKDSIANATVLLDYHLNYL KEVDQLRLERLQIDEQLRQIGASSR PPPNRTDKEKSYVTDDGQGMGRGS RPYRNRGHGRRGPGYTSGTNSEAS NASETESDHRDELSDSLAPTEER ESFLRRGDGRRRGGGGKG\QGGRG RGGGFGKGNDDHSRTDNRPRNPREA KGRRTDGS LQNTSSEGSRLRTGKDR NQKKEKPDSVDGQQLVNGVP |
| 2771 | 8268 | A | 3021 | 1 | 2116 | |
| 2772 | 8269 | A | 3022 | 656 | 883 | |
| 2773 | 8270 | A | 3023 | 303 | 589 | |
| 2774 | 8271 | A | 3024 | 2 | 478 | MAGKQAVSASGKWL MGIRKWYY NAAEFNKLGLMRDDTIYEDEDVKE AIRRLPENLYNDRMFRIKRALDLNL KHQILPKEQWTKYE/EGLCCSSSAL CFLLR*KDQPIECPSRSQEELL*SKLS PL*TAFET*AKENFYLEPYLKEVIRE RKERE EWAKK |
| 2775 | 8272 | A | 3025 | 323 | 400 | |
| 2776 | 8273 | A | 3026 | 2 | 396 | RPPTTTKFAAARQMAGKQAV*STQ AKGLNG/IFKKWYY\NAARIQNKLGL LM\RDDTIY\EDEDVKRSP*EDFPEN LYNDRMFRRH*EGHWTLNLKHQILP KEQWTFNFEENFY\LEPYLKE/VLF RERKERE EWAKK |
| 2777 | 8274 | C | 3027 | 144 | 341 | MYHSLEKFSSCFKHIPDNFLKMTKI KQNIYRDHFLNFLSFQGXQHKKNK TGQHFTSKCTEPFLQD* |
| 2778 | 8275 | A | 3028 | 1070 | 1335 | |
| 2779 | 8276 | A | 3029 | 2 | 303 | |
| 2780 | 8277 | A | 3030 | 149 | 244 | |
| 2781 | 8278 | A | 3031 | 1642 | 1797 | |
| 2782 | 8279 | A | 3032 | 1115 | 1320 | |
| 2783 | 8280 | A | 3033 | 1240 | 1408 | |
| 2784 | 8281 | A | 3034 | 539 | 669 | |
| 2785 | 8282 | A | 3035 | 1155 | 1579 | |
| 2786 | 8283 | A | 3036 | 437 | 666 | |
| 2787 | 8284 | A | 3037 | 51 | 279 | IKGRWEPPPLASFFLTSQGHCS DGP GP*GWGEAVSPRGRNTLSSSSWHW VPYSELRGRGVACRKEVYKIVQNT QH |
| 2788 | 8285 | A | 3038 | 3 | 300 | |
| 2789 | 8286 | A | 3039 | 451 | 760 | |
| 2790 | 8287 | A | 3040 | 183 | 410 | |
| 2791 | 8288 | A | 3041 | 602 | 1145 | |
| 2792 | 8289 | A | 3042 | 2 | 496 | |
| 2793 | 8290 | A | 3043 | 710 | 896 | |
| 2794 | 8291 | A | 3044 | 143 | 601 | |
| 2795 | 8292 | A | 3046 | 120 | 280 | |
| 2796 | 8293 | A | 3047 | 2 | 424 | |
| 2797 | 8294 | A | 3048 | 3 | 452 | |
| 2798 | 8295 | B | 3049 | 240 | 420 | XLKGHGQRKVAERADPKPLPQRGR TCPKRRCPLSDPARCTSFVRDPVN FQASLSHCLAW* |
| 2799 | 8296 | A | 3050 | 310 | 401 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 2800 | 8297 | A | 3051 | 544 | 700 | |
| 2801 | 8298 | A | 3052 | 1 | 568 | |
| 2802 | 8299 | A | 3053 | 686 | 787 | |
| 2803 | 8300 | A | 3054 | 8 | 182 | |
| 2804 | 8301 | A | 3055 | 227 | 547 | |
| 2805 | 8302 | A | 3056 | 1 | 523 | ESLRKQLGQEPFFDMHMMVSKPE QWVKPMAVAGANQYTFHLEATEN PGALIKDIRENGMKVGLAIPGTSV EYLAPWANQIDMALVMTVEPGFGG QKFMEDMMPKVHWLRTQFPSLDI* VDGGVGPDTVHKCAEAGANMIVS GSAIMRSEDPRSVINLLRNVCSSCS RNRSP |
| 2806 | 8303 | A | 3057 | 919 | 1100 | |
| 2807 | 8304 | A | 3059 | 429 | 780 | |
| 2808 | 8305 | A | 3061 | 567 | 682 | |
| 2809 | 8306 | A | 3062 | 148 | 372 | |
| 2810 | 8307 | A | 3063 | 113 | 303 | |
| 2811 | 8308 | A | 3064 | 367 | 449 | |
| 2812 | 8309 | A | 3065 | 48 | 369 | |
| 2813 | 8310 | A | 3066 | 979 | 1254 | |
| 2814 | 8311 | A | 3067 | 173 | 776 | |
| 2815 | 8312 | A | 3068 | 1 | 111 | |
| 2816 | 8313 | A | 3069 | 33 | 494 | |
| 2817 | 8314 | B | 3070 | 100 | 154 | MVHLTPVERVCRCYCPVGQX* |
| 2818 | 8315 | A | 3071 | 559 | 775 | |
| 2819 | 8316 | A | 3072 | 744 | 940 | |
| 2820 | 8317 | A | 3073 | 1 | 255 | |
| 2821 | 8318 | A | 3074 | 1 | 1206 | |
| 2822 | 8319 | A | 3075 | 905 | 1823 | |
| 2823 | 8320 | A | 3076 | 36 | 689 | |
| 2824 | 8321 | C | 3077 | 215 | 325 | MSVYPLDHIQKRIARRSSLTSCMRG TIAWPTNSLTT* |
| 2825 | 8322 | A | 3078 | 1 | 831 | |
| 2826 | 8323 | A | 3079 | 97 | 236 | |
| 2827 | 8324 | A | 3080 | 409 | 602 | |
| 2828 | 8325 | A | 3081 | 818 | 1095 | |
| 2829 | 8326 | A | 3082 | 528 | 714 | |
| 2830 | 8327 | A | 3084 | 91 | 242 | |
| 2831 | 8328 | A | 3085 | 75 | 430 | VSPGLPAARLFQVAYLDShLKCPGC QHVPMTVTFISSKEKP*PRTVPRPP WMRLGHVILFSFLIPSNLSFSPVIFL CGPFKVVIICTELQNVSRSPQTTLAT VYCNKITSYICKKKK |
| 2832 | 8329 | A | 3086 | 1000 | 1145 | |
| 2833 | 8330 | A | 3087 | 225 | 324 | |
| 2834 | 8331 | A | 3088 | 3 | 54 | IHYSLIIV*CWVQF |
| 2835 | 8332 | A | 3089 | 461 | 658 | |
| 2836 | 8333 | A | 3090 | 337 | 408 | GIQDRASHCTQGPPPPPS*VPQASPA AGEGPCDPPGRYPLRDSGQSVTLH AGSSATTIQEPRGA |
| 2837 | 8334 | C | 3091 | 155 | 453 | MLGALGAEELSLDSLPEGLLNFSKP GSEGGRLGLVPAAGEGPCDPPGR YPLRDSGQSVTLHAGSSATTIQEPR GAGHALASXQECQWSRDRAAQAG E* |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2838 | 8335 | C | 3092 | 121 | 393 | MALPGRLPHRKLAGGTLEAPWPGIP SGAVRRHQPPPTTLXXWLGKVKK PLRKRIEAKFLCAEGPEHIRQGSAA VPGGGGRSRNCEQCLI* |
| 2839 | 8336 | A | 3093 | 270 | 573 | |
| 2840 | 8337 | A | 3094 | 15 | 297 | |
| 2841 | 8338 | A | 3095 | 970 | 1098 | |
| 2842 | 8339 | A | 3096 | 127 | 296 | |
| 2843 | 8340 | A | 3097 | 875 | 1075 | |
| 2844 | 8341 | A | 3098 | 171 | 404 | |
| 2845 | 8342 | A | 3099 | 186 | 392 | |
| 2846 | 8343 | A | 3100 | 2 | 202 | |
| 2847 | 8344 | A | 3101 | 2 | 242 | ARGNMAAATLTSKLDLSLLFRRTSTF ALTIIVGVMMFFERAFDQGADAYFT DHINEGVRPCAIPDLGTRLRGDSGV EKLf |
| 2848 | 8345 | A | 3102 | 79 | 1137 | |
| 2849 | 8346 | A | 3103 | 374 | 519 | LDSRRK**C*LESRPHE*TS/DLSSGS LLI*GIWSILFYPMFAF*KFQKEN |
| 2850 | 8347 | A | 3104 | 1 | 1214 | |
| 2851 | 8348 | A | 3105 | 105 | 379 | |
| 2852 | 8349 | A | 3106 | 260 | 421 | LLYGDCTWTSFHLQRLQLHCQVSQ PCRELPLVSSVLCFPFISEELHCVTG HF |
| 2853 | 8350 | A | 3107 | 420 | 848 | |
| 2854 | 8351 | A | 3108 | 664 | 1059 | |
| 2855 | 8352 | A | 3109 | 73 | 269 | |
| 2856 | 8353 | A | 3110 | 307 | 566 | |
| 2857 | 8354 | A | 3112 | 316 | 410 | |
| 2858 | 8355 | A | 3113 | 200 | 403 | |
| 2859 | 8356 | A | 3114 | 258 | 377 | |
| 2860 | 8357 | A | 3115 | 1767 | 1893 | |
| 2861 | 8358 | A | 3116 | 1 | 389 | |
| 2862 | 8359 | A | 3117 | 3 | 569 | RHGEERLQTRTLRAAELSARAPSHS LPAPRSAPTWQKFSSPTEVERCVES LIAVFAQKYAGKIDGYNYNLSLRPE F/L*AFMNTLAAFTKNQEGPWVSL DRMMEETGTPNSDGSARISSGISLI WIGWALAMGLAWNFLPSRAVPFPR KAGPGGDPGPGGFQTPPFSSFGLS VLHLPQAHPSLEAH |
| 2863 | 8360 | A | 3118 | 362 | 712 | |
| 2864 | 8361 | A | 3119 | 2 | 152 | |
| 2865 | 8362 | A | 3120 | 134 | 760 | |
| 2866 | 8363 | A | 3121 | 670 | 891 | |
| 2867 | 8364 | A | 3122 | 44 | 63 | SPSNRNTEEGTLTNIIHNLGMYVFL HAVKGTPFETP*PG*KARAP*PPLGN NWDYGDRTSFTGSFFTISPILYFL ASFYTKYDPTHFILNHSFSS*VVLNS PKWPQLHGVRIFGN*KSKQQEh |
| 2868 | 8365 | A | 3123 | 88 | 207 | |
| 2869 | 8366 | A | 3124 | 2 | 191 | |
| 2870 | 8367 | A | 3125 | 145 | 865 | |
| 2871 | 8368 | A | 3126 | 69 | 118 | |
| 2872 | 8369 | A | 3127 | 1148 | 1323 | |
| 2873 | 8370 | A | 3128 | 197 | 327 | PLGKKFSCSKSLRLLGPFLQL*SLRF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RKTTY |
| 2874 | 8371 | A | 3129 | 154 | 303 | |
| 2875 | 8372 | A | 3130 | 3 | 158 | |
| 2876 | 8373 | B | 3131 | 144 | 274 | XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL* |
| 2877 | 8374 | A | 3132 | 383 | 529 | |
| 2878 | 8375 | A | 3133 | 1981 | 2132 | EKENEDQKLIHLFFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI |
| 2879 | 8376 | B | 3134 | 144 | 274 | XICTLSEKERQIKKQTALVELVKHK PKATKEQLKAVMMISQLL* |
| 2880 | 8377 | A | 3135 | 383 | 529 | |
| 2881 | 8378 | A | 3136 | 1979 | 2131 | EKENEDQKLIHLFFFFSLGVKPTPCL KNINFFNHFASFLCASINKKWKRI |
| 2882 | 8379 | A | 3137 | 296 | 592 | |
| 2883 | 8380 | A | 3139 | 224 | 700 | VLLPPTGKRYPKVYIGVFKGPRKM GSSEIPFQNPFSIFSKEGYFLCREDFP NGAQISLLEEPFQIHLKLTFMFKNTT NFIFTAELCDQCQGL*NLHLSSSP* KKRHLT/HNQTHPHIKTDFHC*FIHY LVV*KSQSTSQHLLFKSTMGKDQRQI DNNIMN |
| 2884 | 8381 | A | 3140 | 761 | 963 | |
| 2885 | 8382 | A | 3141 | 475 | 715 | |
| 2886 | 8383 | A | 3142 | 381 | 698 | |
| 2887 | 8384 | A | 3143 | 2 | 235 | YASLEPPDRPQVGASCPGTYY*GA VPPSPAGVGREGVAGKTGGCTCDK PLSPCSLAG\RRGSFPRRPSWTSPL LCW |
| 2888 | 8385 | A | 3144 | 49 | 353 | |
| 2889 | 8386 | A | 3145 | 174 | 495 | |
| 2890 | 8387 | A | 3146 | 73 | 226 | |
| 2891 | 8388 | A | 3147 | 326 | 421 | |
| 2892 | 8389 | A | 3148 | 1306 | 1444 | |
| 2893 | 8390 | A | 3149 | 53 | 246 | |
| 2894 | 8391 | A | 3150 | 228 | 271 | |
| 2895 | 8392 | A | 3151 | 419 | 599 | |
| 2896 | 8393 | A | 3152 | 1 | 322 | |
| 2897 | 8394 | A | 3153 | 151 | 375 | |
| 2898 | 8395 | A | 3154 | 2017 | 2191 | |
| 2899 | 8396 | A | 3155 | 3 | 234 | LWSASSAQDATWADSQELSMARLP HVRKCVVVVLLQLSLLELLDFPP L/CLGPGCPCHLAHQHPCPRPLFQ LSGR |
| 2900 | 8397 | A | 3156 | 43 | 408 | |
| 2901 | 8398 | A | 3157 | 3 | 374 | |
| 2902 | 8399 | A | 3158 | 1 | 823 | MAVVAPRTL L L L L LSGALALTQTWA GSHSMRYFSTSVSRPGSGEPFIAV GYVDDTQFVRFDSDAASQRMPEPA PWMEQEEPEYWDRQTEISKTNAQI DLESLRIALRYYNQSED/VPPPKTH MTHHPISDHEATLRWALSFPYPAEI TLTWQRDGEDQTQDTEL VETRPAG DGTFOKWASVVVPSGQEQRVYCHV QHEGLPKPLTLRWPSSQPTIPIVGIL AGLVLF GAVIAGAVVAAMWRRK SSDRKGGSYSQAASSDSAQGS D VSL TACKV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2903 | 8400 | A | 3159 | 1 | 1264 | MAVMAPRTL L L L L L SGALALTQTWA GSHSMRYFFTSVSRPGRGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRA PWIEQEGPEYWDQETRNVKAQSQT DRENLRALPLTYNQSEAGS\HTLQ MMYGLGRGGSDGALSFRGLPPVTA YDGKDNIALNEDLRSWTAADMAA QITQRKWET/AAHEAEQWRAYLEG RCVEW\LRRYLENGKETLQRTDPP\ KTHMTHHPISDHEATLRC\WALSFY PAEITLTWQRDGEDQTQ\DTKL VQT RPAGDGTFFHKGASC VGPLGEEQRY TC\HVQHE\GLPK\PTM\RW* PSSQP THPPSWG I HCLALVLLWKL* SLEAV VAACECGRRKSSDRK\GGSYTQAA KPV TSAQGS D VSLTACKSVRQLPCV GLRGKSCFLPFLVDLEPWTLPFA KGT LHVSVFM |
| 2904 | 8401 | A | 3162 | 1 | 342 | GSRTVPSPSPSSGLASPGSPTHRSLG PTTPPMASATEDPVLERYFKGHKA AITS LD LSPNGKQLATASWDTFLML WNFKPHARAYRYDGHKDVVTSVQ FSPYGYLMAAG/SRDLSVRLWIPV** EYS*NGKQLATASWDTFLMLWNFK PHARAYRYDGHKDVVTSVQFSPYG YLMAAGLETYP |
| 2905 | 8402 | A | 3163 | 1 | 583 | DMESRSVTQPGVQWCYLG*LQPPP PRF*RFSCLSLPGSWDYRCVPPHPA NFFIFSRDGVSHHVQAGLELLVSS DPPASASQSAGITGLSHHARPD/YTF LLTVFEPFHGTHVRPPVTCGTLASN WTP TAFISLAENTKVLKVALKEVPF GFDIAISKASGTVQIRAMSFMKTTF SPSFVRECHTHDHVTLLQS |
| 2906 | 8403 | A | 3164 | 1 | 347 | FFILFFLRQSHSVA*AGVQWHNLD LQPLPPGFKQFS/LSLPSSWDYRRMP PRPANF*FLVETGFRHVQAGLELL TSGDPPASTS QSAGITGVSHGAQSC PLL YIEFPLSILAAT |
| 2907 | 8404 | C | 3165 | 13 | 399 | MEKIPVLFVRVANLISIIPAPNKSRLC GKTRISRS AKSKANTRVFLACRFGL AGDNAIANVHAPDADLEAQSDVER TMDLKPCIWVPDTLGEAEQTAPAD RLSMHTQHFGRRRADHEVRRPRP SWLIW* |
| 2908 | 8405 | A | 3166 | 168 | 414 | NPLLLPNTFPANGNTILIKEKVLFLF F*DGSPVLSRPDCGLQWRNLG\SL QSPPPGFTPFSCLSLPSSWDYRHPPL RPANFFLYFLVETGFHRASQG\GLD LLTSRS/IPPRASQSA/RGLQGVSHPR PAYMSLRYNKP AHVPLKIKVKK |
| 2909 | 8406 | A | 3168 | 28 | 123 | |
| 2910 | 8407 | A | 3169 | 2 | 123 | ENRLMAGGE/HMLAAILLFTALRCL CKVKHKPGLHAH*GTAP |
| 2911 | 8408 | A | 3170 | 1 | 402 | QGFSP\ESLRYG\SWEGKALTFFQP DTHKGSVLED**KRKASLQLR*EEG ICL\CLSLGMECLGVKP/VAYILFTEI GESRLMAGGK/HMLAAILLFTALRC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LGKVKHKSGLRAHRTAPFLKLIY DTESFAHMFSC |
| 2912 | 8409 | A | 3171 | 1 | 399 | SSSLQPPPP\GFK*FSCIGLPTSRDYR CVPPRP\ANFVFSVETGFHHVGQAG LELLTSGDPSTSASQSAGMTGVTTV PRPVLLISEAHFWCKNSLFTGENVI EANQNLLALRFISAMDQLSLRIVRN QTTFF |
| 2913 | 8410 | A | 3172 | 1 | 451 | LYGEGWSFALVAQAGVQWCDLRL LQPLLPGFK\YSPASASRVAG/HYR WSL/DSVTQAGVQWHNLGSLQPPPP SFKRFSCLSLPSS*DYRCTPPGLA*/F FIFLVEMGF\LLARLVSNS*PSGDPS TLGLPKVLGLQGVSHHALVPHLLIL QKR |
| 2914 | 8411 | A | 3173 | 2 | 346 | |
| 2915 | 8412 | A | 3174 | 1 | 2430 | |
| 2916 | 8413 | A | 3175 | 576 | 983 | GRSFIVSFLLVNSGKVPTDK/ERLFD RMMNSNWG/RSFAFKVNSNLST*Q FKYKNKGICAACQFSLFPLK*PIRL FFAGEHTIRNYPATVHGALLSGLRE AGRIADQFLGAMYTLPRQATPGVP AQQFPKACETDAF |
| 2917 | 8414 | A | 3176 | 1 | 2930 | RRAGSVKRGEARLFGPTERQSERPL RPSAARRPEMLSGKAAAAAAAAAA AAATGTEAGPGTAGGSENGSEVAA QPAGLSGPAEVGPGAVGERTPRKK EPPRASPPGGLAEPGSGAGPQAGPT VVPGSATPMETGIAETPEGRRTSRR KRAKVEYREMDESLANLSEDEYYS EEERNAKAEKEKKLPPPPQAPPEE ENESEPEEPSGVEGAAFQSRLPHDR MTSQEAACFPDIISGPQQTQKVFLFI RNRTLQLWLDNPKIQLTFEATLQQL EAPYNSDTVLVHRVHSYLERHGLIN FGIYKRIKPLPTKKTGKVIIIGSGVSG LAAARQLQSFGMDVTLLEARDRVG GRVATFRKGNYVADLGAMVVTGL GGNPMAVVSKQVNMELAKIKQKC PLYEANGQAVPKEKDEMVEQEFNR LLEATSYLSHQLDNFVNLNNKPVSLG QALEVVIQLQEKHVKDEQIEHWKKI VKTQEELKELLNKMVNLKEKIKEL HQQYKEASEVKPPRDITAEFLVKSK HRDLTALCKEYDELAETQGKLEEK LQELEANPPSDVYLSSRDQILDWH FANLEFANATPLSTLSLKHWDQDD DFEFTGSHLTVRNGYSCVPVALAEG LDIKLNTAVRQVRYTASGCEVIAVN TRSTSQTFIYKCDVLCCTLPLGVLK QQPPAVQFVPPLPEWKTSVQRMG FGNLNKVVLCFDRVFWDPVNLFG HVGSTTASRGELFLFWNLYKAPILL ALVAGEAAGIMENISDDVIVGRCLA ILKGIFRS\SAVPQP\KETVVSRRWA DPWG\RGs*SYVAQGS\SGNDYDL MAQPYHSWAPSIPGAPQPIPRLLC GENITIRNYPs/TPVHGALAEVGSRE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AGKEIARPSFWGAMY/TRLPRQ\ATP GCFLAQQVPQACETRCIPKGRGPM CPVSCPCKEGSSSNTRSPLEKSTPGI WAPDQLMELPDLTKGACLLNDLE HQGGTCPLVWNCVLRKD |
| 2918 | 8415 | A | 3177 | 62 | 447 | GDRAEESAEPRAWSHSDNSHRYTT LFICLTHTHVHNPVHS\HTHTHTHT HTHTHTHTVSRYRHTETPPLLLKQTG LKFY*NSRDDTPRSRPGSSGLQRLSS SPPVPFQPGTVEASADFCGDDLLTT VRLQ |
| 2919 | 8416 | C | 3178 | 90 | 233 | MRIGYKVKDGTFLDLQMGGLPGX XXSRPKRNHQLSKGEREINLGL* |
| 2920 | 8417 | A | 3179 | 462 | 929 | SLFHTWKADGFFLTGNSSSRPGNNT ICKSKKCPILYLISNHPQIMPLFF CDGSFTLVGPGWEWQWCDLSSLQP PTPR/FN*FSCLSLPSSWDHRHPPSCP ANFLYF**RLGFHHVGQAGLELLAS SDPPASASHSVGITGVSHHTWPMPL LLLI |
| 2921 | 8418 | A | 3180 | 160 | 272 | FFL*DRALLCLPDWSAVV*SWLTAA LA\YRRKRSSYLSLPSSWDYRHLPP CPANFSYFL*RQSLTVLPRLVNSW TQVSLLTQPSVLGLQA |
| 2922 | 8419 | A | 3181 | 6 | 270 | RDRVLLCHTDWSIAVESQLTASSN SW\VK*SSCLSLQTRDYRHEPPYL ANF*IFCRD/RGLTMLPRLV*NSWPQ GILPPWPPKSLGLQV |
| 2923 | 8420 | A | 3182 | 92 | 549 | VWQGLHPQLHPHFASQNLISLALS LKAGVQWHDLSSLQPPRRFKPFS CLSLPSSWDYRRAPLCPANFFLYF** RQGFTMLARLVSNY*PRDPPASASQ SAAITGVSHCARPRLSSLLQCFSNSS RLEHTDGIHFLSEAMSAIHESFPHI |
| 2924 | 8421 | A | 3183 | 16 | 661 | DRVSVTQAGVQWCNLGSLQPLPPR FR*FSCLSLSSWDYRRPPPRPANFC IFSRD/MAFTTLARLVSNS*PQ/CDPP TSASQSAEITGVSHRAWPVLSPPQF FFFDMEHAITQAGVQWRHLGSLQ PPPPMFK*SSCLSLSSWDYRRPPPR PANFFVFL*RDGVSPC*PGWSRSPD LVIHPPWSPKSAGITGLSHCAQPYP QFSKHKDLRVSGKA |
| 2925 | 8422 | A | 3184 | 288 | 489 | CGLILELEKLLLWVIQIQMSLNKA TI*SNDIFCPLST*NQVWCVFKGRSL HFEQKVVPSSNKVTG |
| 2926 | 8423 | A | 3185 | 3 | 166 | WLYSANVAHAPYRGSAWCLRDS RPPAQYWSAQHYSL*PTQFPLEFT TKSLLS |
| 2927 | 8424 | A | 3186 | 3 | 725 | LALLGRVYDVLSARD/YVELGPQYS VSKMTQRRSHVYTTRLNT/ADIYDS DLVPLCPQLSAVPLHSRNSAPYPYN PLYSVP/LPG/VVTGRFYGEDGLPTP ALTQVEAAITRGLEANKLQLEKQ TFPPCNAEWSSARGSRLWCSQKSPK DADDTSIYMFYQKVGDNIDSWNK AGRVFKDSKFDANDPILKDQTQE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | WSGSATFTSDGKIRLFYTDYSGKHY GKQSLTTAQNGVKPEGTTETTMK |
| 2928 | 8425 | A | 3187 | 1 | 1988 | |
| 2929 | 8426 | A | 3188 | 134 | 944 | MLRCGGRGLLLGLAVAAAAMAA RLMGWWGPRAFGRLFIPEELSRYSR GRPRDPGA*YLALLGRVYDD/DPP GRRHYEPGSHYSGFAGRDASRAV TGDCSEAGLVDDVSDLSAAEMTL HNWLSFYEKNYVCVGRVTGRFYGE DGLPTPALQVEACDSTRGFGGQT NYKLQEKQTFPPCNAAGGGAQPGAA RLWCSQKSGGVSRDW/ALAVPRKL YKPGAKEPRCVCVVRTTGPPSGQMP DNPPHRNRGDL\DHPLNAEYTGCP LAITCSFPL |
| 2930 | 8427 | A | 3189 | 1 | 312 | AQPGVQ*RNLSLQPPPPGSKRLSC LSLPSS*DHRPPPCPANF/SVFLVE MGFHHVGQAGLELPTSGDPPASAS QSAGITGASHRTRPES*FY*LRLGIII FR |
| 2931 | 8428 | A | 3190 | 2 | 176 | |
| 2932 | 8429 | A | 3191 | 3 | 67 | |
| 2933 | 8430 | B | 3192 | 1 | 1587 | MVKLSIVLTPQFLSHDQGGQLTKELQ QHVKSVCPCPYLRKVINTLADHH HRGTDGFGSPWLHVIIAFPTS YKVV TLWIVYLWVSLKTFWRSRNGHDG STDVQQRWRSNRRRQEGRLSICM HTKKRVSSFRGNKIVLKDVITLRRH VETKVRKIRKRVTTKINHHDKIN GKRKTARKQLSQHSISHVLAFSDPP FCKKGSLLQAPPSADDNIKIPAERLR IPLPSADDNLKTPSERQLTPLPSAP PSADDNIKTPAERLRGPLPSADDN LKTTPSERQLTPLPSAPPSADDNIKT PAERLRGPLPSADDNLKTPSERQL TPLPSAPPSADDNIKTPAERLRGPL PPSADDNLKTPSERQLTALPSAPPS ADDNIKTPAERLRGPLPSADDNLK TPPLATQEAEEKPRKPKRQRAAE MEPPPEPKRRRVGDVEPSRKPKRRR AADVEPSSPEPKRRRVGDVEPSRK KRRRAADVEPSSPEPKRRRVGDVEP SRKPKRRRAADVEPSLPEPKRRRLS * |
| 2934 | 8431 | A | 3193 | 792 | 1024 | SHRKMFRQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKALCNW RMIISRHLPSVVLHVPLYQPRTRPT LH |
| 2935 | 8432 | A | 3194 | 1 | 1656 | |
| 2936 | 8433 | A | 3195 | 112 | 368 | SHRKMFRQAQELRRRAEDYHKCK/I SLNIQFLMCWLFQIPPSARKPLCNW VSLLVFLAFEHSLPGQDMDTFFSLQ LCAQARTGRSD |
| 2937 | 8434 | A | 3196 | 1 | 1353 | |
| 2938 | 8435 | A | 3197 | 1 | 452 | |
| 2939 | 8436 | A | 3198 | 1 | 510 | |
| 2940 | 8437 | A | 3199 | 2159 | 2958 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2941 | 8438 | A | 3200 | 350 | 927 | LFLVSPLKTISGSRNG\HDGSRDVQQ RA*SSNRRRQ\KKRVSSFRGNKIVLK DVITLRRHVETKVRAKIRKRKVTTK INHHDKINGKRKTARKQKMFQRAQ ELRRRAEDYHKCKIPPSARKPLCNW VSLFVFLAFEHSLPGQMDMTFFSLQ LCAQALQREMAERKAA\YRHHSPIP VGNRVVQKHLHPHPVGPLI |
| 2942 | 8439 | A | 3201 | 1 | 277 | FFFF*ERIWLCCPGWSALARTWLT AAPNSWAQTILPHSWG\YRRLPPCP AFILFYLF\CRDK\SLAMLRLVLNS\ WAQVILPLQPPKVLGLQA |
| 2943 | 8440 | A | 3202 | 1 | 340 | SIHLPKAPPPNHSTGVV\QHRNFFL RWHLTQC/*PGWSAVAQSLLTATST SR\VKQSSHLSLLSSWDHRCAPPHL ANFLYF**RRDFTVLLRLVSNS*A*V ICPRWPPKVLGLQM |
| 2944 | 8441 | A | 3203 | 2 | 354 | ESLTGVQWHEFASLKPL/PCLSLPR GWDYRRAPPRPAYF*FLVETGFHHI GRAGLKLLTSDPPVSASQSAGITG MSHRAWPLLKYFSALQTLNILQKN KNKNLIKTYFISLHVKIF |
| 2945 | 8442 | A | 3204 | 166 | 373 | EGALFCSQASELLSCGLLAVFTRFK LRGPHCCCAKKVYSLPRMGPH TTL H/TALNI*SCPCCLFIFLVC |
| 2946 | 8443 | A | 3205 | 2 | 775 | LHHLPGGGSVSHNKPALCGAVPAG RPDTGDNPAPVGRSNGSALTPVWV LIAKQSPPIVKILKFGWFPILAMVIS SFGGLILSKTVSKQYKGM\AIFTPVI CGVGGNLVAIQTSRISTYLHMWSA\ LGVLP LLMKKFCPNPRSTFC\SQKL NSMSCSRLLLLGGSQGH\LIFFYIY LGGGVVSQS*T/TPDLCGCSNLLGRA* SRVTNPAVTGA\VELVRLTWHQGL \DPDNHCIPYLTGLGDLLGTGPPGDS AFSLTGY |
| 2947 | 8444 | A | 3206 | 2 | 348 | IAFGRYELDTWYHSPWPEEYARLG RL\HMCEF*IKYMNSLTILTMHMVN CAFDPPLGLPKELSLETRMETFFPAL PSFHSIHCLPCVQPELGKAFGCLSVG AWGCRTHLRFTGLH |
| 2948 | 8445 | A | 3207 | 1 | 1503 | |
| 2949 | 8446 | A | 3208 | 1 | 635 | |
| 2950 | 8447 | A | 3209 | 1 | 665 | MQAIKCAGGWKAEAVGKTCLLISY T\TNA\FPGEYIPTVFDN\YSA\NVMV DGK\PVN\WGLWDT\SGQKDYDRV PPYPYPA/QADVFLICFS\LVSPAS\FE NVR\AKWYLNVRHHCPN\TPILVGT KLDLRDDKD/TRIEKLKEKKLT\PIT YPQGLAHG*GRLGAVKYLG/CAPA AHTSEGLKTVFDEAIRA\VLCPPPVK ERGRENCLPVVNVSAPSFLGPVPLE PL |
| 2951 | 8448 | B | 3210 | 1 | 693 | MYGVSAFVVLSP\TGR\PSVLQKEN QQQGV\PN\SP\PLHEQM\QMDTGLCRL TPGLTLAGQWTRGSDSLPGAGEAG RTSFLPMYNANSAASSATHTGAAS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RESCGERECVQFSQRTARDRWCI RAELEQDILDSAAVTIIQKWHIKGR ALHPAGVLGHVEAPFSLVLQLERSR FLKNRWESAGARYPGREEGNEIRH RGCGDRGSQEA AVRCKGPPTPAV ELPPRLPVLS* |
| 2952 | 8449 | A | 3211 | 1 | 627 | FFFGKSILLFKKINVTFDIEKDILKMF LKGLKRHLFWPGMVAPAC*SQHSG RPRRMDHLRSGVRDQPGQVQGETPS LLKNIKKISRAWWQAPVIPATREG*/ E*GESPEPGEKVCRRAEIAATCTP AWGVQSETLSSKKKKS FVLNVPHH PRQASVSFHC FHNQWGSPLWKKA RTFLLLGNGWLSCPHLSTQGNLSA PHLAEAQTLSP |
| 2953 | 8450 | A | 3212 | 114 | 411 | EREF RVPQVELQGPDLG*LNLLLP RLKQFFGLTFQRIWNYKLAPPPVN LEFWAKTGFSHV NQVGFELLT*GDP P/AWASQ RVKMTGPTHQAHLGNF F |
| 2954 | 8451 | A | 3213 | 48 | 1400 | HPMTPI*STPLLYPL/PVTSGLASLSS LTLQNSDS\LLQPLTSAM/PPSAIPT QRTSTPGLALFPGLPSPVANSTSTPL TLPVQSPLATAASASTSVPVSCGSS ASLLRGPHPGTSDLHISSTPAATTLP VMIKTEPTSPTPSAFKGPSHSGNPSH GTLGLSGTLGRAYT\STVPISLSAC LNPALSGLSSLSTPLNGSNPLSSISLP PHGSSTPIAPVFTALPSFTSLTNNFPL TGNPSLNPSVSLPGSLIATSSSTAATS TSLPHPSSTAAVLSGAFCFSTSPAAP FPLNLSTAVPSLFSVTQGPLSSSNPS YPGFSVSNTPSVTPALPSFPGLQAPS TVAAVTPLPVGWPPHPQLPVLPGF GSAFSFHFNSRSLHKKPGFIWDFK AGRQFWFFRAFGPSRVS LGFLRILH NHPCKNYSIMRLHSQHCSRSIQLR LWESYPAQPDGVS |
| 2955 | 8452 | A | 3214 | 2 | 694 | QLLNYAPGPGGPVYDCDLF*NGY HL\WYHD\YGHLEF\RLQATQFEN WYMKYQSPHITKYGAETVSGFPR DPPSDVPVRCPRKSLLEQYHLGLDS KPQKNTCLESPLWNF\ADFMTE\QSP \TKVLGNKKGIFTRAETTQQAFL LRERYWKIAQ*NP GIPHSVARSQCL ENTACCSLSKTDTHLRVPSSPGGQR LPQQQNKCLDCSRQTRTFSGLGFV VIYSSREH |
| 2956 | 8453 | A | 3215 | 2434 | 2765 | GIILFWAQLFPASFFFFFFF*DGVS LC CPGWSAVVRSQLTASSASRVQAILC LSLPSSWDYRHLPPCLANFFVFL/CR DGGFTMLARLVLS*AS*VHPPWPP QSAGDYQA |
| 2957 | 8454 | A | 3216 | 2 | 481 | LFLFLRHSFTLSPSLDVQWRDLGSL QPPPPRFK*FSCLTLPSSWYYRHVPL CLANF*FLVETGFCHVGQSGLELLT SGDLPASASQSVWITGMSHGARLH GHFLGSWENWTCQAPGSSKSDCS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PHMANAVSAGGPGTLLIPSAPSCPC NLAGGRCPLR |
| 2958 | 8455 | A | 3217 | 126 | 364 | RAWAN\LS*LKVLPPGLKGFSGLTL PSTGNNGLVPPPRVNFSGFSKNGVS PCGP/GWF*TTALRELGPLSLLEIGIN PFFL |
| 2959 | 8456 | A | 3218 | 132 | 342 | SLSSLKNMYICLWNVFLFVFGYRAF LCHPGWSTVAQS*LT/IPGT/LWVKP SSLLVLPKRWDYRHEPLRPDLK |
| 2960 | 8457 | A | 3219 | 2 | 264 | QLTATPPPTGFKQFSCLSHPSSWDY RYVPPRPAKFCIFS/VRRGFTMLAR MVSIS*PCDLPTSASQSAGITGVSHR AWPVL*FVFLVETGFHHVQGQDGLN LLTLRSAHLSLPKCWDYRRKPPGLA CFMILNSYLV |
| 2961 | 8458 | B | 3220 | 134 | 3038 | PGMEDGSDDMDTSVEDIGGRSCVT RFVRTLLLIMEHGVKPHSKHLTEYF AFLYEFAKMGEESQFLSLQAIST MVHFYMGTKGPENPQVEVLSEEG EEEEEEEDILSLAEKRYRPAALEKMI ALVALLVQSRSERHLTSLQTDMA ALTGGKGFPFLFQHIRDGINIRQTCN LIFSLCRYNNRLAEHIVSMLFTSIK LTPEAANPFFKLLTMLMEFAGGPPG MPPFASYILQRIWEVIEYNPSQCLD WLAVQTPRNKLAHSWVLQNMEN WVERFLLAHNYPRVRTSAAYLLVS LIPSNFRQMFRSTRSLHIPTRDLPLS PDTTVVLHQVYNVLLGLLSRAKLY VDAAVHGTTKLVPYFSFMTYCLISK TEKLMFSTYFMDLWNLFPKLSEP AIATNHNKQALLSFWYNVCADCPE NIRLIVQNPVVTKNIAFNYILADHD DQDVVLFNRGMLPAYYGILRLCCE QSPAFTRLASHQNIQWAFKNLTPH ASQYPGAVEELFNLMLQFLIAQRPD MREEELEDIKQFKTTISCYLRLCD GRSCWTTLISAFRILLESDEDRLLVV FNRGLILMTESFNTLHMMYHEATA CHVTGDLVELLSIFLSVLKSTRPYLQ RKDVKQALIQWQERIEFAHKLTL NSYSPPELRNACIDVLKELVLLSPH DFLHTLVPFLQHNHCTYHHSNIPMS LGPYFPCRENKILIGGKSNIRPPREL NMCLLPTMVETSKGKDDVYDRML LDYFFSYHQFIHLLCRVAINCEKfte TLVKLSVLVAYEGSKSKCFLEANC GQFGSALFITNLISQYQNLQSDFSNR VEISKASASLNGDLRALAFAPVSTH SQTVPSSNSNSARAFKQMQDLSA TEKLTTPRGKKPKERKTKDDEGGNS HLKGRAC* |
| 2962 | 8459 | A | 3221 | 2170 | 3139 | DLRALALLSVHTPKQLNPALPTL QELLSKCRCTCQQRNSLQEQEAKER KTKALALWTTIITFRVGGGSNTLGV TGLRVVCSAEPK*YKC*KQN*LPTS PPNVILMTFREVSLLACVFTDDEGA TPIKRRRVSSDEHTVDSICISDMKTE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TREVLTPSTSDNETRDSSIIDPGTE QDLSPENSSVKEYRMEVPSSFSED MSNIRSQHAEEQSNNGRYDDCKEF KDLH\CSKDSTLA\EEEE\FPSTSISA VLSDLADLRSCDGQALPSQDPEVAL SLSCGHSRGLFSHMQQHDILDTLCR TIESTIHVVTRISGKGNQAAS |
| 2963 | 8460 | A | 3222 | 3 | 344 | PESHSAAGVQWPDGLSLQLSLP AFKQFSCSLSPSSRDYRRASPRPANF *FLVETGFCHVSQAGLKLLASSDPP VSASQTARITGVSHHAQPRATFYRH KSVLVLPLLKSPQ |
| 2964 | 8461 | A | 3223 | 1411 | 1741 | GYLQFSFSFFLFFFFFFFGLGESHSV T/RGLECSSVISTHCNLRPGSSDSR ASASRVARTRGMHHHTRQIFVFLV QMGFHVHVQAGL/DSS*PSVVHPP\ RPPKVLGLQA |
| 2965 | 8462 | A | 3224 | 361 | 462 | RHFLSTETYCNSFF/RHSSSKNYTK LKRYE*VS |
| 2966 | 8463 | A | 3225 | 3 | 89 | |
| 2967 | 8464 | A | 3226 | 1 | 336 | VCQVCGFRSRLHTNVNRHLLLNKP KIFPHVCDDCGKGFSSMLEYCKHL NSHLSEGIYLCQYCEYSTGQIEDLKI HLDFKHSADLPHKCSDCLMRFGNE RELISHLPVHETT |
| 2968 | 8465 | A | 3227 | 951 | 2075 | RTANLNFCKILDKSQALNVNCPAET GL*LRANSRWP/PINCELCEFNISKYF SDLKQHMILKHKRTDSNVCRCVCKE SFSTNMLLIEHAKLHEEDP/N/YVCK YCEYKPVIFENISRHIADTHFR\DPPI HWCEQCDVQFSSSELYLHFQEHSC DEQYLCQFCEHETNDPEELA*\HVG K*GMHVN**ELSDKV/CNNGWNMG QYSLLSKITFDKCKNFFVCQVCGFR SRLHTNVNRHVAIEHTKIFPHVCDD CGKGFSSNTWKRKRQGQKTFPLLI NLELSTSLTNYRGSPWASELSTSVE VSMAMPLPAAEAETQGHDSGEREPF SQTPGLMQPFSIPVQITLQGSRRRQG RLPVLGDWRPFKLTCSPPALIIAQPI VGAQE |
| 2969 | 8466 | A | 3228 | 2 | 415 | LDPGSLAGFTSYIQFMYDEFVEEYE PTKADSYRKK/VAQDGEEVQIYIINT AGQEDYTAIKDNYFHCVFSTITES FAATVDFKEQ/ILRVKKDENIPFLLV GNKSDLEDKRQVSIEEAKNRAD*W NVIYVETSPKT*AN |
| 2970 | 8467 | A | 3229 | 607 | 1317 | |
| 2971 | 8468 | A | 3230 | 260 | 535 | |
| 2972 | 8469 | A | 3231 | 246 | 985 | KLRHKMAANKPKGQNSLALHKVI MVGSGGVGKSALTQFMYDEFVED YEPTKADSYRKKVVLDGEEVQIDIL DTAGQEDYAAIRDNYFRSGEGFLC VFSITEMESFAATADFREQILRVKED ENVPFLLVGNKSDLEDKRQVSVEE AKNRAEQWNVNYVETSAKTRANV D/KEWPFLKTRWWNTCKYISSHCPR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PAPVSRKTAHWAEVFFDLRMREIRARKMEDSKEKNGKKRKS LAKRIRERCIL |
| 2973 | 8470 | A | 3232 | 1 | 634 | MAANKPKGQNSLALHKVIMVGS GVGKSALT\QFMYDEFVED*E\PTK ADSSRKVVLDGEEV\QIGYPLDTA G\QED\YAAIRD\NYFRSGEGFLCVFS ITEMESFAATAEFREQILRVKEDEN VPFLLVGNKSDLEDKRPGL*EEAK\ NRAEQWNVNYVETSAKTRANVDK VFFDLRMREIRARKMEFEFYLN GTKNTKRLAERIREGGCIL |
| 2974 | 8471 | A | 3233 | 314 | 373 | |
| 2975 | 8472 | A | 3234 | 1 | 2129 | PSVAGAATLWFHVTLPF CARLCGR RSCTHSGIITEFHFFHL/PRPIPI LACGNDDCRIHIFAQNDQFQKVL SLCGHEDWIRGVEWAAPGRDLL LASCSDCLIRIWKLYIKSTSLET QDDDNIRLKENTFTIENESVKIA FAVTLETVLAGHENWVNAVHWQ PVFYKDGVLQQPMRLSASMDK TMILWAPDEESGVWLEQVRVGE VGGNTLGFYDCQFNE DGSMIIA HAFHGALHLWKQNTVNP REWT PEIVISGHFDGVQDLVWDPEG EFIITVGTDTTTLFAPWKRKDQ SQVTWHEIARSQIHGYDLKWL AMINRFQFVSGADEKVLRVFS APRNFVGKFLCHYR\KSLNHV LCNQDSDLPEGAT\APALGLS NKA VF/LREDKAPQPPDE EELLTSTGFEYQQVAFQPSIL TEPPTEDHLLQNTLWPEVQK LYGHGYEIFCVTCNSSKTL LASACKAAKKEHAAIILWE TTSWKQVQNLVFHSLTVTQ MGLLT**GSFLLGCFPEDS NLVIVEKAWIQS/TPEFEP VFSLFAFTNKITSVHSRI IWSCDWSPDSKYFFTGS RADKKVVWGECDSTDDCIE HNIGPLPPSVLDRGWGCD QLSASACSHPSQRYVV AVGLECGKDLLIYLGKRL IKFQK*M T/ATHCVGNK SKPKVIHWAIQKIYC WEGICSGKT*TRREGRR C*VVYTFA SCG*DHTV KIH RVNKCAL |
| 2976 | 8473 | A | 3235 | 451 | 778 | GSGRWKRSRVARAGMQISGAHL QLNCKPPPPGLKADPPWLS\PS SWDPQMCPTPWLLFVCLVETG FTMLPQ AALQLLS*SDLSA* ASQNAGITGMS HHAGPDT VPLF |
| 2977 | 8474 | A | 3236 | 1 | 186 | FFFFEMESRTVTQAGVQWHD LG\SLQPP\PPG\SSDSPVS ASHVAEITGAHHHTWLIF FIFL*GVQWHD LGLTAT SLLGSSDSPVSASHVAEIT GAHHHTWLIF FIFL |
| 2978 | 8475 | A | 3237 | 1 | 353 | KIWLFFVFKTDVSVILVHPR LECSGAI SAHCNLHLPGLS DSTSAFRVAGTTGARHQA QLIFTFLVEMGFHHVGH AGLKLPT*EIRPPRPPEV LGLHACAT VPGHKYVNE PIKMVLLK |
| 2979 | 8476 | A | 3238 | 3 | 453 | GQTGTWQGNTGQRPVQLPP HPPPIH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LVSRRHGKLRHGFRLPMPEPRGLES GKTGSARGVAACTSP*GRSG/QGGG PRDIAQQGGCRGSACGRRSHEALRP RVWCGEGPQWTW\CAVCP\NRSAP GAGLAD\RQHPGESRAWGETRLCE AGGAE |
| 2980 | 8477 | A | 3239 | 232 | 472 | LHSFIHSFIHLFIYLFDRVLLCCPDW STVERSQLTVTLKSR\VK*SSCLS/LP SSWGYRSVPPCPANYFYFL*RQRLT TLPS |
| 2981 | 8478 | A | 3240 | 2 | 345 | MVHVAVAGLNGTHSCPPASSSVLTF GHP\PHEQLQQSVGPTSPHSPLL*PL SSLEVLGWGSEGVGGLQEIQKCSK ALPCKTPCGCFCIYLIFSPTQGDIFPH DPAPLLLSASWV |
| 2982 | 8479 | A | 3241 | 205 | 361 | DAHSPAPAVSTPGQAWAAVLAMFP PGPWGEGSGRL\IPHPAPLLLSAS WV |
| 2983 | 8480 | A | 3242 | 137 | 959 | IPFPVMLDPAGRQQQRWGRIMGY KVSLLGA*NLGRCKNIHKGSCREGL CLISLRAWEGRLVGGFAQN*HTA HPEPGKSSHS*KIPFQRESGL*PATH PVPSKTPPLPGESSRARAWCLKGE DPCPRKPPAP*SLPPGPWGE/P*QGL QPRLGL*TPGLGYEHLKPPF/PSA PAA*PPG\PAKAQAPRKSCAPTIVTH ALLPPNPLPTQLGWKWISADQSQSN PFPRAYP/REPSLFSPNAPLSPSPHP TTFPEFPCSPTPPQIPHQPDPFRS |
| 2984 | 8481 | A | 3243 | 23 | 438 | SRHLGLPKCWDYRQEPLCLALSFFF RVRVS\SVAQVVVQWHDGRSLQPQ TPGPK\YPPATAS*VAGARLIFFK*FL *RWDLTIMPKAGLKLPAATGDPPACL LLSFSLIPTGGFTRFEPTRHSLLEV GLSPMLVRHWLWA |
| 2985 | 8482 | A | 3244 | 1 | 1061 | ASRRALQLFGIPVRQLQKGACPLGL HQLSSPRYKFNFIADVLFKIAVAV HIELFLRHPLFGRNVPLSSSGSFIMS EAGLIITNAHVSSNSAAPGRQQLK VQLQNGDSYEATIKDIDKKSIDIATIK IHPKKKLPVLLLGHSDRTCRPGEVL WVAIRQIPSP*QNTVTTGIVSTAQR EGRELGLRDSMDY\QTDALINNYG NSGGPLVNLDEGIVGINTLKVTAGIS FAIPSDRITRFLTEFQDKQIKDWKKR FIGIRMRTITPSLVDELKASNSDFPE VSSGIYVQEVVPNSPSQGGIQQGGDI IVKVNGRPLVDSSSELQEAULTESPL LLEVRRGNDDLLFSIAPEVVM |
| 2986 | 8483 | A | 3245 | 1 | 268 | QGSPSRDPSPGLGGPNGGIFLAP/AGP NPP/RGTRGNPVFS*NSKICPGWGGP PVGPGS/RGELG*RAALAPGGPGGL DWAPGP*PGGQRGAPF |
| 2987 | 8484 | A | 3246 | 20 | 353 | KEVGRLTHSVNHSGGREKYVWHP GNAL*YGKLPVLPCPIFIVNR*VQ*P *PERHMTVRGSGMNVWIMP/PGKPP RPAEVPVEVEGHLEWTAEDSSNHC QLQG*DQLQWGRWL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 2988 | 8485 | A | 3247 | 2 | 322 | KLDNSSKWLENGTFDLSILQDLDNF C*KMGKWSEVPYVQAFF\SIHSLPSL CSQCHL/CPDFPSFSP/YPLLSPPQT QSPLNPPFPLTPLTSLLRLLARLN QVPILP |
| 2989 | 8486 | A | 3248 | 141 | 924 | PFSSQTVKLSGGATRNPVSSPKASG GQPSEGWEVALEGDS CAALMRQQ CPGLLSRK/RAPGNPTASGSAPGA TKRSLGGRARRGLEFVVSRRFFGGGR AQSSLGNAHPHSGTIPKAPHASQQG LGLRLGGLEPSTPPWVHPPARPRAS PDPSRVAGSPRSLPNPPAAGKGGRG SGEEARYFDLS*ILKSLPYPGHERVY QEPQRGVKTSCSCSPF/HLPLLLFQS SPPPSTLVGAGLKIGFLRCPVGGILI GKGFFFNCLHST |
| 2990 | 8487 | A | 3249 | 1 | 363 | QVSLVINWDLPTNR*NYIHR*AYIW NTPLPLHTWPSLGLKLLIFLIFLEFQ VGRGGRDRKGGAINKGTEYDERT LRDIETFYNTSIEEMPFNVDHMLM GCPATQPLSGLIIGASDQY |
| 2991 | 8488 | A | 3250 | 1 | 87 | LNETVLLWHSWGMSTVVQTQLLPA ASTWVKQSSHLNLSWDHSRVP PHWANFLIFCR/DRSFAMLPKLVSN PWAQAVLPPLPIVL*LNETVLLWH SGWMSTVVQTQLLPAASTWA |
| 2992 | 8489 | A | 3251 | 3 | 270 | CFNSAWTEPGARSPRPAAHSQPSV TSSPHPRTPAPPPPPLQR/SP*SPP*R PRPP/PHVRHNYPSGLKSHH*SAE*P GPLGPIPTVY |
| 2993 | 8490 | A | 3252 | 3 | 452 | |
| 2994 | 8491 | A | 3253 | 1 | 477 | TLLVPQDSERTHPWCLSPADKTNV KAAWGVKGVAHAGEYGAELERM FLSFP\TTKTYFPHFD\LSHG\SAQG* RAHGK\KVA\DALTKAVAHVDDMP KRRCPP*SDLHGAQAFGWDPVQLQ SS*SHLPCLGEPWAAHLPRPSFNPW RLQRLPWGQISWGFC |
| 2995 | 8492 | A | 3254 | 3 | 295 | LFLFFFFFF*MESHSVTRLECSGTIW AH*NLHLPSSDSPALASRVAGTTG MCHHIQLIFFVFLVEKGFHHVG*/D MSLSLDLVIHPPWPPKVLGLQA |
| 2996 | 8493 | A | 3255 | 306 | 519 | GTRVERHSRERPSCHLLCEPSQRYS PLLFLVGL*CPPASPGKSPRTKENNF TADSKSQGQSEKSLWVTLA |
| 2997 | 8494 | A | 3256 | 453 | 626 | HGSCLLHHREQVPIPPGIPNLSDSIL* FPVLRWMLCLYTSCMWFSQSFWI AVMYFV |
| 2998 | 8495 | A | 3257 | 1537 | 1909 | NVLTVEDHPIPIPSKNRPFHNLDPVN LAFFFFFFLNRVSFCHLGWSAVARS HLTCNLLSPGFKQFSCSLSSWDY QACMHHTRLVFGVFSRDGGFTMLA RLVSNS*PQVILPPLPPKVLGLQA |
| 2999 | 8496 | A | 3258 | 1 | 342 | KTESHSVAQAGVQWCDLGSLOPPP PRFKLFSCLSSWDYRGALPRPT DLFA/QFLVEMGFCHVAQAGLELLS SGNLFASASQTARITGVNHHTWPVL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | *F*VKKIPPSLPGLL |
| 3000 | 8497 | A | 3259 | 1 | 338 | FFLRWSL/NSVAQAGVQWRNLSSL QALPPGFRPFSCLSLPNS*DYRCPP RLANFFLYFLVETVFHRLY*RSRMV LIS*PGDPPTSASHSAVVRYLLRRRQ CLRQGLCRASVF |
| 3001 | 8498 | B | 3260 | 188 | 1504 | MRTLLPPALLTCWLLAPVNSIHPEC RFHLEIQEEETKCAELLRSQTEKHK ACSGVWDNITCWRPANVGETVTVP CPKVFSNFYSKAGNISKNCTSDGWS ETFPDFVDACGYSDPEDESKITFYIL VKAIYTLGYSVSLMSLATGSIILCLF RKLHCTRNYIHLNLFSLRAISVL VKDDVLYSSGTLHCPDQPSWVG CKLSLVFLQYCI MANFFWLLVEGL YLHTLLVAMLPPRRCFAYLLIGW GLPTVCIGAWTAARLYLEDTCWD TNDHSPVWWVIRIPILISIVNFVLFIS IIRILLQKLTSPDVGGNDQSQYKRLA KSTLLLIPLFGVHYMVFAVFPISISSK YQILFELCLGSFQGLVVAVLYCFLN SEVQCELKRKWRSRCPTPSASRDYR VCGSSFSRNGSEGALQFHRSRAQS FLQTETSVI* |
| 3002 | 8499 | A | 3261 | 1 | 1047 | MVSISWPRDLPASASQSAGITGLIGA LVLSVGIYAEVER/HEI*NP*KCLPGS SHHPHPPGRRHVHGLLHWCAGVPP *QPELLASRLSRGYGLVLSWLEP RYEKMISGMYLGEIVRNILIDFTKK GFLFRGQISETLKTGRGIFETKFLSQIE SDRLALLQVRAILQQLGLNSTCDDS ILVKTVCVVSRRAAQLCGAGMAA VVDKIRENRGLDRLNVTGVVDGTL YKLHPHFSRIMHQTVKELSPKCNVS FLLSEDSGSGKGAALITAVGVRLRTE ASS |
| 3003 | 8500 | A | 3262 | 178 | 568 | IIFFFFFKMESCSVAQAGVQWWDL SSLQPLPPGFMPFCLSLPSSWDYRR PLLPANFLYF**RRGFTVLARMVSI S*PCDPPASASQSAGITGVSHCAQLE SKFYEGRDVHLFCSPLYFQKARKLP GIE |
| 3004 | 8501 | B | 3263 | 776 | 5218 | MLGDNSSMSVTAPKTFQWDMMW RRKGLILILALCRPKEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEEE EEEEEEEEEEEEEEEEEEEEEDQLDT MLWDSSNTLNTALSKEKTMFSSR AKIVKPNGEKPDEFESGISQALLELE MNLDLKAQLWELNITAAKEIEVGG GRKAIIFVPVPQLKSFOKTQVQLRR ILPKPTQKSCTNNKQKLPRSCTLTA VHDAILEDLVFPSEIVGKRIHVKLD GSHLIKIHLDEAQNNVEHKVEPFS GVYKKLMGKDVNFEPFQLMPGT PGSLEMGLLTFRDVAIEFSPEEWQC LDTAQQNLRYRNVMLENYRNLAFLG IALSKPDLITYLEQGKEPWNMKQHE MVDEPTGICPHFPQDFWPEQSMEDS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FQKVLLRKYEKCGHENLQLRKGCK SVDECKVHKEGYNKLNQCLTTAQS KVFOCGKYLKVIFYKFLNSNRHTIR HTGKKCFKCKKCVKSFCIRLHKTQ HKCVYITEKSCKCKECEKTFHWSST LTNHKEIHTEDKPYKCEECGKAFKQ LSTLTTHKIIICAKEKIYKCEECGKAF LWSSSTLRHKRIHTGEKPYKCEECG KAFSHSSTLAKHKRIHTGEKPYKCE ECGKAFSHSSALAKHKRIHTGEKPY KCKECGKAFFSNSSTLANHKITHTEE KPYKCKECDKTFKRLSTLTCHKIHH AGEKLYKCEECGKAFNRSSNLTIHK FIHTGEKPYKCEECGKAFNWSSSLT KHKRFHTREKPFKCKECGKGFIWSS TLTRHKRIHTGEKPYKCEECGKAFR QSSTLTCHKIHTGEKPYKFEECGK AFRQSLTLNKHKIIHSREKPYKCKE CGKAFKQFSTLTTHKIIHAGKKLYK CEECGKAFNHSSSLSTHKIHTGEKS YKCEECGKAFLWSSSTLRHKRIHTG EKPYKCEECGKAFSHSSALAKHKRI HTGEKPYKCKECGKAFFSNSSTLAN HKITHTEEPYKCKECDKTFKRLST LTKHKIHHAGEKLYKCEECGKAFNR SSNLTIHKFIHTGEKPYKCEECGKAF NWSSSLTCHKRIHTREKPFKCKECG KAFIWSSTLRHKRIHTGEKPYKCE ECGKAFFSRSTLTCHKTIHTGEKPY KCKECGKAFFKHSSALAKHKIHHAGE KLYKCEECGKAFFNQSSNLTHKIIH TKEKPSKSECDKAFIWSSTLTEHK RIHTREKPYKCEECGKAFFSQPSHLT THKRMHTGEKPYKCEECGKAFFSQS STLTTHKIIHTGEKPYKCEECGKAFR KSSTLTEHKIHTGEKPYKCEECGK AFSQSSTLRHTRMHTGEKPYKCEE CGKAFNRSSSLTTHKIIHTGEKPYK CEECGKAFFSSSTLNGHKRIHTREK YKCEECGKAFFSQSSTLRHKRLHTG EKPYKCGECGKAFFKESSALTKHKII HTGEKPYKCEKCKAFNQSSILTINH KKIHTITPVIPLLWEAEAGGSRGQE METILANTVKPLLY* |
| 3005 | 8502 | A | 3264 | 1 | 208 | RDRVLF*HPHWSAVV*SKLTAASTS WVK*FSCLSFLSWCLAMLPRLVLN SWPQVTLLPQPPKVLGLQV |
| 3006 | 8503 | A | 3265 | 78 | 359 | RHSSKNLGNVDSECE*T*FPDIIPFH* KKLTEGEYQKSVNH/MTNAVAHST LSSQLLLALQKTLCLFLMLLTKL PTIHTRTVDAHSLADDDVE |
| 3007 | 8504 | A | 3266 | 48 | 330 | VCGCVWMLRVLCYPGWWSAVAQ S*LTAALISLVNPSSSLSLPSSWDHR RAPPRPANFFNL*RQELPMLRLVL/ NVWAQVILPPWPPKMLELQV |
| 3008 | 8505 | A | 3267 | 200 | 1033 | RSLAPRWHLGHKEKNVTTTSVWG WSPGRNASNSAGVGAGLPFVSTW LAVSSKNIDITEHIDFATPIQQPAME |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PLCNGNLPTSMHTLG\HLHGVSNP QPCTYTGESQLTEVLQNLGQR/RNI HNSRLNRLAPRM/LQSFGKEPRPSW VL/CPAQALYWRV*RPKERRPIEL PSAQLRLHYGPPQMCKDVPLISLANIL PQLPSSGNDVIVATHGQ*SLHHTL L*TPFHLGNVYVAMEEFKALVWY ESTLASLQPEFVPAKNRIQTIQCHLM LKKGRALLP |
| 3009 | 8506 | A | 3268 | 2 | 2956 | LADSSPSNLQIIKELLSMHHPDPA LTKEFDYLPVDSRSSSGFVGLRNG GATCYMNAVQQLYMQPGLPESLL SVDDDTDNPDDSVFYQVQSLFGHL MESKLQYYVPENFWKIFKMWNKE LYVREQQDAYEFFTSIDQMDDEYL KKMGRDQIFKNTFQGIYSDQKICKD CPHRYEREEAFMALNLGVTSCQSLE ISLDQFVRGEVLEGSNAYYCEKCKE KRITVKRTCISLPSVLVIHLMRFGF DWESGRSIKYDEQIRFPWMLNMEP YTVSGMARQDSSSEVGENGSRVDQ GGGGSPRKKVALTENYELVGIVIH SGQAHAGHYYSFIKDRRGCGKKG WYKFNDTVIEEFDLNDETLEYECFG GEYRPKVYDQTNPYTDVRRRYWN AYMLFYQRVSDQNSPVLPKKSRSV VVRQEAEDLSLAPSSPEISPOSSPRP HRPNNDRLSILTKLVKKGEKKGLFV EKMPARIYQMVRDENLKFMKNRD VYSSDYFSFVLSLASLNATKLKHPY YPCMAKVSLQLAIQFLFQTYLRTKK KLRVDTEEWIATIEALLSKSFDACQ WLVEYFISSEGRELIKIFLECNVRE VRVAVATILEKTLDLAFYQDKLKS LHQLLEVLLALLDKDVPENCKNCA QYFFLFNTFVQKQIRAGDLLRHS ALRHMISFLLGASRQNNQIRRWSSA QAREFGNLHNTVALLVLHSDVSS QRNVAPGVIFKQRPPIAPSSPLLPL HEEVEALLFMSEKPYLLEVMFAL RELTGSLAALIEMLVYCCFCNEHF SFTMLAFHLRNQLAETA\PPHEFKGI RFPTTFMEILVIEDPIQAERVVKFVFE TENGLLALMHHSNHVDSSRCYQCV KFLVTLAQKCPAAKEYFKENSHHW SWAVQRLHH\KMSDLYWTPLSNVS NETSTGKTF*RTISDHDTL\PYATALL NEKEHSGSRNGSKSRPANENGHRH LQQGSQSPLDDWVSLRSDLDVDP |
| 3010 | 8507 | A | 3269 | 68 | 301 | NFRDLCDILCSETTRLNTINMSIL SNLTYRFSEIPF*IFRRLFVL*KL/ENS ILKYIWTCKGPRLVKTTFKNNSES |
| 3011 | 8508 | C | 3270 | 224 | 518 | MINKGQAGANIKSNXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXX* |
| 3012 | 8509 | A | 3271 | 342 | 724 | NTYPWAVL/VFFFFFFLRWSLTLVAR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LECRAGVQWCDLGS LQPLPPQFE* FSCLSLQLALPRPAKFFVILVEMGF TMLAKMVSIS*PCDPPALASQSARIT ILDFMLAPACPLLIIPFTWTLFFRNTI |
| 3013 | 8510 | A | 3272 | 3 | 367 | |
| 3014 | 8511 | A | 3273 | 58 | 553 | VARSAPPDGAVCAGPGSRRTMAE QSDEAVKY\YTLERFQMHN\HSKST WLILHHKG\YDLTKFLEEHPGGEEV LREQA\GGD\ATENFEDVG\HSTDAR EMSKTFIIGVELHPVDRPKLNKASGT FKGCV*GNFLFTTI*FLVPSWWTNW \VIP\AISAVGRRLGCIRL |
| 3015 | 8512 | A | 3274 | 41 | 400 | KRLGPRGGVGPSPNGGNQGL*GPKI FPWPSTLGTK/GEPLPSSSSSSSPQK RGFPSSPEK\APGVPPPTPKGPSPPGG GVKKKGRA*KKKPLGLWEKGPNA PGGPGTPTFGGPPGQYPG |
| 3016 | 8513 | A | 3275 | 3 | 146 | WGVITMMVTCSV/A/CTLFWLIAIL AQCNP LYRP*LKDETTWYLKHHWP |
| 3017 | 8514 | A | 3276 | 161 | 472 | |
| 3018 | 8515 | A | 3277 | 3 | 273 | AAAPGN GRASAPRLLLLFLVPLLW APAAVRAGPDEDLSHRNKEPPAP SSCSRSLWAVQGPEPARVEVSGPG WGERGCRAGCAEYQAPGL |
| 3019 | 8516 | A | 3278 | 124 | 672 | FQRTKLLNGPGDVETGTSITVPQKK WLHVISPIFVQSLTLPFLAKWGDR QLLQIELAAREVSDI*EETV*NETYL LLCSRKTLDTLKWAHSIPSYARLF YI**FCSCLKLAFSQFLLPADPYGVA VGGTVGHCLCTGLAVIGGRMIAQKI SVRTVTIIGGIVFLAFAFSALFISPD GF |
| 3020 | 8517 | A | 3279 | 2 | 991 | AAAAPGN GRASAPRLLLLFLVPLL WAPAAVRAGPDEDLSHRNKEPPAP \PSSCSRSLWAVQGPEPARVEKIFTP A\APVHTNTEDPATQTNLGIYPMQF VAIIQLL\VSEIGVSR\TFFIAAIMA MRYNRPGPCWAGAMLCL/AGLMT CLFS/VLFGYATTVIPRGLYILMFQP VLFAIFGIRMLREGLK\MSPDEGQEE LEEVA\ELKKKDEEFQRTKLLNG\ PGDVETGTSITVPAQKKWLHFISPIF GQALTLTFLAEWGDRS*\LTTIVLAA REDPYGVAVGGTVGHCLCTGLAVI GGRMIAQKISVRTVTIIGGIVFLAFA FSALFISP |
| 3021 | 8518 | A | 3280 | 1 | 278 | QHDLQDQDVAFTEEE*RLAGPAQR KLYRDVIVENLRNLLSVGHPPFKQD ISPIERNQDLWIMTTATRIPGNLGKN QTVISSYSKLFICFASS |
| 3022 | 8519 | A | 3281 | 263 | 588 | DSALPQKEELKMNMFKEAVTFKDV AVAFTEELG\LLGPAQRKLYRDVM VEN\FRN\LLSVGHPPFKQDVSPIER NEQLWIMTTS/TPRRQGNLDTLSVK AL\LLYDLAQT |
| 3023 | 8520 | A | 3282 | 1 | 1285 | MEDSELPSARSVLP SKRIGVVQSQQ RPPLGERHYGPTTRDGALHSAYSPT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QARCVSHPTYEKYPHVWRGWPPFS PEKERQRLENLRRKEEAEQLRRQK VEEDKRRRLKEEVKLRKEERLRKVL QARERVEQMKEEKKKQIEQKFAQI DEKTEKAKEERLAEEKAKKKAAAK KMEEVEARRKQEDARRLRWLQQ VRAQ/EGNRSREVK*HLKSHEPVCS GGDSRTHPQPLVHWSQCLP*RLLA RVLRELQEREKALRLQKEQLQRELE EKKKKKEEQQLAERQLQEEQEKKA KEAAGASKALNVTVDVQSPACTSS PITPQGHKAPPQINPHNYGMDLNSD DSTDDEAHPRKPIPTWARGTPLSQA IIHQYYQPPNLELFGTILPLDLEDIF KKSAPRYHKRTSSAVVNSPPLQGA RVPSSLAYSLKKH |
| 3024 | 8521 | A | 3283 | 3 | 262 | FHTEERSYECTECGKA\FKHSSTLLQ HRKVHTPERRQEDRAHGKVVSC*H RVHQERSYSRKEVKESGRESAIRKK LNLAHPNTHPRE |
| 3025 | 8522 | A | 3284 | 1 | 269 | FFFFPQIGSHPI\RLCESDAITFCCSL NLPGRDPPASAS*VAETTGLHHHA GLIF*FFVE/MGL/HQAGLELLDKVIL PPLPPKELGSQM |
| 3026 | 8523 | A | 3285 | 3 | 1191 | KSCFNAFFNFEDMQEITQHFAVCH VDAPGQQEGAP/SPFPTGYQYPTMD ELAEMLPVLTHLSLKSIIIGIVGAG AYILASRFALNHPELVERPLCSLMVD PC/ALKGWIDWAASKLSGLTTNVV\ EII LAHHFGQEELQANLD\LIQTYRM HIAQDINQDNLQLFLNSYNGRRDLE IERPILGQNDNKS\TLKCSTLLVVG DNSPA\VEA\VMADCGGLPHVVQPG KLTEAFKYFLQGMGYIPVCAAQSPE HRVST\SASMT\RLARS\THSTSSSLG SGESPFSRSVTSNQSDGTQESCESPD VLDRHQTMEISLDDVLLSALLRNN GKSAQQKKISAKPKLEFLCPRPGTC DHGSRKFCYTVL\VDPRERSKATAV ALGSFPAGGPAELSLRLGEPLTIVSE |
| 3027 | 8524 | A | 3286 | 3 | 638 | SSKLSGLTTNVVDIILAHHFGQEELQ ANLDLIQTYRMHIAQDINQDNLQLF LKS\YNGRRDLEIERPILGQNDNKS TLKG\STLLVVG\DNSPA\VEA\VECN SRLNPINTTL\LMADCGGLPPG*FS PGKLTEAFKYFLQGMGYIPLVLCYS TSGSMTSVARS\THSTSSSLGSGES PFSRSVTSNQSDGT\QES\CESPDVL DRQQTMEVSC |
| 3028 | 8525 | A | 3287 | 1 | 407 | FSIETESCSVAQAGGKWHDSGSLQP QPPRFK*FSCLSLLNSWDYRPAPP/* PG*LFFVFLVETGF/IHVGQPGKLKL TSSDPPTSASQSAGITGLRDRAQPPP EDSNVQFENHWQRECTMLLFTLGP LKLFP\TELML |
| 3029 | 8526 | C | 3288 | 157 | 468 | MHHIHNASRTFQLIFSSFPRGNAIVF MLKMGGFLELRGPRSGMDHHRGR GEANQPFCTSPAACGQNLPIKHGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PRWSTKGETTADTDSVDLENPILYK YFQL* |
| 3030 | 8527 | A | 3289 | 14 | 348 | EFHSCRPGWSAMTQSRLTLQPPPPG FK*FSCLSLLSSWDYRHTPPHPASF* LLVDTGVFLHVGQAGLKLLTSGDSP TSASQSARITGVNHCARPSTFLRLQ RKAGRCSTSL |
| 3031 | 8528 | A | 3290 | 1 | 2201 | MTNLAMVERDSEAGTAASRFPGNH AAKGKAQAHYKVWRPAEVRCLKL GPEWVTLRYTIKHPYKLCGKRQH VFFFTSRSDVGFMLTTLKPGSVSV ESKMNNKAGSFFWNLRQFSTLVST SRTMRLCCLGLCKPKIVHSNWNILN NFHNRMQSTDIIRYLFQDAFIKSDV GFQTKGISTLTALRIERLLYAKRLFF DSKQSLVPVDKSDDDELKKVNLNHE VSNEDVLTKETKPNRISSRKLSEEC NSLSDVLDAFSKAPTFPSSNYFTAM WTIAKRLSDDQKRFEKRLMFSPAF NQLCEHMMBREAKIMQYKYLFLSLH AIVKLGIPQNTILVQTLRVTQERIN ECDEICLSVLSTVLEAMEPCKNVHV LRTGFRILVDQVWKIEDVFTLQVV MKCIGKDAPIALKRKLEMKALREL DRFSVLNSQHMFEVLAAMNHRSLI LLDECSKVVDNIHGCPLRIMINILQ SCKDLQYHNLDLFGGLADYVAATF DIWKFRKVLFILILFENLGRFPVGLM DLFMKRIVEDPESLNMKNILSILHTY SSLNHVYKQCQNEQFVEVMASALT GYLHTISSVENLLDAVYSFCLMNYFP LAPFNQLLQKDISELLTSDDMKNA YKLHTLDTCLKLDDTVYLRDIALSL PQLPRELPSSHTNAKVAEVLSSLLG GEGHFSKDVHLPHNYHIDFEIRMAD TNRNQVLPL/SLDVGTTSAT\DIQRL LTYISFAGLSELKS |
| 3032 | 8529 | A | 3291 | 3 | 485 | LHTLDTCLKLDDTVYLRDIALSLPQ LPRELPSSHTNAKGGQRS*AALLGG EGTPPSKDVHLAPHNYHIDFEIQN GTPNRNPSAYPLSDVDTTSCQLQFK E*LCYVFPRSA YCLGSSHPRGFLAM KMRHLNAMGFHVILVNNWEDGQT RDGRCQSPFLKT |
| 3033 | 8530 | A | 3292 | 1 | 530 | LRKTFIPNRPLILLPPGNSLATHLFFA ETVSRSAQAGVQWHHLGLLQSPS PGFKRFSCLSLPSNWDYRHAPPRLA NFYIFS*DGVSFHHVGQAGLKLLTS GDPLTLASQSAGITGVSHCTRPLIHK FGLSYRQRIENVSFLLPYTHASSLLQ LLLAPLVTNGQGQEQKPELVREVG |
| 3034 | 8531 | A | 3293 | 115 | 463 | VTKQLFNILSFIFFHTSILIFFFLKME SCSVA\RLCSGTILAHCNLCPLGSS NSPASASRVSWDYKVCATMPG*FL YF**E\QGFHHVGQAGLRTPGPQGD PARPWAPKVLGLQA |
| 3035 | 8532 | A | 3294 | 503 | 1055 | DIDFSPV*LVNVQMRRHALLMNLW DT/QDSHTSLRNAEYCSLMEEDMAP |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | SNKTTWLRPLTQQF*NLPQKKTALA KK*KDFTHRVLFTA*MCLPQSSSLW HL*NWKQSKCPSVGDWEH*FVQW GTPYQKEE*GTPIDKGQSTYNIMQI YICFFLKQYKDKNLKWLLWRTGVS GGSETEIDSEVISGL |
| 3036 | 8533 | A | 3295 | 3 | 304 | FFLVETEFCHAAQAGVQWCDLGLS QPPPPGLQQSSHLNLPKS*DYRCEPP MPG*FLETGFHPSCPRLVPKLLGSSS PPASAS\QSIGIS\GVSHCPEKFPF |
| 3037 | 8534 | A | 3296 | 324 | 650 | KKEHRVTCFSFWEMESRSVA*AEV Q*HDLSLQPLPHGLKRVSLSLPSS WDYRHLPPCLTNVCIFSRNGVSLY* PGWSRTPDLVILPALAPQSAGITGG EPPCPATK |
| 3038 | 8535 | A | 3297 | 2 | 564 | FFFPPPPSPGFKQFSCSLTPSSWD YRCPPPRPANF*FLIETGF/VHVGQA GLELLTSGDLPTPASQNAITGVVRP GTQPASCF*MWQGLIGQNKMTISLL LQSILL |
| 3039 | 8536 | A | 3298 | 352 | 392 | |
| 3040 | 8537 | A | 3299 | 20 | 200 | FTLIQNCFHEIQIEQCGLDAVAHTY NPSTLGGQGG*IA*AQEFETSLGNM VKPHLSLK |
| 3041 | 8538 | A | 3300 | 971 | 9082 | |
| 3042 | 8539 | A | 3301 | 1 | 15447 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLESPPVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSQNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTPVASFSFGIMTDPNF SIFRIRESKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNCTSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSRKTSVSQTSLEAKKWLREGIFD GQPERINTADYVGNLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDSGYLSKNKLDSGIE PVLKNVEDQKNTSFSKVISNVKDA |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | <p> NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVGPPAFRIAS GKIRLCSHETIKKVKDIFTDSFSKVI KENNENKSKICQTKIMAGCYEALD DSEDILHNSLDNDECSMHSKVFVA DIQSEEILQHNQNMMSGLEKVKISPC DVSLETSDICKCSIGKLHKS SVSSANT CGIFSTASGKSVQVSDASLQNAQV FSEIEDSTKQVFSKVLFSNEHSDQL TREENTAIRTPEHLISQKGF SYN VVN SSAFSGFSTASGKQVSILESSLHKVK GVLEEFDLIRTEHSLHYSPTS RQNV S KILPRVDKRNPEHC VNSEMEKTCSK EFKLSNNLNVEGGSSENNHSIKVSP YLSQFQQDKQQLVLGTKVSLVENI HVLGKEQASPKNVKMEIGKTETFS DVPVKTNIEVCSTYSKDSENYFETE AVEIAKAFMEDDELTD SKLPSHATH SLFTCPENEEMVLSNSRIGKRRGEPL ILVGEPSIKRNLLNEFDRIENQE KSL KASKSTPDGTIKDRRLFMHHSLEP ITCVPFRTTKERQEIQNPNTAPGQE FLSKSHLYEHLTLEKSSSNLAVSGH PFYQVSA TRNEKMRHLITTGRPTKV FVPPFKTKSHFHRVEQCVRNINLEE NRQKQNI DGHGSDDSKNKINDNEIH QFNKNNSNQAAA VTFTKCEEEPLD LITSLQNARDIQDMRIKKKQRQRVF PQPGSLYLAKTSTLPRISLKA AVGG QVPSACSHKQLYTYGVSKHC IKINS KNAESFQFHTE DYFGKESLWTGKGI QLADGGWLIPSNDGKAGKEEFYRA LCDTPGVDPKLISRIVVYNHYRWII WKLAA MECAFPKEFANRCLSPERV LLQLKYRYDTEIDRSRRSAIKKIME RDDTA AKTLVLCVSDIISLSAN ISET SSNKTSSADTQKVAIHELTDGWYAV KAQLDPLLAVLKNGR LTVGQKIIL HGAELVGSPDACTPLEAPESLM LKI SANSTRPARWYTKLGFFDPRPFPL PLSSLFSDGGNVGCVDVIIQRAYPIQ RMEKTSSGLYIFRNEREEEEKAAKY VEAQQRLEALFTKIQEEFEEHEEN TTKPYLPSRALTRQQVRA LQDGAE LYEAVKNAADPAYLEGYFSEEQLR ALNNHRQMLNDKKQAQIQLEIRKA MESAEQKEQGLSRDVTTVWKL RIV SYSKKEKDSVILSIWRPSSDLYSLLT EGKRYRIYHLATSKSKSKSERANMP AGRTV*K*S KKQKSFRYKRRGLGCS MSPSTTFKSGIQ*Y*LSIPEKSFI*S*K CQHSYFNSYFQGCSVKPSHDF*RQR IIQNVROAQR*QL*I*C*INQKYSHG KESRCMCFK*KL*KR*AVAT*KIHE SSITFKKGTINQNTNLRVIOKNQEE TTSISKITVNPDS EELFSDNENNFVF QVANERNNLALGNTKELHETDLTC VNEPIFKNSTMVLYGDTGDKQATQ </p> |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VSIKKDLVYVLAEEKNSVKQHIK MTLGQDLKSDISLNIDKIPEKNNNDY MNKWAGLLGPISNHSFGGSFRTAS NKEIKLSEHNIKKSKMFFKDIEEQYP TSLACVEIVNTLALDNQKKLSKPQS INTVSAHLQSSVVVSDCKNSHITPQ MLFSKQDFNSNHNLTSPQKAEITEL STILEESGSQFEFTQFRKPSYILQKST FEVPENQMTILKTTSEECRADLHV IMNAPSIGQVDSSKQFEGTVEIKRKF AGLLKNDCKNSASGYLTDENEVGF RGFYSAHGKTLNVSTEALQKAVKL FSDIENISEETSAEVHPISLSSSKCHD SVVSMFKIENHNDKTVSEKNNKCCQ LILQNNIEMTTGTTFVEEITENYKRNT ENEDNKYTAASRNSHNLEFDGSDSS KNDTVCIHKDETDLLFTDQHNICLK LSGQFMKEGNTQIKEDLSDLTFLEV AKAQEACHGNTSNKEQLTATKTEQ NIKDFETSDTFFQTASGKNISVAKES FNKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPKCKE MQNSLNNDKNLVSITVVPKLLSD NLCRQTENLKTSKSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMGLEKVKISKIS PCDVSLSDICKCSIGKLHKSVSASA NTCGIFSTASGKSVQVSDASLQNAR QVFSEIEDSTKQVFSKVLFKSNEHS DQLTREENTAIRTPEHLISQKGFSYN VVNSSAFSGFSTASGQVSILESSLH KVKGVLEEFDLIRTEHSLHYSPTSR QNVSKILPRVDKRNPEHCVNSEME KTCSKEFKLSNNLNVEGGSSENNHS IKVSPYLSQFQDKQQLVLGTVSL VENIHVLGKEQASPKNVKMEIGKTE TFSDVPVKTNIEVCSTYSKDSENYF ETEAVEIAKAFMEDDELTDKLP SH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKERQEIQNPNTA PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PTKVFPFVKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKN DNEIHQFNKNSNQAAVFTTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEDYFGKESLW TGKGIQLADGGWLIPSNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRAIK KIMERDDTAATLVLCVSDIISLSA NISETSSNKTSSADTQKVAIHELTDG WYAVKAQLDPPLAVLKNGRITV GQKIILHGAELVGSPDACPTEAPES LMLKISANSTRPARWYTKLGFFDP RPFPLPLSSLFSDGGNVGCDVIIQR AYPIQWMEKTSSGLYIFRNEREEK EAAKYVEAQQKRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFSVSFASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDC SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKKRRALDF LSRLPLPPVSPICTFVSPAQAQAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRTAPTSE DYLRLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI |
| 3043 | 8540 | A | 3302 | 1 | 2163 | |
| 3044 | 8541 | A | 3303 | 1 | 5771 | |
| 3045 | 8542 | A | 3304 | 1 | 3395 | MPIGSKERPTFFEIFKTRCNKADLGP ISLWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPMDSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGSFKN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FESGSDKISKEVVPPLACEWSQLTLS GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVS DIKEEV LAAACHPVQHSKVEYS DTFQSQK SLLYDHENASTLILTPTSKDVL SNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTT EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLT DENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVS MFKIENHNDKT VSEKNNKCQLILQNNIEMTTGT FVE EIT/EM*HAFT*GFC*HSE*RNFTT*P KYVWIGESF*NITL*C*FGNFRYM* M*YREAS*VSLICKYLWDF*HSKW KICPGIRCFITKRKTSVF*NRR*YQA SLFQSIV*K*RTFRPAHKRRKYCYT YSRTFNIPKRLFI*CGKFICFLWI*YS KWKASFHFRKFLTQS*GSVRGI*FN QN*A*SSLFTYV*TKCIKNTSSC**E KPRALCKLRNGKNLQ*RI*IIK*LKC *RWFFRK*SLY*SFSISLSISTRQTTV GIRNQLSTC*EHSCFGKRTGFT*KRK NGNW*N*NFF*CSCENKYRSLFYLL QRFRKLL*NRSSRNC*SFYGR**TDR F*TAKSCHTFSFYMSRK*GNGFVKF KNWKKKRRAPYLSGRTL NQKKLIK *I*QDNRKSRKILKGFKKHSRWHNK RSKIVYASCFFRADYLC TSLSHN*GT SRDTESKFYRTWSRISV*ISFV*TSDF GKIFKQFSSFRTSILSSFCYKK*KNET LDYYRQTNQSLCSTF*N*IAFSQS*T VC*EY*LGGKQTKAKH*WTWL**** |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | K*D**Q*DSSV*QKQLQSSSSCNFHK V*RRTFRFNYKSSECQRYTGYAN*E ETKATRLSTARQSVSCKNIHSASNL SESSRRPSSLCVFS*TAVYVWRF*T LHKN*QKCRVFSVSH*RLFW*GKF MDWKRNTVG*WWMAHTLQ*WKG WKRRIL*GSV*HSRCGSKAYF*NLG L*SL*MDHMETGSYGMCLS*GIC** MPKPRKGASSTKIQI*YGN**KQKIG YKCDNGKG*HSCKNCTSLCF*HNFI ERKYI*NF*Q*N**CRYPKSGHY*TY RWVVCC*GPVRSSPLSCLKEWQTD SWSEDYSSWSRTGGLS*CLYTS*SP RISYVKDFC*QYSACSLVYQTWILS* P*TFSSALIIAFQ*WRKCWLC*CNYS KSIPYTVDGEDIWIIHISQ*KRGRKG SSKICGGPTKETRSLIH*NSGGI*RT* RKHNKTIFTITCTNKTASSCFARWC RAL*SSECSRPSLP*GLFQ*RAVKS LE*SQANVE**ETSSDPVGN*EGHGI C*TKGTRFIKGCHNRVEVAYCKLFK KRKRFSYTEYLASIIRFIFSVNRRKEI QNLSSCNFKI*K*I*KS*HTVSSDKK NSVSTTTGFR*NFISDLPATGAPSLQ QIFRSRLSAILF*GGPNRICRFCCEKN RTCPFRLFVRRMLQFTGNKVLD RP* *GHY*ASYVNCCCKQPPVATRIQIRPS YFICWRFFCVFC*SKRGPLSRDIQQN EKYC*EY*HTLQ*SRKQAYAYTAC K*SQVVHPN*RLYFRAVHCSNHSW YRKQASDVFS*L*DILSKSFITLYGQ KEVCFHTCLSPDDFKVL*RGERD*M PIGSKERPTFFEIFKTRCNKADLGPI LNWFEELSSEAPPYNSEPAEESCHK NNNYEPNLFKTPQRKPSYNQLASTP IIFKEQGLTLPLYQSPVKELDKFKLD LGRNVPNSRHKSLRTVTKMDQAD DVSCPLLNSCLSESPVVLQCTHVTP QRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPMDSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGSFKNV SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENNFV FQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNKSKK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPOSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQAEITELSTILEESGSQFEFTQF R |
| 3046 | 8543 | A | 3305 | 1 | 5771 | MPIGSKERPTFFEIFKTRCNKADLGP ISL NWFEELSSEAPPYNSEPAEES KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLT GLNGAQMEKIPLLLHISSCDQNI DLDTENKRKKDFLTSENSLPRIS PKSEKPLNEETV VNKRDDEQHL TDCILAVKQAISGTSPVASSFQGIK SIFRIRESPKETFNASFSGHMTDPN KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFAEPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYM RVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNP DSEE LFSDNENNFV FQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNNDYMNK WAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRD/C/S/YLMIRKLIEAEDRL*KR *WKGMTQLQKHLFSVFLT*FH*AQI YLKLLAIKLVVQIPKKWPLLNLQM GGMLLRPS*ILPS*LS*RMAD*QLVR RLFFMEQNWALLMPVHLLKPQN LLC*RFLTTLVGLLAGIPNLDSTL DLFLCPYHRFSVMEEMLVVLM*LF KEHTLYSGWRRHLDYTYFAMKE RKKRKQQNMWRPNKRD*KPYSLK FRRNLKNMKTQQNHVHHVH*QD SKFVLCKMVQSFMKQ*RMQQTQLT LRVISVKSS*EP*IITGKC*MIRNKL SSWKLGRPWNLLNKRNVYQGM QPWGSCVL*AIQKKKKIQLY*VFGV HHQIYILC*QKERDTEFIILQLQNLK VNLKELTYS*QRQKKLSINNYRFQM KFYFRFTSHGSPFTSANF*IQTFSHL VLRWT**DLSFLL*KKQDLPLSSICQ TNVTIYWQ*SFG*TLMTLLSLIC*L LQATSSGDQNPNAFLLYLLEIFLCF LLVQKRATFKRHSTK*KILLRILTYF AMKQKTSLCIYCMQMIPSGPPQLKT VLQGRLLKSFLVQETSF*CLLLIVR YIKVLYHFVWPKGSLFPHLSQPR*L QSLVKGRKRLMTKRTAKREEPWIS* VDCLYLHLLVPFVHLFLRLHRRHFS HQGVVAPNTKHP*RKKN*ILLR*LH LKNSMKFLFWKVIQ*LTKNLH**IP KLFCLVQKEKNLYLSVNPLGLLPP VQKIISD*NDVVLHL*SKNRRVPRP VRKNVRKISRTQLQLKNIS |
| 3047 | 8544 | B | 3306 | 16 | 10899 | MPNVLEDEVYETVVDTSEEDSFSLC FSKCRTKNLQKVRTSKTRKKIFHEA NADECEKSKNQVKEKYSFVSEVEP NDTDPLDSNVANQKPFESGSDKISK EVVPSLACEWSQLTSLGNGAQME KIPLHHISSCDQNISEKDLLDTENKR KKDFTLSENSLPRISLPKSEKPLNE ETVVNKRDEEQHLESHTDCILAVK QAISGTSPVASSFQGIKKSIFRIRESP KETFNASFSGHMTDPNFKKETEASE SGLEIHTVCSQKEDSLCPNLIDNGS WPATTTQNSVALKNAGLISTLKKK TNKFIYAIHDETSYKGKKIPKDQKS ELINCSAQFEANAFEAPLTFANADS GLLHSSVKRSCSQNDSEPTLSLTSS FGTILRKCSRNETCSNNTVISQDLDY KEAKCNKEKLQLFITPEADSLSLCQ EGQCENDPKSKKVSDIKEEVLAAA CHPVQHSKVEYSDTDFQSQSLLY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DHENASTLILTPTSKDVLSNLVMISR GKESYKMSDKLKGNNYESDVELTK NIPMEKNQDVCALNENYKNVELLP PEKYMVRVASPSRKVQFNQNTNLRV IQKNQEETTSISKITVNPDSSEELFSDN ENNFVFQVANERNNLALGNTKELH ETDLTCVNEPIFKNSTMVLYGDTGD KQATQVSIKKDLVYVLAEEKNSV KQHIKMTLGQDLKSDISLNDKIPEK NNDYMNKWAGLLGPISNHSFGGSF RTASNKEIKLSEHNIKSKMFFKDIE EQYPTSLACVEIVNTLALDNQKKLS KPQSINTVSAHLQSSVVVSDCKNSH ITPQMLFSKQDFNSNHNLTSPSQEQI TELSTILEDGSGSQFEFTQFRKPSYILQ KSTFEVPENQMTILKTTSEECRAD LHVIMNAPSIGQVDSSKQFEGTVEI KRKFAGLLKNDCKNSASGYLTDEN EVGFRGFYSAHGKTLNVSTEALQK AVKLFSDIENISEETSAEVHPISLSSS KCHDSVVSMFKIENHNDKTVSEKN NKCQLILQNNIEMTTGTFFVEEITENY KRNTENEDNKYTAASRNHNLEFD GSDSSKNDTVCIHKDETDLFTDQH NICLKLSGQFMKEGNTQIKEDLSL TFLEVAKAQEACHGNTSNKEQLTA TKTEQNIKDFETSDTFFQTASGKNIS VAKESFNKIVNFFDQKPEELHNFSL NSELHSDIRKNKMDILSYEETDIVK HKILKESVPVGTGNQLVTFQGQPER DEKIKEPTLLGFHTASGKKVKIAKE SLDKVKNLFDERARTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVP SLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDL DYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSDDTFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSDNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me thod | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|------------|-------------------------------------|---|--|---|
| | | | | | | DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKEQITELSTILEDSSGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVVSFMKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFFE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDL FTDQHNICKLKSQFMKEGNTQIKE DLSDLTFLEVAKAQEAHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSLSNELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDERASHQWAK TLKYREACKDLELACETIEITAAPK CKEMQNSLNNDKNLVSIVTVVPPKL LSDNLCRQTENLKTSSIFLKVKVH ENVEKETAKSPATCYTNQSPYSVIE NSALAFYTCSRKTSVSQTSLEAK KWLREGIFDGQPERINTADYVGNY LYENNSNSTIAENDKNHLSEKQDTY LSNSSMSNSYSYHSDEVYNDSGYLS KNKLDSGIEPVLKNVEDQKNTSFSK VISNVKDANAYPQTVNEDICVEELV TSSSPCKNKNAAIKLSISNSNFEVG PPAFRIASGKIVCVSHETIKKVKDIF TDSFSKVIKENNENKSKICQTKIMA GCYEALDDSEDILHNSLDNDECSTH SHKVFADIQSEEILQHNQNMGLEK VSKISPCDVLETSDICKSIGKLHK SVSSANTCGIFSTASGKSVQVSDAS LQNAHQVFSEIEDSTKQVFSKVLFK SNEHSDQLTRENTAIRTPHEHLISQK GFSYNVVNSSAFSGFSTASGKQVSI LESSLHKVKGVL EFDLIRTEHSLH YSPTSRQNVSKILPRVDKRNPEHCV NSEMKTCSKEFKLSNNLNVEGGSS ENNHSIKVSPYLSQFQQDKQQLVLG TKVSLVENIHVLGKEQASPKNVKM EIGKTETFSQVPVKTNIEVCSTYSKD SENYFETEAVEIAKAFMEDDELTD KLPSHATHSLFTCPENEEMVLSNSRI GKRRGEPLILVGEPSIKRNLLNEFDR IENQEKSLKASKSTPDGTIKDRRLF VHHVSLEPITCVPFRTTKERQEIQNP NFTAPGQEFLSKSHLYEHLTLEKSSS NLAVSGHPFYQVSGNKNGKMRKLI TTGRPTKVFPVPPFKTKSHFHRVEQC VRNINLEGNRQKQNIIDGHGSSDDSK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NKINDNEIHQFNKNNSNQAAAVTFT KCEEEPLDLITSLQNARDIQDMRIK KKQRQRVFPQPGSLYLAKTSTLPRI SLKAAVGGQVPSACSHKQLYTYGV SKHCIKINSKNAESFQFHTEDYFX* |
| 3048 | 8545 | A | 3307 | 1 | 12500 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPNSRHKSLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPMDSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPHVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVANQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLLHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISSL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNG/K/TVMS**MPHRLVR*TAA SNLKVQLKLNGLLAC*KMTVTKV LLVI*QMCKMWGLGAFILLMAQN* MFLCLKCKKL*NCLVILRILVRKLL QRYIQ*VYLQVNVMMILLFQCLR*KII MIKL*VKKIINAN*YYKIILK*LLALL LKLLKITREILKMKITNILLPVEILI T*NLMAVIQVKMILFVFIKMKRTCY LLISTTYVLNYLASL*RRETLRLKKI CQI*LFWKLRLKLLKHHVMVILQIKNS *LLKRSKI*KILRLLIHFFRLQVGKI LVSPKSHLIK*ISLIRNQKNCITFP*I LNYILT*ERTKWTF*VMRKQT*LNT KY*KKVSQLVLEIN**PSRDNPVM KRSKNLLCWVFIQLAGKKLKLQRN LWTK*KTFLMKKSKVLVKSPVLAI NGQRP*STERPVKTLN*HVRPLRSQ LPQSVKKCRILSIMIKTLFLLRLWCH LSS*VIIYVDKLKISKHOKVSF*KLK YMKM*KKKQKQVLQVLTQISPLIQS LKIQP*LFTQVVVEKLL*VRLHYLK QKNGLEKEYLMVNQKE*ILQIM*EII CMKIIQTVL*LKMTKIISPKNKILI*V TVACLTAIPTILMRYIMIQDISQKINL ILVLSQY*RMLKIKKTLVFPK*YPM* KMQMHTHKL*MKIFALRNL*LALH PAKIKMQPLNCPYLIVILR*GHLHL G*PVVKSFVFHMKQLKK*KTYLQT VSVK*LRKTTTRINQKFAKRLWQV VTRHWMIQRIFFITL*IMMNVARIH RFLLTFRVKKFYINITKICLDWRKFL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KYHLVMLVWKLQIYVNVV*GSFIS QSHLQILVGFLAQQVENLSRYQML HYKTQDKCFLK*KIVPSKSFPKYCL KVTNIQTSSQEKKILLYVLQNI*YPK KAFHIMW*IHLSDLVQQVESKFP F*KVPYTKLREC*RNLI*SELSIVFTI HLRLDKMYQKYFLVLIRETQSTV*T QKWKKPAVKNLNYQIT*MLKVVL QKIITLLKFLHISLNFNKTNSWY*E PKSHLLRTFMFWEKNRLHLKT*KW KLVKLKFLMFL*KQI*KFVLLTPKI QKTTLKQKQ*KLLKLLWKMMN*QI LNCQVMPHILFLHVPKMRKWFCQI QELEKEEESPLS*WENPQSKETY*M NLTG**KIKKNP*RLQKALQMAQ*K IEDCLCIMFL*SRLPVYPFAQLRNVK RYRIQILPHLVKNFCLNLICMNI*LW KNLQAI*QFQDIHFIKFLQEMKK*D T*LLQADQPKSLFHLLKLNRIFTLN SVLGILTWRTDKSKTLMMDALMI VKIRLMTMRFISLTKTTPIKQQL*LS QSVKKNL*I*LQVFRMPEIYRICELR RNKGNASFHSQAVCILPATTTQNSV ALKNAGLISTLKKKTNKFYAIHDE TSYKGKKIPKDQKSELINCSAQFEA NAFEAPLTFANADSGLLHSSVKRSC SQNDSEPTLSLTSSFGTILRKCSRN ETCNNNTVISQDL DYKEAKCNKEKL QLFITPEADSLSCLQEGQCENDPKS KKVSDIKEEVLAACHPVQHSKVE YSDTDFQSQSLLYDHENASTLILT PTSKDVLSNLVMISRGKESYKMSD KLKGNNYESDVELTKNIPMEKNQD VCALNENYKNVELLPPEKYM RVAS PSRKVQFNQNTNLRVIQKNQEETTS ISKITVNPDSSEELFSDNENNFVFQVA NERNNLALGNTKELHETDLTCVNE PIFKNSTMVLYGDTGDKQATQVSIK KDLVYVLAEEKNSVKQHIKMTLG QDLKSDISLNIDKIPEKNNDYMDKW AGLLGPI SNHSFGGSFRTASNKEIKL SEHNIKKSKMFFKDIEEQYPTSLAC VEIVNTLALDNQKKLSKPOSINTVS AHLQSSVVVSDCKNSHITPQMLFSK QDFNSNHNLTSPQKAEITELSTILEE SGSQFEFTQFRKPSYILQKSTFEVPE NQMTILKTTSEECRDADLHVIMNAP SIGQVDSSKQFEGTVEIKRKFAGLL KNDCNKSASGYLTDENEVGFRGFY SAHGTKLVNSTEALQKAVKLFSDIE NISEETSAEVHPISLSSSKCHDSVVS MFKIENHNDKTVSEKNNKCQLILQ NNIEMTTGTFVEEITENYKRNTENE DNKYTAASRNSHNLEFDGSDSSKN DTVCIHKDETDLLFTDQHNICLKLS GQFMKEGNTQIKEDLSDLTFLEVAK AQEACHGNTSNKEQLTATKTEQNI KDFETSDTFFQTASGKNISVAKESF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NKIVNFFDQKPEELHNFSLNSELHS DIRKNKMDILSYEETDIVKHKILKES VPVGTGNQLVTFQGGQPERDEKIKEP TLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDLELACETIEITAAPCKKE MQNSLNNDKNLVSIE TVVPPKLLSD NLCRQTENLKTSKSIFLKVKVHENV EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDGQPERINTADYVGNYLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYNDSGYLSKNK LDSGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFEVGPPAF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDGKNIHSASN LSESSSRPSSLCVFS*TAVYVWRF* TLHKN*QKCRVFSVS/TLKIILVRK VYGLEKEYSWLMVDGSPMMER LEKKNFIGLCVTLQVWIQSLFLEFGF IITIDGSYGNWQLWNVPFLRNLLID A*AQKGCFFN*NTDMIRKLIEAEDR L*KR*WKGMTQLQKHLFSVFLT*FH *AQIYLKLLAIKL VVQIPKKWPLL LQMGMMLLRPS*ILPS*LS*RMAD* QLVRRLLFFMEQNWWALLMPVHLL KPQNLLC*RFLTLVLGLLAGIPNLDS FLTDLFLCPYHRFSVMEEMLVVL M*LFKEHTLYSGWRRHLDYTYFA MKERKKRKQQNMWRPNKRD*KPY SLKFRNLKNMKTQQNHIYHHVH *QDSKFVLCKMVQSFMKQ*RMQQT QLTRVISVKSS*EP*IITGKC*MIRN KLRSSWKLGRPWNLLNKRNVYQ GMSQPWGSCVL*AIQKKKKIQLY*V FGVHHQIYILC*QKERDTEFIILQLQ NLKVNLIKELTYS*QRQKLSINNYR FQMKFYFRFTSHGSPFTSANF*IQT SHLVLRWT**DLSFLL*KKQDPLSS ICQTNVTIYWQ*SFG*TLMRLLSLI C*LLQATSSGDQNPNAFLLYLLEIF LCFLLVQKRATFKRHSTK*KILLRIL TYFAMKQKTSLCIYCMQMIPSGPPQ LKTVLQGRLLKSFLVQETSF*CLLL IVRYIIKVLVYHFVWPKGSLFPHLSQP R*LQSLVKGRKRLMTKRTAKREEP WIS*VDCLYLHLLVPFVHLFLRLHR RHFHQGVVAPNTKHP*RKKN*ILL R*LHLKNSMKFLFWKVIQ*LTKNLH **IPKLFCLVQKEKNLYLSVNPLGL LPPVQKIISD*NDVVLHL*SKNRRVP RPVRKNVRKISRTQLQLKNIS |
| 3049 | 8546 | A | 3308 | 1 | 9344 | |
| 3050 | 8547 | A | 3309 | 1 | 18345 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TSSSTVLIVRNEEASETVFPHDTTAN VKSYSFNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPSLACEWSQLTSL GLNGAQMEKIPLLHISSCDQNISEK DLLDTENKRKKDFTLSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETSYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSHKVEYSDTDFQSQK SLLYDHENASTLILTPTSKDVLSNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSSE LFSNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNV TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITDACRKDSVKMIQAKKFKQI*KK RSWLQHVVTQYNIQKWNTVILTFNP RKVFYMMKMPALLF*LLLPRMFC QT*S*FLEAKNHTKCQTSSKVTIMN LMLN*PKIFPWKRIMYVL*MKIHK TLSCCHLKNT*E*HHLQERYNSTKT QI*E*SKKIKKKLLQFQK*LSIQTLLK NFSQTMRIJLSSK*LMKGHILL*EILR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NFMKQT*LV*TNPFSTRTPWFYMET QVINKQPKCQLKKIWMFLQRRTKI V*SSI*K*L*VKI*NRTSP*I*IKYQKK IMIT*TNQDS*VQFQITVLEVASEQ LQIRKSSSLNITLRRACSSKILKNNI LLV*LVLKL*IPWH*IIKRN*ASLSQL ILYLHIYRVV*LFLIVKIVI*PLRCYFP SRILIQTI*HLAKRQKLQNFLY*KN QEVSLNLLSLENQATYCRRVHLKC LKTR*LS*RPLLRNAEMLIFMS**MP HRLVR*TAASNLKVQLKNGSLA C*KMTVTKVLLVI*QMCKMWGLG AFILLMAQN*MFLKLCKKL*NCLV ILRILVRKLLQRYIQ*VYLQVNVML LFQCLR*KIIMIKL*VKKINAN*YYK IILK*LLALLKLLKITREILKMKIT NILLPVEILIT*NLMAVIQVKMILFV IKMKRTCYLLISTTYVLNYLASL*R RETLRLKKICQI*LFWKLRLKKHV MVILQIKNS*LLKRSKI*KILRLIH FFRLQVGKILVSPKSHLIK*ISLIRN QKNCITFP*ILNYILT*ERTKWF*V MRKQT*LNTKY*KKVSQLVLEIN** PSRDNPVMKRSKNLLCWVFIQLA GKKLKLQRNLWTK*KTFLMKKSKV LVKSPVLAINGQRP*STERPVKTLN* HVRPLRSQLPQSVKKCRILSIMIKTL FLLRLWCHLSS*VIYVDKLKISKHQ KVSF*KLKYMKM*KKKQKVLQL VTQISPLIQSLKIQP*LFTQVVVEKLL *VRLHYLKQNGLEKEYLMVNQKE *ILQIM*EIICMKIIQTVL*LKMTKII PKNKILI*VTVACLTAPTILMRYIMI QDISQKINLILVLSQY*RMLKIKKTL VFPK*YPM*KMQMHTHKL*MKIFA LRNL*LALHPAKIKMQPLNCPYLVI ILR*GHLHLG*PVVKSFFVHMKQLK K*KTYLQTVSVK*LRKTTRINQKFA KRKLWQVVTRHWMIQRIFFITL*IM MNVARIHIFLLTFRVKKFYNITKIC LDWRKFLKYHLVMLVWKLQIYVN VV*GSFISQSHLQILVGFLAQQVENL SRYQMLHYKTQDKCFLK*KIVPSKS FPKYCLKVTNIQTSSQEKKILLYVL QNI*YPKKAFHIMW*IHLSDLKL QEKY*K*R*QIYCCQ*KFS*LRI*WQ *FK*K*YCLYS*R*NGLAII*SAQHM S*IIWPVYEGGKHS*RRFVRNF SCSSRSMSW*YFK*RTVNCY*NGA KYKRF*DF*YIFSDCKWEKY*CRQR VI**NCKFL*SETRIA*LFLKF*ITF* HKKEQNGHSL*GNRHS*TQNLKE SVPVGTGNQLVTFQGPDERDEKIKE PTLLGFHTASGKKVKIAKESLDKVK NLFDEKEQGTSEITSFSHQWAKTLK YREACKDELAETIEITAAPCKKE MQNSLNNDKNLVSIEVVPKLLSD NLCRQTENLKTSKIFLKVKVHENV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EKETAKSPATCYTNQSPYSVIENSA LAFYTSCSRKTSVSQTSLEAKKWL REGIFDQOPERINTADYVGNLYEN NSNSTIAENDKNHLSEKQDTYLSNS SMSNSYSYHSDEVYND SGYLSKNK LD SGIEPVLKNVEDQKNTSFSKVISN VKDANAYPQTVNEDICVEELVTSSS PCKNKNAAIKLSISNSNFVGPAPF RIASGKIVCVSHETIKKVKDIFTDSF SKVIKENNENKSKICQTKIMAGCYE ALDDSEDILHNSLDNDECSTHSHKV FADIQSEEILQHNQNMMSGLEKVS KISPCDVSLTSDICKCSIGKLHKS VSSANTCGIFSTASGKSVQVSDASLQ NARQVFSEIEDSTKQVFVKVLFKSN EHS DQLTREENTAIRTPHEHLISQK GFSYN VVNSSAFSGFSTASGKQVS ILESSLH KVKGVLEEFDLIRTEHSL HYSPTSR QNVSKILPRVDKRNPEH CVNSEME KTCSKEFKLSNNLNVEG GSSENHNS IKVSPYLSQFQQDKQQL VLGTKVSL VENIHVLGKEQASPKNV KMEIGKTE TFSDVPVKTNIEVCSTY SKDSENYF ETEAVEIAKAFMEDDEL TDSKLPSH ATHSLFTCPENEEMVLS NSRIGKRR GEPLILVGEP SIKRNLLNEFDRIENQ EKSLKASK STPDGTIKDRRLFMH HV SLEPITC VPFRTTKERQEIQNP NFTA PGQEFL SKSHLYEHLTLEKSSSNLA VSGHP FYQVSATRNEKMRHLITTGR PTKV FVPPFKTKSHFHRVEQCVRNI NLE ENRQKQNI DGHGSDDSKNKIN DNEIHQFNKN NSNQAAAVTFTKCE EEPLDLITSL QNARDIQDMRIKKKQ RQRVFPQPS LYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHC IKINSKNA ESFQFHTE DYFGKESLW TGKGIQLADGGWLIP SNDGKAGKE EFYRALCDTPGVDPK LISRIWVYNH YRWIIWKLAAMECA FPKFANRCL SPERVLLQLKYRSTAS GKQVSILESS LHKVKG VLEEFDLIRTEHSLHYSPT SRQNV SKILPRVDKRNPEHCVNSEME EKT CSKEFKLSNNLNVEGGSSSENHNS SIKVSPYLSQFQQDKQQLVLG TKVSL VENIHVLGKEQASPKNV KMEIGKT ETFS DVPVKTNIEVCSTY SKDSENY FETEAVEIAKAFMEDDEL TDSKLPS HATHSLFTCPENEEMVLS NSRIGKR RGEPLILVGEP SIKRNLLNEFDRIEN QEKSLKASK STPDGTIKDRRLFMH HV VSLEPITC VPFRTTKERQEIQNP NFTA APGQE FL SKSHLYEHLTLEKSSSNL AVS GHPFYQVSATRNEKMRHLITT GRP TKVFVPPFKTKSHFHRVEQCVR N INLEENRQKQNI DGHGSDDSKNKI NDNEIHQFNKN NSNQAAAVTFTKC EEPLDLITSL QNARDIQDMRIKKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QRQRVFPQPGSLYLAKTSTLPRISLK AAVGGQVPSACSHKQLYTYGVSKH CIKINSKNAESFQFHTEDYFGKESL WTGKGIQLADGGWLIPSNDGKAGK EEFYRALCDTPGVDPKLISRIWVYN HYRWIIWKLAAMECAFPKEFANRC LSPERVLLQLKYRYDTEIDRSRRSAI KKIMERDDTAAKTLVLCVSDIISLS ANISETSSNKTSSADTQKVAIHETD GWYAVKAQLDPPLLAVLKNGRLT VGQKIILHGAELVGSPDACTPLEAP ESLMLKISANSTRPARWYTKLGFFP DPRPFPLPLSSLFSDGGNVGCVDVII QRAYPIQWMEKTSSGLYIFRNEREE EKEAAKYVEAQKRLALFTKIQEE FEEHEENTTKPYLPSRALTRQQVRA LQDGAELYEAVKNAADPAYLEGYF SEEQLRALNNHRQMLNDKKQAQIQ LEIRKAMESAEQKEQGLSRDVTTV WKLRIVSYSKKEKDSVLSIWRPSSD LYSLLTEGKRYRIYHLATSKSKSKS ERANIQLAATKKTQYQQLPVSEIL FQIYQPREPLHFSKFLDPDFQPCSE VDLIGFVVSVVKKTGLAPFVYLSDE CYNLLAIKFWIDLNEDIKPHMLIAA SNLQWRPESKSGLLTLFAGDFSDFS ASPKEGHFQETFNKMKNTVENIDIL CNEAENKLMHILHANDPKWSTPTK DCTSGPYTAQIIPGTGNKLLMSSPN CEIYYQSPLSLCMAKRKSVSTPVSA QMTSKSCKGEKEIDDQKNCKKRA LDFLSRLPLPPVSPICTFVSPAQK AFQPPRSCGTKYETPIKKKELNSPQ MTPFKKFNEISLLESNSIADEELALI NTQALLSGSTGEKQFISVSESTRTAP TSSDYLRLLKRRCTTSLIKEQESSQA STEECEKNKQDTITTKKYI |
| 3051 | 8548 | A | 3310 | 1 | 7988 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESLH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLRTVKTMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVCGLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTD ENTNQREAASHGFGKTSKNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVVPPLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVNKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFYAIHDETFYKGGKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSIDIKEEV LAAACHPVQHSKVEYSDFQSQK SLLYDHENASTLILTPTSKDVLNLV MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDSEE LFSDNENNFFVQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIEKNNNDYMNKWAGLLGPISNH SFGGSFRASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHNL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTT EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEVGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTFFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKELFNKIVNFFDQKPEEL HNFSLNSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVS ETVVPPKLLSDNLCRQTENLKTSKSI FLKVKVHENVETAKSPATCYTN QSPYSVIENSALAFYTSCS*KSQNIK KYLFES*ST*KCRKRNSKKSCNLLH KSVPLFSH*KFSLSLHLK*RKTSVS QTSLLLEAKKWLEGIQDQPERINT ADYVGNYLYENNSNSTIAENDKNH LSEKQDTYLSNSSMSNSYSYHSDEV YNDSGYLSKNKLDGIEPVLKNVED QKNTSFSKVISNVKDANAYPQTVN EDICVEELVTSSSPCKNKNAIKLSI SNSNNFEVGPAPFRIASGKIVCVSHE TIKKVKDIFTDSFSKVIKENNENKSK ICQTKIMAGCYEALDDSEDILHNSL DNDECSTHSHKVFADIQSEILQHN |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | QNMSGLEKVSISKISPCDVSLETSDIC KCSIGKLHKSVSANTCGIFSTASGK SVQVSDASLQNAQVFSEIEDSTKQ VFSKVLFSKNEHSDQLTREENTAIR TPEHLISQKGFSSYNVNSSAFSGFST ASGKQVSILESSLHKVKGVLVEEFDLI RTEHSLHYSPTSQRNVSKILPRVDK RNPEHCVNSEMEKTCSEFKLSNNL NVEGGSSENNHSIKVSPYLSQFQQD KQQLVLGTVKSLVENIHVLGKEQA SPKNVKMEIGKTETFSQVVPVKTNIE VCSTYSKDSSENYFETEAVEIAKAFM EDDELTDKSLPSHATHSLFTCPENE EMVLSNSRIGKRRGEPLILVGEPSIK RNLLNEFDRIENQEKSILKASKSTPD GTIKDRRLFVHHVSLEPITCVPFRRTT KERQEIQNPNTAPGQEFLSKSHLY EHLTLEKSSSNLAVSGHPFYQVSGN KNGKMRKLITGRPTKVFPVPPFKTK SHFHRVEQCVRNINLEGNRQKQNI GHGSDDSKNKINDNEIHQFNKNNNS NQAAAVTFTKCEEEPLDLITSLQNA RDIQDMRIKKKQRQRFVPPQGSLEYL AKTSTLPRISLKA AVGGQVPSACSH KQLYTYGVSKHCIKINSKNAESFQF HTEDYFGKESLWTGKGIQLADGGW LIPSNDGKAGKEEFYRALCDVKAT |
| 3052 | 8549 | A | 3311 | 1 | 14305 | MPIGSKERPTFFEIFKTRCNKADLGP ISLNWFEELSSEAPPYNSEPAEESSEH KNNNYEPNLFKTPQRKPSYNQLAST PIIFKEQGLTLPLYQSPVKELDKFKL DLGRNVPSNRHKSRLTVKTKMDQA DDVSCPLLNSCLSESPVVLQCTHVT PQRDKSVVCGSLFHTPKFVKGRQTP KHISESLGAEVDPDMSWSSSLATPP TLSSTVLIVRNEEASETVFPHDTTAN VKSYFSNHDESLKKNDRFIASVTDS ENTNQREAASHGFGKTSNGNSFKVN SCKDHIGKSMPNVLEDEVYETVVD TSEEDSFSLCFSKCRTKNLQKVRTS KTRKKIFHEANADECEKSKNQVKE KYSFVSEVEPNDDPLDSNVAHQKP FESGSDKISKEVPSLACEWSQLTSL GLNGAQMEKIPLHHISSCDQNISEK DLLDTENKRKKDFLTSENSLPRISL PKSEKPLNEETVVKRDEEQHLESH TDCILAVKQAISGTSPVASSFQGIKK SIFRIRESPKETFNASFSGHMTDPNF KKETEASESGLEIHTVCSQKEDSLCP NLIDNGSWPATTTQNSVALKNAGLI STLKKKTNKFIYAIHDETIFYKGKKIP KDQKSELINCSAQFEANAFEAPLTF ANADSGLLHSSVKRSCSQNDSEPT LSLTSSFGTILRKCSRNETCSNNTVIS QDLDYKEAKCNKEKLQLFITPEADS LSCLQEGQCENDPKSKKVSDIKEEV LAAACHPVQHSKVEYSQDFQSQK SLLYDHENASTLILTPTSKDVLNLV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MISRGKESYKMSDKLKGNNYESDV ELTKNIPMEKNQDVCALNENYKNV ELLPPEKYMVRVASPSRKVQFNQNT NLRVIQKNQEETTSISKITVNPDS LFSNENNFVFQVANERNNLALGN TKELHETDLTCVNEPIFKNSTMVLY GDTGDKQATQVSIKKDLVYVLAEE NKNSVKQHIKMTLGQDLKSDISLNI DKIPEKNNDYMNKWAGLLGPISNH SFGGSFRTASNKEIKLSEHNIKKSK MFFKDIEEQYPTSLACVEIVNTLAL DNQKKLSKPQSINTVSAHLQSSVVV SDCKNSHITPQMLFSKQDFNSNHL TPSQKAEITELSTILEESGSQFEFTQF RKPSYILQKSTFEVPENQMTILKTTS EECRDADLHVIMNAPSIGQVDSSKQ FEGTVEIKRKFAGLLKNDCKNSASG YLTDENEGFRGFYSAHGTKLNVS TEALQKAVKLFSDIENISEETSAEVH PISLSSSKCHDSVSMFKIENHNDKT VSEKNNKCQLILQNNIEMTTGTTFVE EITENYKRNTENEDNKYTAASRNSH NLEFDGSDSSKNDTVCIHKDETDLL FTDQHNICLKLSGQFMKEGNTQIKE DLSDLTFLEVAKAQEACHGNTSNK EQLTATKTEQNIKDFETSDTFFQTAS GKNISVAKESFNKIVNFFDQKPEEL HNFSNLSELHSDIRKNKMDILSYEE TDIVKHKILKESVPVGTGNQLVTFQ GQPERDEKIKEPTLLGFHTASGKKV KIAKESLDKVKNLFDEKEQGTSEITS FSHQWAKTLKYREACKDLELACET IEITAAPKCKEMQNSLNNDKNLVS ETVVPKLLSDNLCRQTENLKTSKSI FLKVKVHENVETAKSPATCYTN QSPYSVIENSALAFYTSCSRKTSVSQ TSLEAKKWLREGIFDGQPERINTA DYVGNYLYENNSNSTIAENDKNHL SEKQDTYLSNSSMSNSYSYHSDEVY NDSGYLSKNKLDGIEPVLKNVEDQ KNTSFSKVISNVKDANAYPQTVNE DICVEELVTSSSPCKNKNAAIKLSIS NSNNFEVGPPAFRIASGKIVCVSHET IKKVKDIFTDSFSKVIKENNENKSKI CQTKIMAGCYEALDDSEDILHNSLD NDECSTHSHKVFADIQSEELQHNQ NMSGLEKVKISPCDVSLETSICKC SIGKLHKS SVSSANTCGIFSTASGKSV QVSDASLQNAQVFSEIEDSTKQVF SKVLFKSNEHSDQLTRENTAIRTP HLISQKGFSYNVVNSSAFSGFSTAS GKQVSILESSLHKVKGVL EEFDLIRT EHLHYSPTS RQNVSKILPRVDKRN PEHCVNSEMEKTCSKEFKLSNNLN VEGGSSENNHSIKVSPYLSQFQQDK QQLVLGTKVSLVENIHVLGKEQASP KNVKMEIGKTETFS DVPVKTNIEVC STYSKDS ENYFETEAVEIAKAFMED |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DELTDSKLPSHATHSLFTCPENEEM VLSNSRIGKRRGEPLILVGEPSIKRN LLNEFDRIENQEKS LKASKSTPDGT IKDRRLFMHHVSLEPITCVPFRTTKE RQEIQNPNTAPGQEFLSKSHLYEH LTLEKSSSNLA VSGHPFYQVSATRN EKMRHLITTGRPTKVFPFPFKTKSH FHRVEQCVRNINLEENRQKQONIDGH GSDDSKNKINDNEIHQFNKNSNQ AA AVTFTKCEEEPLDLITSLQNARDI QDMRIKKKQQRQVFPQPGSLYLAK TSTLPRISLKAAVGGQVPSACSHKQ LYTYGVSKHCIKINSKNAESFQFH/T *RLF*WKFMWKRNTVG*WWM AHTLQ*WKGWKRRL*GSV*HSRC GSKAYF*NLGL*SL*MDHMETGSY GMCLS*GIC**MPKPRKGASSTKIQI *YGN**KQKITNILLPVEILIT*NLMA VIQVKMILFVFIKMKRTCYLLISTTY VLNYLASL*RRETRLKKICQI*LFW KLRKLKKHVMVILQIKNS*LLKRS KI*KILRLLIHFFRLQVGKILVSPKSH LIKL*ISLRNQKNCITFP*ILNYILT*E RTKWTF*VMRKQT*LNTKY*KKVS QLVLEIN**PSRDNPNVMKRSKNLL CWVFIQLAGKKLKLQRNLWTK*KT FLMKKSKVLVKSPVLAINQRP*ST ERPVKTLN*HVRPLRSQLPQSVKKC RILSIMIKTLFLLRLWCHLSS*VIIYV DKLKISKHQQVSF*KLKYMKM*KK KQKQVLQVLTQISPLIQSLKIQP*LF TQVVVEKLL*VRLHYLKQKNGLEK EYLMVNQKE*ILQIM*EHCMIQIT VL*LKMTKIISPKNKILI*VTVACLT AIPTILMRYIMIQDISQKINLILVLSQ Y*RMLKIKKTLVFPK*YPM*KMQM HTHKL*MKIFALRNL*LALHPAKIK MQPLNCPYLIVILR*GHLHLG*PVV KSFVFHMKQLK*KTYLQTVSVK* LRKTTRINQKFAKRKLWQVVTRHW MIQRIFITL*IMMNVARIHIFLLTF RVKKFYNTKICLDWRKFLKYHLV MLVWKLQIYVNVV*GSFISQSHLQI LVGFLAQQVENLSRYQMLHYKTQD KCFLK*KIVPSKSFPKYCLKVTNIQT SSQEKKILLYVLQNI*YPKKAHIM W*IHLSSLDLVQQVESKFPF*KVPY TKLREC*RNLI*FRTEHSLHYSPTF*T KMYQKYFLVLIRETQSTV*TPEMEK TCSKEFKLSNNLNVEGGSSENNHSI KVSPYLSQFQQDKQQLVLGTVKVS VENIHVLGKEQASPKNVKMEIGKTE TFSVPVKTNIEVCSTYSKDSSENYF ETEAVEIAKAFMEDDELTD SKLPSH ATHSLFTCPENEEMVLSNSRIGKRR GEPLILVGEPSIKRNLLNEFDRIENQ EKSLKASKSTPDGTIKDRRLFMHHV SLEPITCVPFRTTKE RQEIQNPNTA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGQEFLSKSHLYEHLTLEKSSSNLA VSGHPFYQVSATRNEKMRHLITTGR PTKVFVPPFKTKSHFHRVEQCVRNI NLEENRQKQNIIDGHGSDDSKNKIN DNEIHQFNKNNSNQAAAVTFTKCE EEPLDLITSLQNARDIQDMRIKKKQ RQRVFPQPGSLYLAKTSTLPRISLKA AVGGQVPSACSHKQLYTYGVSKHC IKINSKNAESFQFHTEYFGKESLW TGKGIQLADGGWLIPSNNDGKAGKE EFYRALCDTPGVDPKLISRIWVYNH YRWIIWKLAAMECAFPKEFANRCL SPERVLLQLKYRYDTEIDRSRRSAIK KIMERDDTAAKTLVLCVSDIISLSA NISSETSSNKTSSADTQKVAIHETDG WYAVKAQLDPPLLAVLKNGRLTV GQKIILHGAELVGSPDACTPLEAPES LMLKISANSTRPARWYTKLGFFPDP RPFPLPLSSLFSDGGNVGCVDVIIQR AYPQWMEKTSSGLYIFRNEREEEEK EAAKYVEAQQKRLEALFTKIQEEFE EHEENTTKPYLPSRALTRQQVRALQ DGAELYEAVKNAADPAYLEGYFSE EQLRALNNHRQMLNDKKQAQIQLE IRKAMESAEQKEQGLSRDVTTVWK LRIVSYSKKEKDSVILSIWRPSSDLY SLLTEGKRYRIYHLATSKSKSKSER ANIQLAATKKTQYQQLPVSEILFQI YQPREPLHFSKFLDPDFQPSCEVDL IGFVVSVVKKTGLAPFVYLSDECYN LLAIKFWIDLNEDIKPHMLIAASNL QWRPESKSGLLTLFAGDFSVSFASP KEGHFQETFNKMKNTVENIDILCNE AENKLMHILHANDPKWSTPTKDCT SGPYTAQIIPGTGNKLLMSSPNCEIY YQSPLSLCMAKRKSVSTPVSAQMT SKSCKGEKEIDDQKNCKRRALDF LSRLPLPPVSPICTFVSPAQAQAFQ PPRSCGTKYETPIKKKELNSPQMTPF KKFNEISLLESNSIADEELALINTQA LLSGSTGEKQFISVSESTRAPTSSSE DYLRLLKRRCTTSLIKEQESSQASTEE CEKNKQDTITTKKYI |
| 3053 | 8550 | A | 3312 | 11089 | 17637 | NHCHRFHLEWMPWCGCRSPSGPRH VNQKPEELHNFSLNSELHSDIRKNK MDILSYEETDIVKHKILKESVPVGT GNQLVTFQGQPERDEKIKEPTLLGF HTASGKKVKIAKESLDKVNLFDE KEQGTSEITSFSHQWAKTLKYREAC KDLELACETIEITAAPKCKEMQNSL NNDKNLVSIVTVPPKLLSDNLRCRQ TENLKTSKIFLKVKVHENVKETA KSPATCYTNQSPYSVIENSALAFYTS CSRKTSVSQTSLLLEAKKWLRGIFD GQPERINTADYVGNLYENNSNSTI AENDKNHLSEKQDTYLSNSSMSNS YSYHSDEVYNDGYLSKNKLDGIE PVLKNVEDQKNTSFSKVISNVKDA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NAYPQTVNEDICVEELVTSSSPCKN KNAAIKLSISNSNNFEVSDEILFQIY QPREPLHFSKFLDPDFQSPSCSEVDLI GFVVSVVKKTVRNEEASETVFPHD TTANVKSYSFNHDESLKKNDRIAS VTDSENTNQREAASHGFGKTSNGSF KVNSCKDHIGKSMPNVLEDEVYET VVDTSEEDSFSLCFSKCRTKNLQKV RTSKTRKKIFHEANADECEKSKNQV KEKYSFVSEVEPNDDPLDSNVAH QKPFESGSDKISKEVVP SLACEWSQ LTL SGLNGAQMEKIPLLHISSCDQNI SEKDLLDTENKRKKDFLTSENLPRI \SSLPNPEEPLNEETVVNKRDEEQHL DSHTDCILQ*KQAISGTFPVASSFQG IKKSIFRIRESPKETFNASFSGHMTDP NFKKETEASESGLEIHTVCSQKEDS LCPNLIDNGSWPATTTQNSVALKN AGLISTLKKKTNKFIYAIHDETSYKG KKIPKDQKSELINCSAQFEANAFEA PLTFANADSGLLHSSVKRSCSQNDS EEPTLSLTSSFGTILRKCSRNETCSN NTVISQDL DYKEAKCNKEKLQLFIT PEADSL SCLQEGQCENDPKSKKVSD IKEEV LAAACHPVQHSKVEYS DTF QSQKSLLYDHENASTLILTPTSKDV LSNL VMISRGKESYKMSDKLKGNN YESDVELTKNIPMEKNQDVCALNE NYKNVELLPPEKYM RVASPSRKVQ FNQNTNLRVIQKNQEETTSISKITVN PDSEELFSDNENNFVFQVANERNNL ALGNTKELHETDLTCVNEPIFKNST MVLYGDTGDKQATQVSIKKDLVY VLAENKNSVKQHIKMTLGQDLKS DISLNIDKIPEKNNDYMNKWAGLL GPISNHSFGGSFRTASNKEIKLSEHN IKKSKMFFKDIEEQYPTSLACVEIVN TLALDNQKKLSKPQSINTVSAHLQS SVVVS DCKNSHITPQMLFSKQDFNS NHNLTSPQKAEITELSTILEESGSQF EFTQFRKPSYILQKSTFEVPENQMTI LKT TSEECRADLHVIMNAPSIGQV DSSKQFEGTVEIKRK FAGLLKND CN KSASGYLTDENEVGFRGFYSAHGT KLVNSTEALQKAVKLFSDIENISEET SAEVHPISLSSSKCHDSVVS MFKIEN HNDKTVSEKNNKCQLILQNNIEMTT GTFVEEITENYKRNTENEDNKYTAA SRNSHNLEFDGSDSSKNDTVCIHKD ETDLLFTDQHNICLKLSGQFMKEGN TQIKEDLSDLTFLEVAKAQEACHGN TSNKEQLTATKTEQNIKDFETSDTFF QTASGKNISVAKESFNKIVNFFDQK PEELHNFSLNSELHSDIRKNKMDILS YEETDIVKHKILKESVPVGTGNQLV TFQGQPERDEKIKEPTLLGFHTASG KKVKIAKESLDKVKNLDFDEKEQGT SEITSFSHQWAKTLKYREACKDLEL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ACETIEITAAPKCKEMQNSLNNDKN LVSIETVVPKLLSDNLCRQTENLK TSKSIFLKVKVHENVEKETAKSPAT CYTNQSPYSVIENSALAFYTSCSRK TSVSQTSLLEAKKWLREGIFDGQPE RINTADYVGNYLYENNSNSTIAEND KNHLSEKQDTYLSNSSMSNSYSYHS DEVYNDSGYLSKNKLDSGIEPVLKN VEDQKNTSFSKVISNVKDANAYPQ TVNEDICVEELVTSSSPCKNKNAAI KLSISNSNFEVGPAPFRIASGKIVC VSHETIKVKDIFTDSFSKVIKENNE NKSICQTKIMAGCYEALDDSEDIL HNSLDNDECSTHSHKVFADIQSEEIL QHNQNMMSGLEKYSKISPCDVSLETS DICKCSIGKLHKSVSANTCGIFSTA SGKSVQVSDASLQNAQVFEIEDS TKQVFSKVLFSNEHSDQLTREENT AIRTPEHLISQKGFYNVNVSSAFSG FSTASGQVSILESSLHKVKGVLLEEF DLIRTEHSLHYSPTSQRNVSKILPRV DKRNPEHCVNSEMEKTCSEFKLS >NNLNVEGGSSENNHSIKVSPYLSQF QQDKQQLVLGTKVSLVENIHVLGK EQASPKNVKMEIGKTETFSDPVVKT NIEVCSTYSKDSENYFETEAVEIAK AFMEDDELDSKLPSHATHSLFTCP ENEEMVLSNSRIGKRRGEPLILVGEP SIKRNLLNEFDRIENQEKSLEKASKS TPDGTIKDRRLFMHHVSLEPITCVPF RTTKERQEIQNPNTAPGQEFLEKSKS HLYEHLTLEKSSSNLAVSGHPFYQV SATRNEKMRHLITTGRPTKVFPVPPF KTKSHFHRVEQCVRNINLEENRQK QNIDGHGSDDSKNKINDNEIHQFNK NNSNQAAA VTFTKCEEPLDLITSL QNARDIQDMRIKKKQQRQVFPQPG SLYLAKTSTLPRISLKA AVGGQVPS ACSHKQLYTYGVSKHCIKINSKNAE SFQFHTEYFGKESLWTGKGIQLAD GGWLIPSNDBGKAGKEEFYRALCDT PGVDPKLISRIWVYNHYRWIIWKLA AMECAFPKEFANRCLSPERVLLQLK YRYDTEIDRSRRSAIKKIMERDDTA AKTLVLCVSDIISLSANISSETSSNKTS SADTQKVAIIELTDGWYAVKAQLD PLAS |
| 3054 | 8551 | A | 3313 | 1 | 207 | CNLCLPDSSDSPASASQVAGKTGLC HHTGVVVFVFLVEMGFHHAGQAGLE LLT*VICVPQPPKALGLQV |
| 3055 | 8552 | A | 3314 | 279 | 625 | SLYVCMHVCMYVFILRRSFALVAQ ARVQWCGLGSLQPPPPGFKRFNSCL SLPTS*DYRRAPPHTNFFVFSAEME FHRVSQDGLYLLTSGDLHPRLASQS AGITGVSHRTRPFL |
| 3056 | 8553 | A | 3315 | 1 | 418 | GSIPPPGVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPQ PPGPAPPGARTRTRPESE*SQPGRSP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VSRQSLTGADALEGPCGLATKQPS WPHRCGTSGSSPGWLLARGFQETQ QDCIVPLNAQDIG |
| 3057 | 8554 | A | 3316 | 1 | 354 | GFIPPPGVVYCVPYPLKHAPAPALP* TRQRGSPQSPGALRAK*HVLLETPQ PPGPAPPGARTRTRPESGAWRWVR AGSSPPPPSPHPTPPCFFQVHQGLRS GSANEASLEDPQSRDRA |
| 3058 | 8555 | C | 3317 | 299 | 365 | MSCPECNLTGISSTKNKLNQ* |
| 3059 | 8556 | A | 3318 | 33 | 302 | PSSWDYRHAPPRLTNF*FLVEMGF HYVG/QAGLELLSSGDPPALASQSA RITGMSR\RAWPK*HNVLRKFTNLS LGHQNHGPRVGGQAKP |
| 3060 | 8557 | A | 3319 | 3 | 409 | SNFRSNFGYNIPLKHLADRVAMYV HAYTLYSAVRPFGC/SGYWGCAIGK ARQAAKTEIEKLQMKEMTCRDIVK EVAKIIVHDEVKDKAFELELSWV GELTNGRHEIVPKDIREAEKYAKE SLKEEDESDDDNM |
| 3061 | 8558 | A | 3320 | 1 | 255 | |
| 3062 | 8559 | A | 3321 | 1 | 395 | FGYNIPLNHLPDRVAMYVHAYTLY SAVRPFGCSFMLGSYSVNDGAQLY MIDPSGVSYGYWGCAIGKARQAAK TEIEKLQMKEMTCRDIVKEVAKIIV HDEVKDKAFELELSWVGE\ESLKE EDESDDDNM |
| 3063 | 8560 | A | 3322 | 515 | 560 | |
| 3064 | 8561 | A | 3323 | 3 | 661 | KDGVVLGVRKISPS*TYEEGFQTKR LF*CLIGNVEMA\VAGLLADARSLA DIAREEASNFRSNFG\YTIPLKHLAD RVAMYVHAYTLYSAVRPFGCSFML GSYSVNDGAQLYMIDP\SGVSYGY WG\CAMRQAR\QLAKTELERLQLK KLPSGDIVKEVAKIIVHDEVKDK AFELELSW\VGDLTK*RHEILPK\D\ LRDEAEKYAKESLKEEDESDDDNV |
| 3065 | 8562 | A | 3324 | 3 | 634 | |
| 3066 | 8563 | A | 3325 | 2 | 487 | HIFGKAKEYANSQVVTKDQYAVIC LGGDAVPSASLHVSETMEKT*KK/H RMSHFVTCLTEGRRKCIKPVHYD RVKKITQRKKEIPVVFLNRVPEALG KCTHADPEAAEGK/LSRAMHFILQS APDIRRELQKILEARPQTPAVDFGR RLLRFSITDRTQMGR |
| 3067 | 8564 | C | 3326 | 373 | 727 | MKPRLWEFSLHREGNTGTTGLDSL LWPPARTTKWAHLTKRNQAQPGY AGPASPTSHVLCAPAQAYLTHDVNS QVSLIKTSLQASSGSXXXXXXXXXX XXXXXXXXXXGAQAFFLGGGFF* |
| 3068 | 8565 | A | 3327 | 2 | 536 | VHLVPRQNACAIRLTEPCPPRLK*FS CLSLPSS/WDSQ/HAPPH/PGS/FCIFR RDGGSPMLS\GWFQTPDLRRSTRLSI PKCWDYRREPPHPVKIFLKLFFSY WVFPVCALNLSLSLFVYTFLSNLS LLYSSHTGSKLQCYEMLHVETHIPK GEGVLSRVERRKVRLLSHTKPCQFS HESA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3069 | 8566 | A | 3328 | 3 | 334 | FLRQGL/NSVTQAGVQWGDGLGSLQ PPPPKLGSSHPSPSSCRHYRHTP/ RSG*FFVFL*RWGFAMLPRLV*TS G\PSDMPALASQGAGTTSMSSH TWR PYLNF GKFP RKKN |
| 3070 | 8567 | A | 3329 | 1 | 148 | PKLKGLCLSFHEGKKRLSYF/CIMA* P*YPLDFGEQWPLHGSHAYSTIL*L DLFCKKEEE*DEIPYV*CFMLLWKS TTM*KKRLSYFLSWLNLNTHWIS EN SGHCMVLMMLTVRSCS |
| 3071 | 8568 | A | 3330 | 3 | 267 | FFFFLDRFSLCGPGWSAV/VQS*LT VNS/TFLGPSNPPLSLWSSY/DVR/R MPANLS*FFRS*/SLAMLPRPVLSW PQAIFLRHAPKVLGVEV |
| 3072 | 8569 | A | 3331 | 3 | 269 | FETESHSVTRLECSG/TILAHCNTCL PGSSNSHASASQVAGIAGEHHHAQI IFIFLVETGFHHVQGAGLELLT*VIC LPRPPIVLGLQA |
| 3073 | 8570 | A | 3332 | 1 | 299 | FSLIKISMMLLMKMEK*NLQFIW/KP RRLQIAKARLNASSSSSSSSSSSSSS SSSVVWYWHKKRHIDHWNRLENS NINRHICSQLILTKVPGANTKDHP |
| 3074 | 8571 | A | 3333 | 3 | 261 | RQDLSLCHPGWSA VVQS*LIHALTS* \VKQSTYLRHPTSWG*RCVPPCPAN FC\FFCRDRIL/TISPRLVSWAQVIELP QPPKVLGLQV |
| 3075 | 8572 | A | 3334 | 3 | 290 | VDFFFFFFSRRSNVLSHRLECSGTISS HGNLCLLGSSDSPASASQVARITGV HHHTQLIFIFLIETGFRHVDQAGLDL LT*VILPPQPPKMLGLQA |
| 3076 | 8573 | A | 3335 | 3 | 358 | |
| 3077 | 8574 | A | 3336 | 76 | 386 | VLPPPSSPALHSPAPPSTCPYLPGA/P PPLLPPCAGRSPAAAAPHCPAPCA PRH*GSR*LESPAPQG PQSRAARMP AWPLPPAPPTDPTAPPAPRSHWPAA PPT |
| 3078 | 8575 | A | 3337 | 66 | 381 | VLPPPSSPALHSPAPPSTCPYLP GAL PPLE/GPPSRPPRPTFIGNPGGQGPGE VSPIVLRSPSQPH*PGNQGPCSSQP PGSPRSEHGC*HRCWALYGQKEKP APS |
| 3079 | 8576 | A | 3338 | 1 | 303 | KDRFSFCGPG*SAVTQLNLTADP*T PALK*SFHRSLLSRWDYRRAPPYLA N*KKFL*SRGLAMLPRLVFHSWPQ VILSPLSRARATAPSFPLFSSKDEPI |
| 3080 | 8577 | A | 3339 | 2 | 212 | RFSCLSLPSSWDMHHSPG*FFIFLVE TGFAHVQGAGLELPASNDPPASTS QSVVITAMSHRRALVPIF |
| 3081 | 8578 | A | 3340 | 2 | 273 | RRSSTQPRLQCSGTIPAHCNLHPPS PSDYPAPASRVAGTTGARYHHAQPI SAFSSAETGFHHAGQDGLKLLT*AI HPPRPPKVP GPQA |
| 3082 | 8579 | A | 3341 | 135 | 494 | IKHRGMGLDFAVLPLQVKWPPDPG FLECIHFLQLKGTIPDLKERAPVTSR VEPGHAGHC/TSYGQVCHL*GRC/V EKRKGIA CDCAFSMYDGLFCSNSNS RADWSHCTVSGTYQHTENSIMS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3083 | 8580 | C | 3342 | 71 | 217 | MPQPNFFVLLVDRGFHHVDQAGLD LLTSSDSPALASQSARITGVSHHA* |
| 3084 | 8581 | A | 3343 | 1 | 106 | |
| 3085 | 8582 | A | 3344 | 2 | 1926 | MAAAAVDSAMEVVPALAEAAPE VAGLSCLVNLPGEVLEYILCCGSLT AADIGRVSSSTCRRLRELQSSGKVW KEQFRVRWPSLMKHYSPTDYVNW LEEYKVRQKAGLEARKIVASFSCR FSEHVPCNGFSDIENLEGPEIFFEDEL VCILNMEGRKALTWKYYAKKILYY LRQQKILNNLKAFLQPPDDYESYLE GAVYIDQYCNPLSDISLKDIQAQIDS IVELVCKTLRGINSRHPSLAFKAGES SMIMEIELQSQVLDAMNYVLYDQL KFKGNRMDYYNALNLYMHQVLR RTGIPISMSLLYLTARQLGVPLEPV NFPSSHLLRWCCGAEGATLADIFDYI YIDAFGKGKQLTVKECEYLIGQHVT AALYG\VVNVKKVLQRMVGNLLSL GKREGIDQSYQLLRDSL DLYLAM PDQVQLLLLQARVYFHLG\ILPEKS FCLVLKVL DILQHIQTL\DPGQHGA VG\YL\VQHTLEHIL\ERKKEEVGVE VKLRSDEK\HRD\CY\SFGFIMKA* RGMGY*LC*FYGWDPPTWHGSGHE LDSRNMNV\HSLPHGHHQPFYNVL VEDGSCRYAAQENLEYNAEP\QEI SH\PDVGRVYSQRFT\RTHYIP\NAEL \EIRYPEDLEFV\YETVQ\NIYKCKRK ENIE |
| 3086 | 8583 | A | 3345 | 59 | 339 | |
| 3087 | 8584 | A | 3346 | 1 | 342 | FCSCQPQAGVQRRDLSSLQPLPP\GF K*FSCSLPSSWD\YRRPPP/RPGYFL YYLVEIGFCHICQAGLKLLRSGDPP AWASQSAGITGMSHHAQPHLLLLN CLLPFLGIPLHSPL |
| 3088 | 8585 | A | 3347 | 1 | 294 | ETESHSV\RLCSGTILAHCNLHLP GSSNSPASASQIAGTIGARHHTWLIF VFFVEMGFHHVGQTLELPGLK*SAC LKPLKVLG*QAGVQRHNLGSLQPPP PRFKQFSCSLPNSWDHRCPTPHLA NFCIFCRDGFPPCWPSRTPWPQVI CLPQASQSAGITGVEPLQPQRSYP |
| 3089 | 8586 | A | 3348 | 2 | 268 | EAESHVA\RLCSDAISAHCNLRLP GLNSPASASRVAGIIGACHHDWLI FVFLVETGFCHVGQAGL/DNS*PQVI HPPRPPKVLGLQA |
| 3090 | 8587 | A | 3349 | 3 | 444 | FFFEIWSGSVA\RLCEGGTIFAHCN RLLGSSHPPPTSAS*VAGTKGTCHHV QLIAFFVDTGFHHVARLVLS* TQAICPPRPPKVLGSYASITAPGPTFFFL TIILGVQVDKRFYGNLTRKDIQKLG NYVWEGLELLSPQKFMKLP |
| 3091 | 8588 | A | 3350 | 1 | 318 | FFFFFLRQSFALAQAGM/QWHDLGS LQPPPPGFK*FSYLSLPSSWDYRYVP PRPASFEFLVEMGFHHVGQAGFELL TSSDPPASASQSAGIIGVS*RTQPGT NDFL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3092 | 8589 | A | 3351 | 16 | 848 | VGSGLVSAQQTGCGPGNPSPPGVS GAMELRVEPAARGQGS LGDPPA\VL LPGALELPIPGSFFASQSCSPWVML QLTFPHF*LLLAPLPPVSPAPTGWDL VSQLOPVSSPRGRCPRSGPDLLPLH GQPFHSSSFSSSMQASGEVPQPCPS RSSGS/VKGGLQTVESGPGALKC EALAWLRG*GLLGHSGFAGSVPEV TPGSPHVLNP\GRGLPCAGYCLHPA AL*GMVFGLPPLPGSSLV*PTIWLLT LKSPTS*GIP*HRKPWFVSVMHKVG WKV |
| 3093 | 8590 | A | 3352 | 1 | 293 | VLRQGLSLSTQDRMQWHYDSSLQP *TPGLK*SSASQVAATTGTCHHTWL TFLFVF/DFWRWSL/NCIAQAGLE/PP GFK*/CPKHWDYRHEPGMPGWVFLI S |
| 3094 | 8591 | C | 3353 | 127 | 345 | MFDFELELFXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXLI AQGECLYVWKINSQHSVFLLKKL CF* |
| 3095 | 8592 | A | 3354 | 2 | 215 | AHCNLC L PGSSDSPASASRVGTIG VHRTQLIFVFLEEMGFCHIGQAGL ELLT*VICLPRPPKVLVLR |
| 3096 | 8593 | A | 3355 | 164 | 311 | QRSQGIWVWRFIRRF*II |
| 3097 | 8594 | A | 3356 | 1 | 381 | YINVIIHFVHINCWRECQKVQLT*K\ SF*QFLKNLNIHLSYDLAIPVLGICPR EMKAYVHIKTCK*MLIAAFHIAQN WNQ/P/RCPSTGEWYKQTVIFYTMQ HYS AIKNNE*LIHKTTWKNLKEARA SGV |
| 3098 | 8595 | A | 3357 | 2 | 764 | RTLHLFAGGCGGTGVAIFTCPLEVI ETRLQSSRLALRTDYYPHVHLGTIS GAGMARPTSATPGLFHGLKSILEKE GPKSLFRGSRPNLVGVAPSRAVYFA CYSKAKEQFNGIFAPNSNIVHIFSAG SA/GVRGSKQMNTLQCARYVYQTE/ GIRGFYRGLTASYAGISETIICFAIYE SLKKYLKEAPLASSANGTEKNSTSF FGLMAAA/GSF*GLSSCIAY/PHEVIR TRLREETSTSFQCTARLVFREESYL PL |
| 3099 | 8596 | A | 3358 | 155 | 875 | DQHPVTPGLFQVLKAVYFACYSKA KEQFNGIFVPNSNIGHIFPAGSAAFIP NPLMD\PIWMVKTRMQLEQKVRGS KQMNTLQCARYVY/HDRKAFGGFY RGLTASYAGISETIICFAIYESLKKY LKEGPLAFFGKWD*GKIPQVFLDL WPAAALSKGL\ASCMAYSHTEVH* GRRL\REKGHPSTKSFCPERRALGVP GEEGYPCLFIEGLFAPSFIRQIP\NTA\ IVLGYLWRLIVYLLGRP |
| 3100 | 8597 | A | 3359 | 1 | 281 | FFFAPETESYSVARLECSGTILVHCT LCLPGSSDSPASASQVAGTTGACHH TWLILVILVEIGFHHVQGAGLG/IS*L QVIRPPWAPKVLGIIG |
| 3101 | 8598 | A | 3360 | 135 | 218 | TLQFTSLISYSFCQSWGSKVPLSLPP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | P*/PANF/*FLVETGFLQVGQVGLKL LISSDPPTSASQSAGITDVSHCAGPE F |
| 3102 | 8599 | A | 3361 | 198 | 390 | |
| 3103 | 8600 | C | 3362 | 5 | 316 | MPAKLFLMVEFSGVACSSAKXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX YYRLLFSPCHSF* |
| 3104 | 8601 | C | 3363 | 186 | 323 | MPWLEHTAHFPDKAWITRMALLRN GIVPYDSLPLWITLGRWPNGGT* |
| 3105 | 8602 | A | 3364 | 2 | 3096 | TPRLQSNTRALYQYCPPIINYPQLE NELFCNIYYLKQLCDTLRFPDWPIK DPVKLLKDTLDAWKKEVEKKPPM MSIDDAYEVNLNPQGQGPHEDESKIR KAYFRLAQKYHPDKNPEGRDMFEK VNKAYEFLCTKSAKIVDGPDPENIIL ILKTQSILFNRHKEDLQPYKYAGYP MLIRTITMETSDDLLFSKESPLLPAA TELAFTVNCSALNAEELRRENGLE VLQEAFSRCVAVLTRSSKPSDMSVQ VCGYISKCYSVAAQFECEKITEM PSIHKDLCRVLYFGKSIPRVAALGVE CVSSFAVDFWLQTHLFQAGILWYL LGFLFNVDYTLSESGIQKSEETNQQ EVANSLAKLSVHALSRLGGYLAEE QATPENPTIRKSLAGMLTPYVARKL AVASVTEILKMLNSNTESPYLIWNN STRAEGLEFLESQQENMIKKGDCDK TYGSEFVYSDHAK*LIVR*IFVRVYN EVPTFQLEDPKAFAASLLDYIGSQA QYLHTFMAITHAAKVESEHQHGDRL PRVEMAFEALRNVIKYNPGSESECI GHCRCIFSLLRVHGAGQVQV/AL* EVVNIIVTSNQDCVNIAESMVLSSL LALLHSLPSSRSAFWETLYALDIR VQKLIKEAMAKGALIHLLDMFCNS THPQVRAQTAELFAKMTADKLIGP KVRITLMKFLPSVFMAMRDNP AAVHIFEGTHENPELIWNDNSRD VSTTVREMMLEHFKNQDNPAN WKLPEDFAVVFGEAEGELAVGGVF LRIFIAQPAWVLRKPREFLIALLEKL TELLEKNNPHGETLETLTMTATVCLF SAQPQLADQVPPLGHLPKVIQAMN HRNNAIPKSAIRVIHALSENELCVRA MASLETIGPLMNGMKKRADTVGLA CEAINRMFQKEQSELVAQALKADL VPYLLKLLEGIGLENLADSPAAT*GS ELVKALQGG*LEVLQYGENRVNEIL C/RFLSVWECLSKIQEHLDFIS*/ESH TAGYLTGPGVAGYLTAGTSTSVMS NLPPPVDHEAGDLGYQT |
| 3106 | 8603 | A | 3365 | 1 | 358 | NRLNATPIKIPTAFFAEMDKLNPKFL KLNS*NLRYNARDST*PKQY**RKR TWINKNNAGGLILPYCILLQRNNNQ DIG*KNVLKIM**WHRDRHDQ*NR NQSPEINP*YIGKLFSTVL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3107 | 8604 | A | 3366 | 2 | 40 | LPRLKQFS\CLSLPSSWDYKR\RP PANF/SVFLVETEFYHVGQAGLELFT SSDLPTLASQIAGITGVSHCAWPE*S AS |
| 3108 | 8605 | A | 3367 | 1 | 223 | IIVKKWKQPKCPPTDEWINKMWDI QAIEYNLAI*/DKVVIHATTCMKLEN IMLSERSQLQRATYCNDAIYKNPE |
| 3109 | 8606 | A | 3368 | 307 | 332 | TTYHFFF*TESHAAQAGAHWRDLS SLRPPPPGFKPFSCLSWDYRRTPPH PAN\FLAFLADTGLHHAGQAGLKLL TSNDPPTPASQSAGTTGVSHRAQPF FSELPITIFFSL |
| 3110 | 8607 | A | 3369 | 3 | 411 | QTLPSATVSPEQAGAFPLALHSAQE SLGPAQTVPGSTGPPQAPSGPGPPG EPG*ERLCASHKAFISHKQSH*SPQ* PFQGRFDAFPQYKQQTRPGHT/GQK GLRGPRTQTLSTLSQPTACSENSQG SQSPKRTLS |
| 3111 | 8608 | A | 3370 | 3 | 166 | EESCSVVQGGVQWCDLS*LQTLPP\ GSSNFCASASRVAGITGAHHHAQL KKKMLF |
| 3112 | 8609 | A | 3371 | 4 | 312 | FLR*SFTLIVQAGVQWRYLGLSLQPP PPGFKRLSCLSLPSSWDYRHVPP/*P GYFFVFLVKMGCLHVGQAGPKLLT SGDPAASASQSAGITGPHRTWLRS FLI |
| 3113 | 8610 | A | 3372 | 3 | 282 | FFFETGSNSVAQAGVQWCNHSSLR PRPSG\SSDPPNSSSQVAWTTGVHH TQLLFKFFCKDEVSLCFDWSQTV* RVEHIRDEYETTQHCLYPSN |
| 3114 | 8611 | A | 3373 | 1 | 164 | ETEFRSVAQAGVQWRDLGSLQPPPS GFK*SSCV/SLPSTWDYRYMPPCPA TLLNT |
| 3115 | 8612 | A | 3374 | 1 | 114 | ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS |
| 3116 | 8613 | A | 3375 | 363 | 1246 | DTEQIYCIQEPEYGGKKYCTKQSRS YVSWTTHFSSSFIDQSLLSESMA*KS TAPHSSDF*DFLT*KT*NLFFFLRRSL ALSPQAGVQWRDLGSLQAPPPGFTP FSC\ASPSSW\DYRHLPPCPANFFVF FLVETVSIFVFTVLAGMVISI*PQ/CD PPTLASQSAGITRLSHRAR\LCFVF* KKRNAREGGRLLTIKADFLIFFSFF FEMESCSVSKAGVEWHGLSSL*ALP HRFTPFSCLSLLSSWDYRRPPQLA NF\CIFSRDEVSPC*PGWSGSPDLVIH LPWPPKVLGLHA |
| 3117 | 8614 | A | 3376 | 3 | 324 | DRISLCCPGWSAIVQSQLTAA\SPLG LKQSFYISLPSS*GHLAPLHPANIF GFPL*KWGLPMLPMLVLNSWAQVI LPKCWGLQASATVPGLFINFYDYIM DQSSFN |
| 3118 | 8615 | A | 3377 | 3 | 673 | RWSHSVQAGVQWRDLSSRQPPPP GSRDSPASAS*VAGTTGTTHHAQFF FFFFFLRRS/LSSV/SQDGVQWHDH SLQPVPPGFKQFSCLSLPSSWDYRC AAPRPANFFVF**RRVFSTLARLVSI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | S*PCDLPTLASQTAGITGVSHCTQLA KFCIFS*DGVCHVGQAGAVLILCLF LHSKINMFSPLHCTPASTVYSHLPQ RPTRKRLYIRWRWERTWPANAEL |
| 3119 | 8616 | A | 3378 | 2 | 323 | RRSFTLVAQAGVRWHILGSLQPLPP GFKRFSCLSLPSGWDYRLMPPCPAN F*FLVEMRFHHVQAGPERLTSGD LPA*ASQSAGITGVATTPSQYKLCSL IIMKLN |
| 3120 | 8617 | A | 3379 | 1 | 311 | DFFF*ETASHSVTQAGVQWCDPSSL QPPPPVFKQSSCLSLPSSWDYRHVP PCSVDT/CISILLIPFLRSGE*SPLLS WSSCDLGQGTAPLGFWFPMGKARP V |
| 3121 | 8618 | A | 3380 | 3 | 404 | PCLANFF/VFFVETGTHYAA*CGLRL LGSSALPV*TS*SAGIIGMSHCTC/LQ ITLLKTESHSVAQAEVQWHDLGSL QPLTPRFKRFSCLSLPSRWYRCAS PRLANFCTFKFLYFLVETGVSPCWP GWSGTPDLR |
| 3122 | 8619 | A | 3381 | 739 | 1003 | NLYLNY/CFF*IETGSHSVTQSGMQ WHNLASLQRLPLRLKQTSLSLLSS WDCRHMPNLA/NF/CVLRDKISPF CPGWSQTPGLKQCIEF |
| 3123 | 8620 | A | 3383 | 1 | 299 | ETESGSLPRLECSGTISAHCNLRLL GSSNSPVAS*VAGTGACSHAQLIF VFSVESGFRHVGQAGLNF*PQVIHP PRPRKVLGLLPVSHHTRPISFFL |
| 3124 | 8621 | A | 3384 | 12 | 336 | SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTRDPP/CLGLPKCW DYKREPPRPAH |
| 3125 | 8622 | A | 3385 | 2 | 318 | FLSSHFLTQSL/DSVAQAGVQWHN LGSLQAPPPGFTPFSCSLSPSSWDYR RPPRPANFFVFLVKTGFTVLARM VSL*PHDPPASASQSAGITGVSHW CPANN |
| 3126 | 8623 | A | 3386 | 1 | 325 | ASTAQAGVQWPAAQLQTPPPGFTF FSCSLSPSSWDYRRPPSPANFLYF* *RRGFTMLARMVSIS*PCDPPASSQ SAGITGLSHRAPVIRILRRAGRNT IGGLD |
| 3127 | 8624 | A | 3387 | 3 | 530 | RQSL/DSVAQAGVQWRNLGSLQVL PPGFMPFSCSLSPSSWDYRRPPRPA /NFFVFLVET/GFTRGSIS*PRDPPAS ASQSAGITGVSHRTRPKDCYS*RCS YCKVLTRLCFRKLLTGEEAPMP/PF* RQS*CLTSVTLSSAWRSICYDRLVDI QFKILFMKTKLPLLFSSQNELYFIIL |
| 3128 | 8625 | A | 3388 | 3732 | 4979 | NFVFLYLRELSSQAKSLTSHPLSNFF FKRQGLAMLPRLECS/GLFTGAVIA HYSLQLLGSSNPASANQVAGTTGA CYHAQSIF*S*NFFIFLSSVS*NLCLN QNAGFYLLFFYF*Y*MCRYASSTFLT NELCGKKK*TLSIEIKSIFFKHHVLY WLFGLVFLNLLLILPVLNEHRKIL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | E*GRKVYQDILPGFGCKF*RMVFLIF VHIL*APRYPSQ*GKLIPCI*LLYL*W LSPSPSTVSLAFHDKFVNLHFYIDMS LFHGQACSIKMIFLKDVNCA*LIGYI LFCFFFFFFFFLRCGV\SVAQAGVQ WRNLGSL\QAPPPRFMPFS\CLSLPS SWDYRRLPPRPANFFFFFLDF**RPL VFL/SFTVLARMGL\IS*PRDLPTSAS QSAGITG\VSHHVQLPYFVLNKFV LGSNSGF |
| 3129 | 8626 | A | 3389 | 1 | 585 | AFFFFLRQGLALV/THAGVQGQDYS SLQPLPPGLKAILLPQPECWDYRC MSPCLA/N/FFVFFVAMGFRMLPTL/ VLELLGSSDPPTLAS*SAGITGVSHC TWPLFI*VWSFGKV*ELS*HRFCISSF IHI*KFWKRWG\SLCSPGWS*TAGL KRSS*LGLPKYRDYRHEPPCPAFFTF LLECYDLHILLICSHFYLR |
| 3130 | 8627 | A | 3390 | 3 | 459 | QPGVQWHDLSMMPPPRFKCFSC SLL/SS*DYRCPAMPQPNFCIFI*RY GFT\MLASLVLD*L*VIRPPWVSQS AGITGVSHHTWARDRADF*MGVW ASPIARVPRGQQVRSCQPL*GS/WDP ET*HNGHFHFWIKQSEPIFKGRR*N P |
| 3131 | 8628 | A | 3391 | 1 | 258 | FFFKTDSCSVA\REYSGAISAHCNL RLPGSSDSPALAPQITGTTGMC/RS* FFIFLVETGFHHIGQAGLKLTLWIH CPPKMLGLQA |
| 3132 | 8629 | A | 3392 | 3 | 316 | VAQAGVQWWYLSSLQPPPPGFTSC LSPQCSWDYRHAPPCSANF*FLVET GFHHDGQAGLELLTSSDPPALASQS AGITGVHPPAPNSSCLHTDKRVHT WHKPS |
| 3133 | 8630 | B | 3393 | 49 | 279 | SSSDSDDEEKKHEKLLKALNAEEA RLLHVKETMQIDERKRPNYSMYET REPTTEEMEAYRMKRQRPDPMAS FLGQ* |
| 3134 | 8631 | A | 3394 | 2 | 357 | |
| 3135 | 8632 | A | 3395 | 1 | 1765 | MSATVVDAVNAAPLSGSKEMSLEE PKKMTREDWRKKKELEEQRKLG NAPAEVDEEGKDINPHIPQYISSVPW YIDPSKRPTLKHQRQPQEKQKQFSS GEWYKRGVKENSIITKYRKACEN CGAMTHKKKDCFERPRRVGAKFTG TNIAPDEHVQPQLMFDYDGKRDRW NGYNPEEHMKIVEEYAKVDLAKRT LKAQKLQEELASGKLVEQANSKPKH QWGEEEPNSQTEKDHNSEDEDEDK YADDIDMPGQNFDSKRRITVRNLRI REDIAKYLRNLDPNSAYYDPKTRA MRENPYANAGKNPDEVSYAGDNF VRYTGDITISMAQTQLFAWEAYDKG SEVHLQADPTKLELLYKSFVKKE DFKEQQKESILEKYGGQEHLDA PPELLLAQTEDYVEYSRHGTVIKQ QERAVACSKYEEDVKIHNHTHIWGS YWKERRGMKCCSHFSKYSYCTGEAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KEIVNSEECIINEITGEESVKKPQTL MELHQEKLKEEKRRKMKKKKHR KSSSDSDDEEKKHEKLKKALNA*E A\RLHVKETMQ\DERKRPYNSMY *TSRP\IEEEMEA YRMKRQRPDDPM ASFLGQ |
| 3136 | 8633 | C | 3396 | 106 | 426 | MFLKEPVXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXRLXXXXG* |
| 3137 | 8634 | A | 3397 | 25 | 435 | TKYWLLFFLILILPFFFWRRSRSVT QAGGQWHDLSLQPPPPGFKQFSC LSLPSSWDYRRAPLHLANFYIFSRD/ MDFTMLARLVNSRSQ/CDPLASAS QSAGISGKSQHTRPVLVLLKTYTNS H/SF*VKGLGWEFIL |
| 3138 | 8635 | A | 3398 | 3 | 320 | KTESHSVTQAGAQQDLSSVQSP PGFKRFSCSLSPSNWDYRRVPLHPA NFL*/FLVETGFHHAG*VGLELLTSG DPPTLASQNAGITGVSHCARPIVIFL YLITSR |
| 3139 | 8636 | B | 3399 | 70 | 199 | XMQVTGFGRGQNHNVQGSTPTDAS PRRRDVCTAQTQDSKLVNS* |
| 3140 | 8637 | A | 3400 | 198 | 397 | TKNRNTLSRFLLEAPRVFGPPSP/RP PKP/ASGP*PPIACPAGTHIPCGPYPC CHVGGGWPAQPLAALG |
| 3141 | 8638 | C | 3401 | 164 | 313 | MTLHFQELKSLKFYLNXXXXXXXXXX XGGRFKGSLGGPKFTRACNVKAFS L* |
| 3142 | 8639 | C | 3402 | 165 | 361 | MVKFCANNQGKTKLIFMFFHKESHI IIGRPRAQREKKEKEEGNPNECLLD VSLRTGFSGLPGRV* |
| 3143 | 8640 | C | 3403 | 146 | 389 | MTPISLKGRCRQLGDGKRCSLEDLA LIEGCPHAGRPPPRKSTLEPAFGSPR CQDPVSAMCMTRSPANLDSAERQ APGLGR* |
| 3144 | 8641 | C | 3404 | 157 | 404 | MLSLTSSPLNQGVVSFVHIAILKY QGCKPHFIKKLSRXXXXXXXXXXXXX XXKXXXXXXXXXXXXXXXXXXXXXP PAPSFLWGEG* |
| 3145 | 8642 | C | 3405 | 73 | 252 | MHTPLLAWPGMAWCYRQPLSTPRL ILNYVKPRKMIFRTFAYIRLYLCTYF AVFHRRKWP* |
| 3146 | 8643 | A | 3406 | 2 | 617 | IYIFLKALNFCREVPISPPPKVRVLF KDSQVTSFPVPAL*KGGQGLGYKT APYKEKTNSLQARVNLGPSRGLK RPPSSSSSPNPALLFIQTRVKLVNG KRPEATCLGRKASYSVRFSAAWDP\ PAGCAQPPTVSPDTPKQVSRTKAR N*TKNRNTLSRFPS*KLPRVSGPTQV PNPPKPRSRGD*QRTFPFVPDGNPV LN |
| 3147 | 8644 | C | 3407 | 129 | 281 | MSSHARVNLGPSKDPLKRPPXXXX XTQRQLFKTFINRCLQFVDFFEKIKL * |
| 3148 | 8645 | A | 3408 | 1 | 303 | QAGVHWRNLG\SLQPPPPPTLRRFS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CLSLPSSWDYRHPPSHPANFFFFLL LVEARFHHVGGGLELLTSSDPSTS ALQIAGITGVSHRAEPAPFFK*CFG |
| 3149 | 8646 | A | 3409 | 3 | 1039 | QQPFVNPALPPGYSTGLPYTGM SAFQYGPMTFVPPASAK*HGVNLT PTPPFQQPVGYGQHGYSTGYDDL QGTAAGDYSKGGYAGSSQGTKQV CRFWGLGKGVSVSSSTGLPDMTG SVYNKTQTFDKQGFHAGTPPPFSLP SVLGSTGPLASGAGPWLCTPTIPTH LASPPAAPLTAAAPPSAGCTEWLG SAQPAQLPAAQVSSLQTCRLQSLIL GQLNPGERGGAGAKAYPGQERTTR ARIWEPKCPFSKNSPTCVSHALCGE SASPDWATVCNVFMYVFNVIEVW GGVGGWRQMLARSAPPHSKPPSPN CSKISTPNPHLPFRSFLHSLATAQWA H |
| 3150 | 8647 | A | 3410 | 2 | 344 | LRQSVSLLPRTQAGVQWPNLGLSLQ PPPRFQRFSCLSLLSSWDYRHAPPC PTKFFVFLVETGFTMLARLVIS*PH DLPALASQS/AGITGVSHCAQHGV YIRCFRELA\SYSL*SLQ\WPHV*SL AYSIL |
| 3151 | 8648 | A | 3411 | 52 | 174 | |
| 3152 | 8649 | A | 3412 | 2 | 692 | RPP/QADPPRCWPR/PLGLGGCVPW GAGRLRRGHGPEPDSPPRRSPRGP ASPQR*PPRPDPWPPRQASPCRPT D*SRTAGRTTDPQEEAVGGQGPSR GG*APSNSSEPPLYGSGPLDSAFSLG TAFRKTLRIDLTSQSRPPHRSLSLYS GKGLAPGELADALNFLIYPTDFGL HCTIGDVATGPWRCNQIKRRKHCQ LGKSKLIYFFFPPTPSAKNFFSRY RHHS |
| 3153 | 8650 | A | 3413 | 3 | 367 | MLNYPLDFHPSFFVGGFFFEMESRS\ VARLEVPGVISHCHVCLPGSVSDS PASASQVAGTTGVCH*AQLIFVFLV ETGFHHFDQDGLDLT*SVHLCPS KCWDYVIHPPQPPKVLGLQA |
| 3154 | 8651 | A | 3414 | 1 | 595 | MGIHHVQGASLELLTSGDLPASASQ GRGVRLYYNEGRSSQSASVTALFLS SLPTVTSAMAGTRPPSARSHQTLQA CRAQKTKTRMSSI*GTGAKHQASSP GKAPLSTSPYFWKPSLQTSPCSGSR SLWASLPSPLAALFLCFWQDAT*RS STTRSSLPSWPSRSTRALRLSTS*PE CAPSA*ASSKAGERSTGDRL |
| 3155 | 8652 | A | 3415 | 259 | 941 | PVSWSLNSCRFFFF*QDQLPSVV/Q AGSGQ*RNLDLQPLASRFK*FSSS RL\SSW\DYRHMATMARLIFLVE MGFTMLARLVNFLTSSDPPTSAPF KWLGLQGKPNTRAVGFN**LGY SIILYHSNSPGTDLVFILFIYLFYFL RQEQNSAAQARVQ*WHNLGSLQSP PPGV\H*FLCLSLPSSWDYRCAPPHQ ANFFIFSRDGVSPCWPGWS*TPDLR |
| 3156 | 8653 | A | 3416 | 165 | 289 | ISGLSGLYHIDRLIVCNCKQKPTYS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | *NPGLSW*TDFKCLI |
| 3157 | 8654 | A | 3417 | 3 | 796 | PGPRAPPIRCSPLRSAPRRPST*SAA AWPASAAAGFCPCFYSA PPSSTSSR WPAAAGCSLATTAKTSSRVVEMLP RRAAAAGSYEGRAVRA/VMEYAW GRAAA/DHALSVASSILVILFHPLLL RPLCWTPECLSS*EVIGLLALAAV FQIISLGNLPREVHPDLHPSCQAPLS LTSITGAYGFGVGQPRIILTRLCLLL LAASPTTEDGPSGAMPSPGTSTHLP NLGMKCGRKSLPAEMGLPEGRKLF LPGGLWNPIFWPVFHHY |
| 3158 | 8655 | A | 3418 | 2 | 603 | GFFFFKIVLIQDLFPSTPLPSSVHSGD YGD SGQDP SGT RNTFRFCSPSPFPS COLPRPEAHTHANTRNPPSPHLLSF PHQSSEP*EGVKSLEEA*KWGEMA ITP*PTPLWR*LWRTPNSFPLSGQPF STPARPSVPSPIQPKTKHVQQHPPAS T*KTGSVPTSLTPSTGVLGEWPPEDP AKGLMPEGKEEQKAFGP |
| 3159 | 8656 | B | 3419 | 34 | 375 | MLLGRLTSQLLRAVPWASLPRKGA QLELEEMLVPRKMSVSPLESWLTA RCFLPRLDTGTAGTVAPPQSYQCPP SQIGEGAEQGDGVADAPQIQCKN VLKIRRRKMNHKKYRKL* |
| 3160 | 8657 | A | 3420 | 2 | 361 | YSTSPAGQVGR LSPSQGGPAGAGG DAG/TPGRCP SAPWRAGSRPAASCP DWIPG/PAGHVAPPQSYQCPPSQIGE GPGGTPETQADQVRERPEAHLAG GAKGSPRRAGRPPRSTCGANESG |
| 3161 | 8658 | A | 3421 | 1 | 417 | RITAATGGKGGARLICPAGR/CLGV CQPSGASFSPAFSQMPSSPCSAPSPI WLGGHW*DCGGAT/CPCGPGIQSG QEAAGREP/GSPGG*RTSSWGPASPP APAGPPCEGERPPYLGRPAMCCKG ARRPGCPALQRRAKAGGR |
| 3162 | 8659 | A | 3422 | 31 | 756 | GRRALRQAGPGSSREGPGARQRDS RGGEPEGAGLPVLGPF GASERDTA RVGGLGASGRELCWKQSPPCGLGW RREK GSEGRGGTRRPSGPPTTEG AAA*PE/PGTCVPAPLGP/GPPPTDH APGAPDFPAVEGRSLGRRPPALAQ S/P/GSAGQPGLRSPFTH/QPAGPGR GLSPSQGGPAGAGGDAGPQEDVRQ PPGELGSRPARFLPQTGLPGPAGTC GLHRNPTQCPPSPDRGKPGKQG |
| 3163 | 8660 | A | 3423 | 69 | 258 | PRTNRCATNHTPANF*FFVETGLH VAQAGLELLGSSSPALAPKQLVTG ASHHTRPQ*NFLQ |
| 3164 | 8661 | A | 3424 | 8 | 292 | QSFLFLKTRYLLRHP/GWNTVAQ*Q LTVVTSRLN*SFHLSLPSSWAI AVR MPPCPANFLFF/TRDRVSLC*PRLVS NTWVQMILLPQPPEMLGLQA |
| 3165 | 8662 | A | 3425 | 123 | 357 | WGKRPGQGGRNPWGPPLPGGK/PP KKGFLGPFTGRFQGSSPGL*KGPFL KGGP/QF*KPKPGSQNRVFKPPKIWE TPLGN |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3166 | 8663 | A | 3426 | 2 | 311 | FHSCYPGWSAMVRSQLTATSASQF K*FSCLS/LPSSWDYKCAPHPANFL FLVEMRFHHVLVRLVLNS*TQVIHL PRPPKVLGITGVRLGAQPCTFFFFYC SSV |
| 3167 | 8664 | A | 3427 | 7 | 534 | TSDFIYKALKLQQEVPAKSHLVQN YRFFFFFFLWWSLAPVAQTGVQWH DLSSLQPPPGFKRFFCLSLPSSWDY RCPPRPANF*FLVETGFHHVDQAG LKHLTSDDPASASPSAGITGVHPRP GQENQDLPGLCVDQLYTENSRRFFSK NYYQTPNFTSRKRDCLKISVFFFA |
| 3168 | 8665 | A | 3428 | 368 | 688 | LTVEFLNLLNILSLVCFIHQTN*IICY FNT/SSSHQNA*YI*EPHVP*GQRGK ASRQRG*TPPRSGTAASWPRVEK*R EARPQNPAQQTYYVRESPTDASPSS PKMAA |
| 3169 | 8666 | A | 3429 | 1 | 90 | FFVFLSHQRNLCLRRYSRDMAAIK SKFFL\WPGRVAYAYNPSTLGRRGG QIT*AQEFKCS*AAIKSKFFL |
| 3170 | 8667 | A | 3430 | 259 | 331 | RNE*LLTRFSPLSLSH*VLGVSMF |
| 3171 | 8668 | A | 3431 | 1 | 639 | LGKFHTFQMSPGGGVGLLSL*SYRN SCLAG/GGCDHMSVHVCIRARGVK VRKNSNHPTETRK\VLGMRSLT RESSISDSMWLARKQTLHTPVMMQ TPHLTPTI*EEPQRIARPE\DTFMSV/Y YPMQTEHHQTPLDYNRRGTSLLD DEEPIVEDVMMSSSEGRIEDLNEGM DFDTMDIDLPPSKNR\RETE\LKAD FFDPA\ASIMDESVLGVSMF |
| 3172 | 8669 | A | 3432 | 1 | 354 | LETSPLMFTMLDRDMSG/TMGFNEF KELWAVLNGWRQHLSSFDTRSGT VDPQELQKALTMTGFRLSPQAVNSI AKRYSTNGKITFDDYIACCVKLRAL TDSFRRRDTAQQFIQCVMSV |
| 3173 | 8670 | A | 3433 | 1 | 788 | MAYPGHPGAGGGYYPGGSPVVKEE NLIRQNDVYVFPVSQYGGAPGGPA FPGQTQESL\YGYFAA\VAGQDGOID ADELQRCLTQSG\IAG\GYKPFNL\ET CRLMVSM\DRDMSGTMGFSEIF\K ELLGLLLEWAGRIQHFI\STDREW EQ*DPQELPEGP*QTMGF*V*VPPGC *ISFAKRYSTNGK\ITFDDYIACCVQ T*GVFTDSFSKTGILAQGGCLLNFI WIDFHFNVCVHGVFKSLGSCMNVIN DSNWSSPLLVLFAFG |
| 3174 | 8671 | A | 3434 | 6222 | 7046 | RTVTTFLSKDSHGVIYCAQGGKIPDH QNPQCNRKQHPVSTILMLDKASF QLRK RKHNLSVNCINRNPMSLKN TSWHSSLSVTQRHQQQSKLHFQGS LLH*PSQNIL/SNI*KCINYC*HCSV LLSYLFIETESYSVAQAGVQWHDLG LLQLLPLRFKQFSCFSLPSSWDYRS APSCPANFCILVEMGFCHVGQAGL KLLASSDPPALASQSAGITGVSHYT QPCSPFLKSTGLFSCVKLSNPYHKG RIYLGRMCFLNSTWHLVKSTLFCPL FI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3175 | 8672 | A | 3435 | 3 | 287 | SRSVAQAGVRWRDLSSLQPPPPRFK QFSLNFPSSWDYRCAPPRPANFV*I LAEMRFRHVGQVGLLELLTSGDPPA SASQSAGITDTSCHAWPFTF |
| 3176 | 8673 | C | 3436 | 88 | 303 | MTFLESSAVPPHWTGQDGRVCWTG WIPQCQAGSAPEVLECLSTQQVKSL QTLGGAAVSHKTNICLPFTKLW* |
| 3177 | 8674 | C | 3437 | 354 | 416 | MKESPGGELPQTGKKPVFLF* |
| 3178 | 8675 | A | 3438 | 274 | 460 | TLKNLRSAASTLGNPASPAHSSILS CPMRGHCRTL*KCHDWSFRAKMPS PFPQVGIYPPPN |
| 3179 | 8676 | A | 3439 | 480 | 613 | LSFRAKMPSFPQVGIYPPPN*GPIC LLCFSFLCECVFYRNHLD |
| 3180 | 8677 | A | 3440 | 1 | 864 | YPTTPYQHHPISPPPIPTHNHHQKP PTPSHRPQPTQRYTYHHNHTALTI APTRQSNPPHNTHHHTPS/TPRTNSS PPH\HHTLPQRIPPYPPT*HTPQAHS HPAG*RASSQPRRAPSPASRPSPTDP ALRANPLSRSYGSGLPFTFYLHCSN MPKACSPWRPAADMCTARPRFRPF KPDFQGPARRHRTTPETRRFRHGPI SRGEP\PGQPCPSQRKENSTPEFPPA SSGIGRVTDGTGLAAAPSPPLRIRGS EPDSPFESAEGHRRPSRPFRTALAQ SLRNE |
| 3181 | 8678 | A | 3441 | 23 | 266 | EMESHSVTRLECSGAISAHCTLRLP GSSDSPASAS*EAGITGMCTT/ARLIF GFHHVGQAGLKLL/NIVILLPRPPKV LGLQA |
| 3182 | 8679 | A | 3442 | 840 | 887 | |
| 3183 | 8680 | A | 3443 | 127 | 593 | DKATKLTFRSYAAVILKIHVLTW VILFRRKIIRDETLKLLDLISLVGKG QCYRVVFFWFFFFFEMKSHSVTR LECSGAISAHCNLCPLGSSDSPASAS LVAGVTGM*HHTQPIFVFLVATGFH HVGQGWSRTPDIRVIRPPWPPKVLG LQA |
| 3184 | 8681 | A | 3444 | 2 | 514 | FFFFLRLQSL/DSVAHTGGQ/WGGG/ LQPPPPRFEGFLGLKLLGS*HYK/PP RMANFIFSRDGVFAMLARLVNSS ASSDLPGLASHSAGITG\VSHHARPI FSYKEHQSY\GLRACPAPV*PHLSYL QPQPQYFQIRSHTEAPGST/WNFGE DTIQPSTFSFYLT*KIIPILYRVKK |
| 3185 | 8682 | A | 3445 | 2 | 147 | FFFCRD/RSLTMLPRLVLYSWAQVIL PSWPPKMLG*QAQATVPSPPKSIN |
| 3186 | 8683 | A | 3446 | 2 | 328 | TITYRGAKIRITSDSSSETMQAREE* SEIF*VLK/ESSSPH*PKILYSGKLSFK SKGEIK/YF*GKQN/LKEFVSSRPVL QGMLKVVLQREGKLYRSETQTYKK KEKASEKE |
| 3187 | 8684 | A | 3447 | 1 | 357 | GDRVLLCCPG*SADHSSLQS*PSGL KRYFCLGLLSNWKHRCMPPCPANF FNFYFCRDK/SLPMLPRLVSNSWAQ GIFLSQPPVSVGDYRCGAYHALTLFI YGRMGVFAMLAQAGPQTPL |
| 3188 | 8685 | A | 3448 | 2 | 84 | GLTLLPRLVSNSWPQEILLPW/PPKV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LKL*AQAGLKLLASGNPPALAPKVL KL |
| 3189 | 8686 | A | 3449 | 1 | 439 | |
| 3190 | 8687 | A | 3450 | 1 | 552 | GNEFSILKSPGSSVFRNGNWPPIGER IPDVAALSMGFSVKEDLSWPGLA ^{AV} GNLFHRPRGYPSWVM\VKSGGTKL ALTPQAVVISYPLENRVYVMVGKAN SVFEDLSVTLRQLRNRLFQENS ^{VLS} SLPLNSLSRNNEVDLLFLSELQVLH DISSLLSRHKHLAKDHSPDLYSLEL AGLDEIGKRY |
| 3191 | 8688 | A | 3451 | 3 | 1111 | ILKSP\GSSVFRNG\NWPPIPRE\RDPP DVAA\LSHGLPL*KKDLSWPGLA ^{VG} NLFHRPRATVVMVNVNGVNKLDLP P\GSGIS\YPLENAVPFSLDSVANS\IH SLF\SEET\PVVLQLAPSEERVY ^M /VK GRANSVFEDLS\VTLRHSRNRLVFK KTLFLSFTPPQILLSRNNEVDLLFLS ELQV\LDISSLSPRPKHL\ARDHSPD LYFTGSWAGL\DEIGKALLGEDSEQ FRDASKILVD\ALQKFAD ^H VPVFM VGNPVVELVHCPSHLNTSPPLGKTR DLPLRPKQAQEPQQVPYNLA\YKYN FEYS\VFNMVLWIMIALALA\VIIT SYNIWNMDP\GYDSIIYRMTNQKISE WIECYLWPRIRKRGFGNWLFC |
| 3192 | 8689 | A | 3452 | 3 | 371 | MLPLARCSSSCLAPLSTYQTQVK ^{TQ} VHTETCI*MFIAALFII ^{VRR} *KQPKCP SENK\WNKIWHIHTMK*YSATKKN KVLTYATI*MNTENMLSQRSY*QKT T*YLFLLMYMKIQNREMYRYKVD |
| 3193 | 8690 | A | 3453 | 2 | 318 | ETESRSVAQAGVQ*RNLS ^{SLQ} /PLPP GFK*FFSLSLRSSWDYRCMHDA*LI FLFLVETGFCHASQAGLELLTSSDPP ASASQSAKITSMSHHALPLFSNKVT FWDSW |
| 3194 | 8691 | A | 3454 | 33 | 504 | GLHNFLTYKATHISAVWYAVRVEN RSTEQNRVQK*TYMYVVKDAR*VN GNRILF*YC/WNN*IITWRKMNLNL DLTLHRKVYLKWWIDLNVKAKTVS PLGQNITESLHNFGVGKYFLDT*SI/ MPHKFFFNKLDIIRIKIFCS*KDAINK MKKWPGVVAH |
| 3195 | 8692 | A | 3455 | 16 | 1011 | WPVRAQAGQRPVLHTQVASL ^{FAGV} PCVL ^{SHPKKGLLVPPFPSSKKGHLG} KPHCPLPSAGRGAAGLGPLAQ ^Q PVS PAPASPMAPCKPKGLPPLPMG ^{VEPE} ILATMPVLTSHPP/SPEPMQSGNMPP S/PPSLCAFVPRWSHPPVPGWARWS CP/ALPAAPPSL*HWTRMQPPFCVPL RVPWVPSSGARGMKESGLDGQ ^{GFL} GPTPSASPWGPWFDIRLPGCKQ ^{GIL} AFKVTGPPTGFPDFEGKRFK ^{KENKP} PG*LESKAPDTVK*NPPSTNPP ^{PAPA} FLTWDGAYRGPA ^{GFL} LVCQPSLLS LILKNIDDTLKCVERFEKLTASK ^Q P KATVVLARRS |
| 3196 | 8693 | A | 3456 | 1 | 348 | PQQLRCFSFWRKDTKVDWLLN ^{RG} |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ARWLEKKTRLHRGPWARPRLMRA QREEALRREGGNPPPRGPGGEEAPL LRSSSGRPAR/HQT*QKSGASPSDPR SASR*ALRREGGNPPPRGPGGEEAP LLRSSSGRPARLRPSRSPERHPPTLA PPPARPSCPALPRLSMSAG |
| 3197 | 8694 | A | 3457 | 2 | 247 | PGCTILAHCNLCLSGSSDSPASAS*V TGNNRHAQPCPLI*RTGFCHVG/R MNMLVFNSLTSSDPLEVST*GPQPP KVLGLQA |
| 3198 | 8695 | A | 3458 | 1 | 515 | GLGSLGPPAAVPTCPPRSPPP/GSPE GALQCGTLPAGTATPDGHVGVAVP FPPTVAPTRRSRSPSPQSC*WGLQH QLCPGSMEEHMTPHGLALPGASHIV PPTLCAPGGSEGARGI*PPA*AGYAL SLPTQFQTLILHPSCCRPGVP/PINLA AQLPPQVPHAPHAWQLPSAPK |
| 3199 | 8696 | A | 3459 | 2 | 223 | IYISPKALKFCREVGPICPPK\KGSF PKIPR*QIFPPRC*KTGKGQGIKRP IRGKVLRCCKPGLNLGPPRVL |
| 3200 | 8697 | A | 3460 | 2362 | 2696 | |
| 3201 | 8698 | A | 3461 | 1586 | 2325 | SPQRSGAARARPAPHRALLGRVPA RDAGSGRRTRSSRTRCGGCARRWS SISRRRRSSETSAGSWRRLSKPSGPG RWRHCARNTGRRCPWWQISVVP RPSSRP/WLAALAEALKDSGEKPGK GASRPEDLQLIGRLQTRLKEREDIK QLTKKKVEDVPSRVVSVPNLASYA KNFLSGDLSSRINAPPITSPSLDPSP SCGRITYKPNQSTDAKTATRTPDGET AQAKEVQQKQGSPPHQEWFTKYFSF |
| 3202 | 8699 | A | 3462 | 125 | 489 | YYLFFFFFFLRLQSLTLVAQAGGQW RNLSSLQPLPPGFKRFPCLSLSSWD YKCPPP/RPG*FFVFLVETGFHHVAQ AGLELLTLGDPPTSISQSAGITGVSH QARPD*ETLEFQGDRVNL |
| 3203 | 8700 | A | 3463 | 1503 | 1511 | LFPVPFACPSLNCPSPPPIGVHLP QRLETPP*EEGRWIPRRTCGPARPGP PPGAPSVTLPPRTVHFHGHAKGIHFR KP/RHPG*CVFILTLDCVHLH*KIND FIDTNFAMKSGYPNRIVRISFLIHT |
| 3204 | 8701 | A | 3464 | 54 | 593 | RTALPAQHVASTWPGRPSRLLLRG GPGAPRSMQTGDSVGRGASKEPN*\n PHSGLPKHPLARSPPQRPSHRAMGQ GSPMPAGPT*TCAQALPPSQDGLD LGNRAGWGCSPECLSKAPGGEGPA QAHGPNPHTYRKPQWCWKLSPGH ALAPSPPRREVALNLNYSFIVPRDSP RPCIISL |
| 3205 | 8702 | A | 3465 | 2 | 324 | FFFFFLKWSLA/SFAQAGVQWCDLG SLQALPPGFTPFCLSLSSWDYRRP PPHLA/NFFVFLVDMGFTVLARMV SIS*PHDPPALASQSAGITGVSHACP AYNVFKDDG |
| 3206 | 8703 | A | 3466 | 142 | 413 | AQEFKTS LGNMAKPCLYKKYKKM SWDYRRPSRPANFSCFLVETGFCH VAPAGLELLGSSNSPT*ASQSAGITG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VSHHTRPQIFLLPLSN |
| 3207 | 8704 | A | 3467 | 241 | 523 | NISGSFCMPILTAPLFTVAKRWKQY VPISG*MINKMWYIHTVEYYASKR KIR*/PCAAATWMNLEDMMMLSEVSQS LEDKYSMLPFM*SIYVKYLEQSNA |
| 3208 | 8705 | A | 3468 | 137 | 382 | NSAVHQKFISIPNTSLPHSLAILKPQI NSLEEET*PFWCKKSSPVPKMRGER NDDNFHKVLLNVTNVDPQGLRSP KWFCWG |
| 3209 | 8706 | A | 3469 | 2 | 363 | FFFDTESYSVAQAGVQWHDLCSLQ PPPAGFKOFFCLSLPSSQDYRHLP WLANF*FLVETGFHHVGQAGLKL TSSDLPASGSQSAGITGMSQRTLQQ LSLKTTELNRNFCVPYCIINA |
| 3210 | 8707 | A | 3470 | 135 | 466 | GIDTILTLNQ*SLKTRQ*FTLIIF/IFF FFLRWSL/DSVAQAGVQWRDLGSL QAPPRGFTPFSCSLPSSWDYRRPLP RPANFFYF**RRGFTMLARMVISIS*P RDLPAEFL |
| 3211 | 8708 | B | 3471 | 27 | 21189 | MKVSAARLAVILIATALCAPASASP YSSDTPCCFAYIARPLPRAHIKEYF YTSGKCSNPVVFVTRKNRQVCAN PEKKWVREYINLEMSMICSGHHV YPNLPTDSFGLDQFRGNYLHSRDY KNPEAFKGRVLVIGLGNSGSDIAV ELSRLATQVHDVKVLGNKPKVHIIST RSASWVMSRVWDDGYPWDMMYV TRFASFLRNVLPFSISDWLYVQKMN TWFKHENYGLMPLNGSLRKEPVFN DELPSRILCGTSLIKPSVKEFTETSAV FEDGTMFEAIDSVIFATGYDYSYPFL DETIMKSRNNEVTFLKGIFFPLMEK PTLAVIGLVQSLGAAIPTADLQAW WAAKVFANSCTLPTTNEMMDDTD EKMGGKCLKCPYQFRLMGPGKWDG ARNAILTQWNRTVKPTRTRVVSEV QRPHPFYNLLKMLSFPLLLLAVTLT FY* |
| 3212 | 8709 | A | 3472 | 9 | 339 | ITLSLLSFFNLRPSFALLAQAGVHW RDLDSLQPPPLRFK*FSYLKSP*RSW DYGHAPPRPANSVLLVETGSLHVSQ GGLILPTSGDPPASASQSAGITGVN CARPPSLFS |
| 3213 | 8710 | A | 3473 | 1 | 50 | |
| 3214 | 8711 | A | 3474 | 1 | 1256 | MAAAAAQGGGGGEPRRTEGVGPG VPGEVEMVKGQPFVGPRTYQLQY IGEGAYGMVSSAYDHVRKTRVAIK KISPFHQTYCQRTLRENQILLRFRH ENVIGIRDILRASTLEAMRDVYVVQ DLMETDLCKLREKPSKLSNDHILLT FLLPDSLAPSSYIH\SANVLHLRS* SPPTWLIQHHLADLKVCGFGLAGIC RSWRHDHTGFLT EYVATRWYRAP EIMLNSKGYTKSIDIWSVG\CILGAE MLSTRAIFP\GKHYLDQLNHILGILG SPSQEDLNCIINMKARNYLQSLPSK TKVAWAKLFPKSDFKAL\DLLDRM LTFNPNKRITVEEALAHPLYEQYY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DPTDEPVGEGSPSPFGMELDDLPE RLKELIFQETARFQPGSAGRPPSPR QTSLHPGGWTCPPARPLSRRDC |
| 3215 | 8712 | A | 3475 | 877 | 1463 | LPFTAWP*E/QLQQA VHAGLPQQA KILFDGGSEIGKILPAFQSGNLSCQLH **IGQRAGRGGRLRIGRQGGFSFHQ* DGQQIALH/QPGPERVAASGPRWF APAGENPV*WWFRNRQNPLIALRSL PAFQSGNLSCQLH**IGQRAGRGG RIGRQGGFSFHQ*DGQQIALHRLA LRELQQA VHAGLPQQA KILFDGGSE IGKIPV*GLLRWPPLPRDVQWDSAP LLRARWGL*GER*PREVPAALQGE* PQALLPGGGEPGWQPAEPHPAGGV HRAGPPGGGCWARAGGHQKHL RPAAGVPPDRGCLLQLGQIPH*AGE QVQAGPGTGQPAGEQAQRGLSGNA GPHQVPAEGDTGHLCD |
| 3216 | 8713 | A | 3476 | 29 | 1076 | EQRDPQDIFSQRKSSAFPPSPEIEILS GGKSLSLQLHTPSPG/QQGETPRGG QQSQH/PCQPGGGVPRYACAGGV PVTERGAQGWVHPALRRARYPDA GVQSHMKPAGDWGPGSNKPAGTD ADAVSGRR*LPKTLPSLGLGKKSPP GVPGHPEYPE/HGGSEALLHEFLLP VSRL/HGPLYPQMSNGTLHHYFVP DGDYEENDDEKCCQL/PLQGE*PQA LLPGGGEPGWKPAEPHPAGGSSPC WAARWEDAGRVLGGHQQKHLR RRGRELWQVPAAGVPPDRGCLLQL GQIPH*AGEQVQAGPGTGQPAGEQ AQRGLSGNAGPHQGAEGDTGHL GAQGLIRAAGPHH |
| 3217 | 8714 | A | 3477 | 3 | 591 | ERNYLFFLRWSLTLSSRLRGQWRN LG*MQPPPP\GFKA\FSCSLPSSWD YRRMPPCPANFCILVEIGFHCLAKL VLNSRPHDPPTSASQSAGITGVSHR AQT*KGIHLNELCTALAKEGRAWS GR*RAGAATPAP/PAPFTL*PGCIPES WSPMPPPHLPLTALCKATHAGTK HPLHTKTVSSCGAVLQPTPQRKD |
| 3218 | 8715 | A | 3478 | 1 | 235 | RDHPGQH/GETPSLRKIEILAGHGVR HL*SLLGRLRQENCLNSGGRCSE PRSCHPTLAWAIEQGSVSRKEGHF RLA |
| 3219 | 8716 | A | 3479 | 2 | 928 | RPPRPGTERALPSRLRSRPRVRTETP SPSSSGPPPSRNTGMAPLRR*RV*R GTVPRSG*KGR*PCSRRRRSVPSGR TPALRGTRAPSDQKGKARPPEP APSRPCGSRFCRASRSRTSPRPPTP ARESGNPGRSP\DGGEKAAAQGS*K ESAACSNRAWS*WAA\SPPWITVTR QKRRGTLDPQPNQEDKPGARTLKS EPGKQAKVPERGQEPVKQADFVRS KSFLITPVKPAVDRKQGA KLNFKEG LQGISLSHQNLAAQSALMMEKEL HQLKRASYASTDQPSWMELARKKS QAWSDMPQIIK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3220 | 8717 | A | 3480 | 1 | 435 | EKINKIRWLPQQNAAHFLGTNDK AIKLWKISERDKKAEGYNLKDEDG RLRDPFRITALRVPILKPMDLMVEA SPRRIFANAHTYHINSISVNSDHETP NIVDIKPANMEELTEVITAAEFHPPH QCNVVFYSSSKGTIRLCDMR |
| 3221 | 8718 | A | 3481 | 204 | 397 | VPILKPMGSYG*EASPRIRIFANAHT YHINSISVNSDHETYL SADDLRNL WHLEITDRSFNIV |
| 3222 | 8719 | A | 3482 | 1 | 1462 | PLRSWLPRLPDSQADIISTVEFNYS GDLAT/GDKGGRVVIFQREQEVLQ PRRALP*SVSSFLSTSCREVWQGCE FSLPFRERIK/GRPHSRGEYNVYS/TA FQSHGTGGFDYLSLEIEEKINKIRW LPQQNAAHFLSTNDKTIKLWKISE RDKRAEGYNLKDEDGRLRDPFRIT ALRVPILKPMDLMVEASPRRIFANA HTYHINSISVNSDHETYL SAR*PGGI NLWHLGNHR*EAFNIVDIKPANME ELTEVITAAEFHPPH QCNVVFYSS SKGTIRLCDMR/SSALCDRHS/KSFFE EPEDPK/SSRSFFS/EIHSIS/DVKF/SH SGRYM/MTRGLPVRWKVWGPSTW EEAGPVGGPTRVHEYL/RTKL/CSL/ YENDCIFADKFECCWNG/SDSAIMT GSYNNFFRMFDRDTRRDVTL/EASR ESSKPRASLKPRKVCTGGKRRKDEI SVDSLDFNKKILHTA WHPVGQCYL PWLATN/NLYIFQDKIN |
| 3223 | 8720 | A | 3483 | 603 | 659 | MCGFFFVFFFWRRSL/DSVTQAGVQ WRDLGSLQPLPPGFKRFSCLSLPSS WDYRRPPCLANFLFLVEMGF/TTV LARLVSNS*PRDLPTSASPSAGITGV S*HASSRL |
| 3224 | 8721 | A | 3484 | 84 | 202 | |
| 3225 | 8722 | A | 3485 | 3 | 577 | ILGFPPFVRWGSHTVAQAGVQWCD HGSLQPRSPGVK*SSHLSLLGSWNH RHATTTTPG*FCFFSRIRSHCVAQAGL *LLTSNHPPALASQT/VGITGVSHWT WPNTGFSVLTATNKNLKFHYAISK CLVRAKLSSRLKIEERNKALSAPV VSVSIFDRVLRLLGYSASDWQPEFV ETAVSNFVIYGIFRGQ |
| 3226 | 8723 | A | 3486 | 3 | 248 | SLYIEIPGGALPEGSKDSFAVLLEFA EEQLRADHVFICFHKNFSFLGFEIV RPGHPLVPKRPD ACFMAYTFERESS GEEEE |
| 3227 | 8724 | C | 3487 | 185 | 340 | MDNFCSSLCDFCHQNKNLRLVXXX XXXGGRFKGPLEGPKFTRACNELV FSL* |
| 3228 | 8725 | A | 3488 | 1 | 546 | NDRLN*TRELTSHERRRFRPSSRLT DAQ/RINWRQVLSAGSLYIEIPGRR AAEGGARN SFAVLLEFAEGVQLRAD HVL/ICFHKNREGQKPPL/RTFSFFG LED FEDRG NPLVPKETPDACFHGLT TFERE/SSG/EEEEVGARLRGLGQFP RPGAHP LVKPGWGKEPVDSPHLAL GLSPML |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3229 | 8726 | A | 3489 | 1 | 526 | FFFLERDPCSVTQAGMQWHDLGSL QPPPPGFKWFSCLSFPSSWDYRCP HPANFCIFSRD/MGFTILARLVNS*P HDPPTSASQSAGTTGVSHSAWPVC/ LFEIEFHS\VAQAGVQWRDLGSLQP LPPEFK*FSCLSLPSSRDHRHLP KFIHFSRDRVSPCWPGWS*TPDLR |
| 3230 | 8727 | A | 3490 | 276 | 735 | FFFFFFLRQSFSLSVQAGVQWHNLG SLQPPPPGFRQFSCLSLPSSWDYRHP PPCPANFCIFNRELIIVYLIKTGF/IHV GQAGLELLTSGDPPALASQSAGIPG MSHCAQSTH*FLLAQQLFCSIYPSFH AQGVIPRIVTHKRETGSQTLYSIV |
| 3231 | 8728 | A | 3491 | 2 | 344 | FIFIF/NFLRWSL/DSVAQAGAQWRD LGSLQGPPPGFTPVSCSLPSSWDY RCLPPRANFFAFLVETGFTVLARM VSI*PRDPPASAYQSAGITGVTTAP GLLF*INICLAAFYFV |
| 3232 | 8729 | A | 3492 | 109 | 559 | QFLHRLVHDSGEVWMKLV**NTL LAKMVSISWPRDLPASASQSAGITG LIGALVLSVGIYAEVER/HEI*NP*KC LPGSSHPPHPPGRRHVHGLLHWCA GVPP*QPGKH |
| 3233 | 8730 | A | 3493 | 1 | 593 | ETESRSIVQAGVQGRELGSLQTLPP GFTPFSCPSL\SWDYRHPPQHSANFL AFLVETGFTVLARIVSIS*PHDPPAS ASQSAGITGVSHHARPQTGRLLFL FFFFETESCSVTQIGVCSGHDLGSL QLRPPGITPFSCSLPSSWDYRRPRL RPANFFFFVFFSRDGVSLC*PGWSRS PDLVICPPRPPKVLGLQA |
| 3234 | 8731 | A | 3494 | 3 | 484 | RFFFFFFLRRSFT/SVAQAGV*WHDL GSLQPPPPWFR*YLCGLPLNSWDYR RGPPRLVNL CIF/M*R*SFTVLARLV SNSWPQ/CDLPP/SASQGAGNTGVS HARPDEIFYQC*Y*ETEMVRRST TQDRAGSTTVLKLGLQLPEREIVN LALGALVYRNITPN |
| 3235 | 8732 | A | 3495 | 104 | 288 | GEVICGRRRSEVSRCNLVDLEPKGP WGHWQGG*GDRRAGGT*GE/GHL RKKAI*GLQVQGRPRTEGPLGA/PG KGD*PTTEGPRGDARNCDACPRPR ARPVLVW |
| 3236 | 8733 | A | 3496 | 3 | 641 | RPPFFFFFFFRRSL/NSVTQAR LQWHYVLGSLQAPPPGFTLFSCLSLP SSWDHRRPP/RMPG*LFFAFLVETGF QVVSQGWVSIS*PQ/CDPPASGLSKC WGLQGVSHLRPSHLSFLAFFFSET GS\FSVAQAGLQWA\NHSSLQAPSP GFTPFCHSLPSSWDCHRPPRANF /CCIFSRDGVSPC*SGWSRSPVLVIRP PRPPTVLGSQG |
| 3237 | 8734 | A | 3497 | 1 | 296 | VSRRFKQSIPP*AS*GWDHRCVPPAS LANFFFLLEMG\FPMLPRLVLNSWA QVILPSQPSQSAVITGMSHCACLYW LLKTKQIKIKQTGMSKVIKLFPL |
| 3238 | 8735 | A | 3498 | 1 | 347 | KKTGRRKRNMIDYEKKKNKEQEER |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RKKRKKRKSSSSSSSPEEKKEEKKK KREEEENRKKEEEEE*DK/KEED RRKHESRRRLRAVGDEVINKVCQE LKRTIPVGRDYRPLDPSS |
| 3239 | 8736 | A | 3499 | 2 | 286 | PQPCSLAPNPPRMPPGSF/TPCPSPPR SNITL*KQRPPSPPPSPEPPRIAQQRV AQNLTSPRPAAAKPPGWLSTNLSK ALPETPTVAQSPVLFTHF |
| 3240 | 8737 | A | 3500 | 3 | 954 | RPRAGAAGGGGGGSRPSGAHPSRS AC/GCPAGTRPGRAPPAASARPSRS KRGGEERVLEKEEEEDDR*R*R*RR SMCQRRSEVAPSSDRPGRCAPPSP TASGDLRVPRRGRSGPPGTAPGPG *RAGASPGQRHPPGCSWPQ*TRKG EQVFFSFPASVATGPDSPSPVPLPPG KPALPGADGTPFGCPPGRKEKPFDP RSSWNVMGFRSNILLEA*FPEQATA FPRAGN*WQIFAAHAHRCASPACP S\PRASPENLRAPHQGASARPL*GM MDPDGFL/ALSAQPHPCPKPIAPISP KIPQSPGSWTGDTLSPH |
| 3241 | 8738 | C | 3501 | 68 | 199 | MPIIPALWEAQAGGLLRPGVCDQPG QYSKTSSLINKLKNPPSL* |
| 3242 | 8739 | A | 3502 | 11 | 520 | IRVDDFVAHRSRCCVAFPSSTPRSR RRPKRRRRRRRENDPAASSLPAPHL CSVSQSAAGARLVLRPRACGAQAQ RP*LASGLRTSALRRRGHPRAELRS GPQRRQASE/PSPRGVAGARWRR EDG/RPSKRSRMAQREAQQTSPQR GNRPKTSEKCPPEEKAVCRTPG |
| 3243 | 8740 | A | 3504 | 78 | 595 | NQNRLKEAGWRLKLADETSSSSHQ QVCGTHHVSACYS/GSPYS*KHPD SPSPATSRKQNLSTQSCISPMWPCSQ RSICQFGHGGTESGGILLGLLRKAI GSPGKRSAPVQPNWEGNG*EAAW ASSSSPCKVTAPLAPSELPFSKFL RNKKAQRKISHLLEVTVGHLLC |
| 3244 | 8741 | A | 3505 | 2 | 267 | ADLSAEAL*TRREWDDIFKVLKTSS/ LGQPKILYPSKLSLINEASSSSSSSS SS/REFTTRLVL*EMLKGILHMEAQ QYLPS*KHTKV |
| 3245 | 8742 | A | 3506 | 1 | 323 | IAGEVNTPRSVTDRSS*Q/IIQEGIVQ LNSAIH/QTGCTNINRILPLTTAEYTF FSHLYRTFT/KIAHILGHMTHLNKG KRIEIIQSMLSDHNGIQPEISNRKIAG KSPNT |
| 3246 | 8743 | A | 3507 | 3 | 814 | SSGLAGTPFPSEGAVCRSQPG*GSG S\PLPVGPACWYLP CGP*DQRCPPG SLGPSAEPGS*NLSCPRPMCSPAGT SCPAPV/PDSVTPVLRARGTACLPS TFPAWSVPRFQPGAAPSSADLVH AASGPSASLSSSLSTKAPSLPLGACL PAGGV*TLFGPPSG/RLWRPP*GLTG GGLVWAAGVHWACLWPGQASGG SIRHVCVAVGVQGAPAQKEGGAGL GKGLGSFACGRPHLPAYFACGRPH LPAYFVLDLPFAKVLNRINI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3247 | 8744 | C | 3508 | 112 | 252 | MFRSMYNXXXXXXXXXXXXXXXXXX XXXXLGMSEXXXXXXXXXXXXXX LGF* |
| 3248 | 8745 | A | 3509 | 448 | 715 | FFIISIKIIEFFFFETESCSSVTQTRVQ WFDLGS\LOPPPPGFKQFSCLSLSIS WHYTHVPPHLANYRIFSRDGV*PC WPGWSQTHDLE |
| 3249 | 8746 | A | 3510 | 55 | 295 | SQYAYTKEMESIVNNLPKKKTPGL HSFTGEFYQTFKNEMIL/YIL*FLPEI* SRG/IYPSSSSSSSL*LPKLDKDIHRK EN |
| 3250 | 8747 | A | 3511 | 2 | 853 | DLMCKKMKHLWFLLLVAAPRCV LSQLSSSSSSSSSSSSSSSSSSSSSS DSVRHNSYYWGWVRQPSGKELEW IGSLYFTGTTHYSPSLKSRVTISADT SENQFSLTLTSVTAADTAVYYCARP RNIVGSSSSSSSSSSSSSSSPSTKGPS GFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPA/V LQSSGLYSLSSVGTVPSSSFHGPRT Y\CNCKSQSPATTKVDKGELSPK\A CDKNSTHAPPGPQHLETPWGGPVS LFFFPKKT |
| 3251 | 8748 | A | 3512 | 3 | 2310 | QLLTMDWTWNILFLVAAATGAHSQ VQLVQSGAEVKKPGASVKVSKAS GYTFTNGLAWVRQAPGQGLEWM GWTIASNGKTNYAQKFQGRVTMTT DTSTNTAYMELRSLRSDDTAVYYC AREKDNATGAWFAYWGQGTLT VSSGES*AWYPGIQICSMLEL*ISAF WGRPGLTLAGGREGAKVTQVAPA RCTPNAHEPRHWTLHGPRIDKNR GASAPWAQLCPTPRSHGTTSLAAS TGPSVFPLAPCSRSTSESTAALGCLV KDYFPEPVTVSWNSGALTSGVHTFP AVLQSSGLYSLSSVVTVPSSSLGK TYTCNVDPKPSNTKVDKRVW*EA STGREGVCWKPGSALLPGRTPAVQ PQRAARHAPSVSSPGGL*PPHSCSG RGSSGFFHQAPGRHRLDAPTPGPAH KGAGAGLRPAKSHIREDPAPDLSP QRPNSPLPQLGHLSSQIPVTPNLLS AEPKSCDKTHTCPPCPGKPAQASPS SSRRDRCPRVACIQGQAPAGC*HVV LHLFLAPELLGGPSVFLFPPKPKDT LMISRTPEVTCVVDVSHEDPEVKF NWWYVDGVEVHNAKTKPREEQYNS TYRVSVLTVLHQDWLNGKEYKC KVSNAKALPAIEKTISKAKGGTRGV RGPHGQRPARTLCPESDRCTNLCP YR\QPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPE NNYKTTTPVLDSDGSFFLYSRLTVD KSRWQEGNVFSCSVMEALHNHY TQKSLSLSLGK |
| 3252 | 8749 | A | 3513 | 1 | 1677 | AEVQLVESGGGLVQPGGSLRLSCA ASGFSFSKAYMNWVRQAPGKGLE WVGRIKTKKDAAGTTDYAAPVKGRF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TISRDNSKNTLYLQLNSLRAEDTAV YYCAKDEFSSTRKNFLTGQSKTFAA YYGMDVWGQGTLLTVSSASTKGPS VFPLAPSSKSTSGGTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVL QYSGLYSLSSVTVPSSSLGTQ\TYT CNVNHKPSNTKVDKTVELKTPLGD THTCPPCPTP*LALGGPSVFLFPPKP KDTLMISRTPR\VTCVVVDVDPKRT PEGQVPTWYV\DGLE\EVHKCQDKSR GKEQYNSY\YRVV\SVLTVV\HGDW \LNGK\EYK\ICRVSHKSPQAPIEETH LPKPKGSPQNPQVYTLPPSRDELTK N\QVSLTCLVKGFYPSDIAVELESN GQPGNNFK\TTPPVLDSDGSFFLYSK LTVD\KSRWQQG\NVF\SCSVME\A LHNPYTQKSLSLSPGKMIPTADKPP LPGSLAGRTKDAWHGTPVYILPRAP KHGNAKPTPWPWAKKKKKKKKKK KGGRSRVSLEGPKLTRTQLS |
| 3253 | 8750 | A | 3514 | 1 | 164 | TRVNENQIESKAAYALFYKRQDVA RRLSPAGS/SGAPASPACSSPPSSEF MDVN |
| 3254 | 8751 | A | 3515 | 1 | 712 | EILIIHLKRFSYTKFSREKLDLVEFP IRSGARERMAGGRQGKEGVYQY*P SPHPQ\DLDFSEFVIQPNESNPETY KYDLIAVSNHYGGMRDGHCMCQA VGGACPGSGGQGGDQDLPSE*LGM *ASGEGSSVVGRK*TRSEIWTLSEEA RKGRRG*LSFPFR\TFACNKDSGQ WHYFDDNSVSPVNENQIESKAAYV LFYQRQDVARRLSPAGSSGAPASP ACSSPPSSEFMDVN |
| 3255 | 8752 | A | 3516 | 3 | 3090 | IPLLQLLLRRLWRRHGRWTEPREPQ HEELPGLDSQWRQIENGESGRERPL RAGESWFLVEKHWYKQWEAYVQG GDQDSSTFGCINNALTFQDEINWR LKEGLVEGEDYVLLPARAWHYLVS WYGLEHGQPPIERKVIELPNQKVE VYPVELLLVRHNDLGKSHTVQFSH TDSIGLVLRARERFLVEPQEDTRL WAKNSEGSLDRLYDTHITVLDAAL ETGQLIIMETRKKDGTWPSAQLHV MNNNMSEEDDFKGQPGICGLTNL GNTCFMNSALQCLSNVPQLTEYFL NNCYLEELNFRNPLGMKGIEAEAY ADLVKQAWSGHHSIVPHVFNKV GHFASQFLGYQQHDSQELLSFLLDG LHEDLNRVKKKEYVELCDAAGRPD QEVAAQEAQWQNHKRRNDSVVDTFH GLFKSTLVCPDCGNVSVTFDPFCYL SVPLPISHKRVLEVFFIPMDPRRKPE QHRLVVPKKGKISDLCVALSKHTGI SPERMMVADVFSHRFYKLYQLEEP LSSILDRDDIFVYEVSGRIEIEGSRE DIVVPVYLRRTPARDYNNSYYGL MLFGHPLLVSVPDRFTWEGLYNV LMYRLSRYVTKPNSDDEDDGDEKE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DDEEDKDDVPGPSTGGSLRDPEPEQ AGPSSGVTNRCPFLLDNCLGTSQWP PRRRRKQLVQLQTVNSNGHNRLH HSPCTKSNAKPVHCYSTWKP\EMK K\RYIDE*EGEGLREGNAFRRGYV* RKAPVRLQECIELFTTVEPPPPFGGK\ EREKPWYCP\SCCKQHQLAT\KKL\Δ LWMLPEILIIHLKTFFPYTQVLPEKK LEHPSWKFPYPGTLD\FS*/EFVIQAH QNEVEIRELYK\YDLI\AVS\NH\YGG MRDGTLTQHLACNKDSGQWHLLLI DNSVFPLFN*GIQIRVPRAAYVL\FY QRQ/DTLARLLSPCRAHLAPSVLP CLHAPSPQLVSSCDVILRALGPAPPE KKKKKALSALSLLVSAPLLLFVLGA PARHCRLSRGYCSPVPLNRSPLGKN RSCLLLA VRAPPCVCPSSSDPPF |
| 3256 | 8753 | A | 3518 | 1 | 271 | PLPPGFK*FSYLRLPSSWDYRCPPPH PTNF*FLVAMWFCVHGQAGFELLT SGDPPTSASQSAGITGVSHRSRPVD FLNYLLRKSYPFT |
| 3257 | 8754 | A | 3519 | 3 | 633 | FFFI*DRVSLIAQAGVQWRNCGSLQ PPPTGFKQFSCLSLWRSWHYCRH HAQLIFVFLVKTGF\TMSVKADLEL LTSGDPTASASQSAGITGVNHQCPA SKQF*FHCKSW/CLF*MQSLSF\FLG GGQSRVSGQAGVQWHDLSLQPLS PGLKQFSSLSLPSSWDYRGVPLRLA NFCIFSRDGVSLCWPGWS*TPDLKA NPTRLGLPKGWGL |
| 3258 | 8755 | A | 3520 | 2 | 430 | CLKNMVGAGEVDEDELEVETKEECE KYGKVGKCVIFEIPGAPDDEAVRIF LEFERVESAIKG*WYS*ILKNKKVEF TALIFTSKAYCLIKVKPLSYRIPALF CLLFAFQRLTLN\GRYFGGR\VVKA CFYNLDKFRVLDLAEQV |
| 3259 | 8756 | A | 3521 | 3 | 1076 | HEERQRQRELERQKEIEEREK\RRK DRHEASGFARRPDPDSDEDEDYER\ ERRKRSMGGAAIAPPTSLVEKDKE PRDFPYEEDSRPRSQSSK\AAIPPPVY VEEQDRP\RSPTGP\SNSFLANMGGT VAHKIMQK\YGLPGGPRVLGKHEQ GLSTALSVEKT\NKRGGKIIVGDATE KDASKKSDSNP\LTEILKCPTKVLL RNMVGAGEVDEDELEVETREECEK\ YGKVGKCVIFEIPGCPLMMEASTG YFLEI*EELNSAIKAVVALN\GRYFW CTGW*KAMFLQIWAKFRVLDLARN QVWIFKEPRARVISGDPLNELQAVE KKEKGPQPPWLFAYPRLLEGLLRY MLIDPFFYFVVF |
| 3260 | 8757 | A | 3522 | 1381 | 1787 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3261 | 8758 | A | 3523 | 1147 | 1553 | LEYVAHPLHQLLILNNFYSVLNEKY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3262 | 8759 | A | 3524 | 1456 | 1862 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3263 | 8760 | A | 3525 | 889 | 1295 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3264 | 8761 | A | 3526 | 743 | 1149 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3265 | 8762 | A | 3527 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS/DSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSA/PGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLRYPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGFTVLARRVLIS* PRDLPASASQSAGITGVSHHT/LIF/ NFFETGTHSVTWAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYIYLFYFHRDEGSLCCPGWS* TPELK |
| 3266 | 8763 | A | 3528 | 1966 | 2372 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSIS*PRDPPTSA SQSAGITGMSH |
| 3267 | 8764 | A | 3529 | 10304 | 11097 | FAFSPK*HSCLRCPCI*FSSGLLHEVL *LLPLCWP*THGWDPGSREANKSPK LHAIRCWWLEENLWSSNSQSLQ TVKN*ESHIN*SCRSNLI/HH*FWNQ VK*K*LLNISGNCFFFLRWSL/DSVA QAGVYWRDLGSLQPPPGFKRFSCSL SLPSSWDYWHLPCLAKFCIFSRDG/ GFTIWARLVLS*SCDLPASGSQSA GITGVSHHTWLQVITYFLKEMRSCY FSQVGWPQTPGLKQCSHLKLLSSW DYRHMSPHLAISGS |
| 3268 | 8765 | A | 3530 | 87 | 411 | ARLVQNTVAQLKEVQYKLFGLF FE*/QSHSVAQAGYSAVIIAHCNLSL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LGSSDPFFSAS*VAGTTGMCQHA W LIFDR*WR*GLAMLPRLEM*IFLISH LRLIWSAWS |
| 3269 | 8766 | A | 3531 | 31 | 403 | THLNGLQIRGSPLFFF/FELESSVA\ RLQCSGVISSHCNLRPLGSSNSPASA S*IAGITGAHHNPG*FF/VFFSRGRFH HVGQAGLELLTSSDPPRPSTLPQSG WGFTRHGAIA PQWGQVPFHRS |
| 3270 | 8767 | A | 3532 | 7 | 1047 | |
| 3271 | 8768 | A | 3533 | 3 | 53 | |
| 3272 | 8769 | A | 3534 | 7 | 960 | |
| 3273 | 8770 | A | 3535 | 1538 | 2287 | WWSSSKLRLIYYYYSLFFFFFFFFFG M*SYSVTQARVQWHHLGSLQPLPP GFKQFSCSLPSSWDYRHPHPLANF LYF**RWGFTMLARLISNS*PQ/CDL PASASQSAGTTGLSHCAQ/LLFAFLT DNSVLIETALT*LQSCAS*KLN*IPL ESSDFYTTTTFETESHV/TQAGVQCR NLGSLQPPPPRFKQFSCSLPSSWDY KCTLPRPANFCIFTRQGFTMLARIVS PGSLGLMISLPRPPKVLGLQV |
| 3274 | 8771 | A | 3536 | 3 | 263 | LGVGDRVSLCHPVWSASSL*SQT PG LK*SSHLSLPSRWDNRHAPPCLA/SL KNFCRDRGLTMLPRLVSNWAQAI LPPQLPEVLGLQV |
| 3275 | 8772 | A | 3537 | 33 | 295 | AGMQWCSLGS LQPPPPVLRSSHLS LPSSWEYSHTCNFCIFCRDGFVLP RLLG*SNRPASSS*NTGITGVSHRAQ PSLFLSYFFF |
| 3276 | 8773 | A | 3538 | 3 | 33 | |
| 3277 | 8774 | A | 3539 | 1 | 375 | |
| 3278 | 8775 | A | 3540 | 3 | 340 | HEVVAA*YY\G*PSIAQEVAGTLAE LDVTLQLEDKFLQNKVFLTGP HIS LADLVAITELMHPAGAGCHVF*GLP TLATWRQLVEASPGEDLFQEVHEVI LKATDFPPADHTI |
| 3279 | 8776 | A | 3541 | 30 | 284 | YSVSTPLRDSNPNNHLSLGHCPASS QTEPQAPQALGQPATKLLPHQP PP /MPQPSSKP*VSATSLCTSPPLPLCP AGGSSGTT |
| 3280 | 8777 | C | 3542 | 127 | 435 | MAASXNPEVLDITEETLHSRFL EGV RNVASVCLQIGYPTXASVPH SIINGY KRVLALSVETDYTFPLAEK VKAFLA DPSAFVAAAXLGCCHHSC SXCCCS P S* |
| 3281 | 8778 | A | 3543 | 3 | 417 | |
| 3282 | 8779 | A | 3544 | 2 | 881 | RGKLCAYGRPPMMRRSIEGN/LENN PASEELLPH*RGHLGFCFTREDLT EIRDMLLA\NKVPTAARCWCQLPP CEVTVP\QNTGLGPEKTSFFPGL* VSPTKNLPGGTH*K S*SYVQL\K TG DKMGSQTKAKAAEKM LKNLPPSP F GAGQPKQGVVRKNGKHPTNPESA*I STRGKLCHSRFLGGCPANVAKCLS CKIGYPTVASSTPII\NGYKRVGP CLWTPDYTFPLAEKVKAF\ADPSC LCVLLPPVGAATTACFALLQPPA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KVEAKEESESEDEDMGFGALFD |
| 3283 | 8780 | A | 3545 | 2 | 311 | DGVSLLLSPRLQWHNLGLLQPPPP* FKGFSCSLSPGSDYRHV/PPCLAN FVFLVETGFRHVGQTGLELLTSGDP PASASQRAGITGVSHRTWQKMYFL SQKYF |
| 3284 | 8781 | A | 3546 | 1 | 290 | KTFFFFF*DRVLFCCPG*SAVAQ\SW LTAALTSWAQSS*DHRLKP/HMLS FFYFCRQGLTMLPKVVLNSWAQAI LPPQPPM*PGLQACTYAWSRAL |
| 3285 | 8782 | A | 3547 | 229 | 486 | IKIKINQAWVCACLSLPSSWDYRHG PPHPANF\FVFFLVETGFTMRARLA SNS*PCDPPTSASQSAGITGVSHRAG CSEAFRSQV |
| 3286 | 8783 | A | 3548 | 2 | 431 | ARGSIYQNDTTI*NMYLDNRASECT VRELVKQK/R*MEKPTIIFGDFNNPV SLIEGSSK*KISGTMENLKNTANFT* LIFIKCSAQQHQNAHSFPV/PHRTF/S KIDHFLWCKRGLNCKMIQIIQNVV CDHTALNKKPMPERSLEK |
| 3287 | 8784 | A | 3549 | 2 | 194 | VDDFFFFLWWSI/NSVTQAGVQWRN LGSLQALPLGFMPFSCSLSPSSWDY RCPPPAHPANFFLHF**RRGFTVLAR MVSIS*SHDPPASDSQSAGITGLSHR AR/LKGHYDF*EMAC/HLICKRGRQ VP*LFFFFFFEMEYHSVTQAGVQWR NLGSLQALPLGFMPFSCSLSPSSWD YRCPPPAHPANFFLHF |
| 3288 | 8785 | A | 3550 | 2 | 489 | ARGTQALMMMT/GTACHASPH*GG RLTS*PGAICFTHGDMAA*WREESC LLVT/WDLVMSEGLGMR\YAFIGPLE TMHLNAEGML\SYCDRYSEGIKHV VQTFGPIPEFSRA\TAEKVNQDMCM KVP**PGSTLAAR\RHWRDE\CLMR LAQV*RSSSCSPQLNFLC |
| 3289 | 8786 | B | 3551 | 13 | 441 | MEGVEEKKKEVPAVPETLKKKRRN FAELKIKRLRKKFAQKMLRKARRK LIYEKAKHYHKEYRQMYRTEIRMA RMARKAGNFYVPAEPKLA\FVIRXR GINGVSPKVRKVQLLRLRQIFNGT FVKLNKASINMLRDCRAIYCMG* |
| 3290 | 8787 | A | 3552 | 1 | 775 | RRVPA\VPETLKKKRRNFAELKIKR L\RKKFAQQML\RKAR\RKLIYEKAK H\YHKEYRQMYRT*NFEWARMGK KKLANF\YVPAEPQIWR\FVIRIG\N GVSPKGSERFFQLLRLRQIFNGNLL *KLNQGFRFNMAEDF*SPYIAMGGT PNLKVSKMN*SYKRGLWAKSNKK R\IAL\TDNAL\IARSLGKIRHILawe DLIHEIYTV\GKRFK\EANNFLWP\FK LSFSTKVEMKKKTTHFVEGGDAGN R\EDQINRLIRRMN |
| 3291 | 8788 | A | 3553 | 1 | 356 | SHHVQLLEFFVEMGSPCVSQA\VL* LLGSSDPPVLASENVGIK/GPPHPA* S*F*IIACVFVYIYFLEMGS\CSFAQA GVLWYNHSSLQR*TPGL*QISLLSPL SSWDYRHVPPCLVIYF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3292 | 8789 | A | 3554 | 3 | 352 | HEGFTMLVRLVSNS*HRDPQASASQ SAGITGVSHHANP/CFFLTESNWVA QAGVQWRVLS*LQPPPA*FKGFSC SILSSLS/WGYRCLPP/HPANFFFF*K GFFFWFPSWNAMGKKWFN |
| 3293 | 8790 | C | 3555 | 55 | 201 | MPKNYPRLWWQHVCNPQPTWEAE VGELLEPQEA EVAVSQDHATALQP G* |
| 3294 | 8791 | A | 3556 | 3 | 212 | QEFFFFFFEM*SRCVTRLEGSGAISA HCKLCLPGSCHSPASASQDSIFNTQ HLNVGRNSTSKSKPIDYF |
| 3295 | 8792 | A | 3557 | 2 | 265 | EKESRSVTRLECRGAISAH*NLHLP GSSHPPSASHVAGTTGACTT/AQLI FFVFLVETGIHHVGQDGLNHL/NLVI RLPQPPKVLGLQA |
| 3296 | 8793 | A | 3558 | 354 | 675 | HFISYFPDGAELTSSIRVPFFYSNVLF FF/CRQESRCHQAGVQWHDLGS LQP PPPFGKRFSCLSL*SS*DYRQAPPRP ANFCIFNRGPVSPCWPGWSQSPDFV LVPNS |
| 3297 | 8794 | A | 3559 | 1 | 1203 | |
| 3298 | 8795 | A | 3560 | 2 | 634 | VNTEKLTAFVNTLNGKNGTGSHLV TVPPGPS*ADALISSPILAGESGAML GLGASDFEFGVDPSADPELALALRV SMEYQRQRQEEYARRAAAASAAE AGIATTGTEGERDSDDALLKMT\SQ QE\FGRT\GLPDL\SSMTEEEQIAYA MQMSLQ\AEFGQAESADIDASSA MDTS*PAKEEDDYDVMQDPEFLQS VLENLPGVDPNNEAI |
| 3299 | 8796 | A | 3561 | 506 | 930 | IRTTQIGLCLSQVYFIVFDLHAQYEH KATNITPTLSKIISIRPRRFIPVT*L LNMFAFSSPMVPVLSQRIGTI*FLF RFFNT*IFSDGLTNRLTCSR FANCKV NPVIGSISKYVLCSSSFGFNPSIGSET SGLAYRK |
| 3300 | 8797 | A | 3563 | 3 | 271 | FFLET*SCSVG\RLCSGVILAHCKL RFPGSSDSPASASGVVGTGAHHHT RLFCIFSRDGFHHVGQDGLDLL/NL VIHPPWPPKVLRLQA |
| 3301 | 8798 | A | 3564 | 1 | 218 | ETGSPSVTRLECSSIQSAHCNLDLP GSSDPVVS\APQVAGTTGTCHNTQLI FVFFVEMGFCHLSQAVLQLLG*TIH PLWPPKVLGL*AQVILLSQTPQVAG TTGTCHNTQLIFVFFVEMGFCHLSQ AVLQLLG |
| 3302 | 8799 | A | 3565 | 1 | 294 | ASTFFFFFFGDRVSLFLPRLEYNGAIS AHRNLC/LPGFSSDSPASAS*VAQD YRHAPPHLANFVFLVETGFLHVGQ AGLKLPELSVIHPPWPPKVLGLQA |
| 3303 | 8800 | A | 3566 | 3 | 292 | FFETKFSSVTQAGVQWHNLGSLQPP PPAFKRFSCLSLPSSWDYRHLPPRPA NF*FLVEMGFHHVDHADLELPTSS DPPTLASQSAGIIGVSHRARP |
| 3304 | 8801 | A | 3567 | 3 | 389 | |
| 3305 | 8802 | A | 3568 | 1 | 672 | |
| 3306 | 8803 | A | 3569 | 1 | 2018 | MSDNGVRTGAPSTDQRTGMSVRAE |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | WRRGEFLVTGRRPLVGGGAGEEGE LGGDARSSRDPELQSYAAFVAVVT RIWLPAPRCPALGGLASGPGKAEQF SRSLYLPDHLGEGNGLLGKSLEPY RSACMSAAGLKITGSKETKRLLLLI SIDWSRDLNLCIYFRVYCQEKQEE RRELPRITGPPPEAAVVAFEWLKTS TLTGLHPQLPLSLPQPECALPYLVR AFSRGDYMGRIQEVGWVTAGLVIW AGTCYIYKFTKGRAQSVRTLARN GSTVKMETVVGVQSQT LAINEAEIK TKPQVEIGAETGARS GPRAEVETKA TAIAIHRANSQAKAMVGAEPETQSE SKVVAGTLVMTEAVTLTEVKAKAR EVAMKEAVTQTD AEAGKIVKKEAV TQTKAKAWALVAKTEAKREAMTQ TKAETHILAEKETEINRVMVTQSET LAVPREVAKMGATNKTGIVDETKT RALEETVSVAKTQSEARPGATVDA RGNPNGMSREVAGVDMKSCAQSQ AVTKIQGDDMPGTGVEDMGNCKT MSRAESGADTRASAQPQIFAKTQTE AIPGAKIDAGGNTNAMCKVGAGAD VRACIQPQTVAKKQAEVTS GARVD GRGNTNVISKAITGADMRAAAQPQ AVASTHAEAMSDAKVKNRGNPNA MTKAGAKANLRANSQVEALPDAR DKSRGNPNVMAKVGDGTDMLSCT QPQLVASVQADTLSDGKIKV RGNV NTMPKEGAGVDMKAQGMASQSGE ALPNTRGKARGKAKAKCKTGPGM DMKTCTQPQAGVKTPAEALLDSRV DGRGNPNATSKAGTKADQRVCGQP LVVANPQGEALPGAKNKVKGNPHT VLKVGAGEGTTDSAQPEAVVSFQG EALLGTKNKVKGNPNVVLKAEVGE GAMGTAQLQIMASSKGEALLDSKN KVKGNSNAVSKAGAGTDTTGSVQP QIVANSQGEVLPGAKNKIRGNPTTV PNSGVGPYTTDSARLQAVANSQGE VLPGAKNKVKANLNAVSKAEAGM GATGSVQPQAVANSHCETLPGAKN KVRGNWNAVSKAGAGMDTRGSAQ PQAVANSQGEVLPGAKNKVKGNPN VVS KAGAREDTVGSTQPQVLASSQ RETLPGARNKVKGNSNVVSKAGAR EDTMGSAQPQVVANSQRETLPGAR NKVKGNSNAISKA EAGAGIMGSVQ VQVVASFQGEVLPGAKNKVRGNSN AVPKAEAGADTVGSAQPQAVANSQ SETLLGARNKVKGNTIAVPKAGTG AGTRHSAQPQIVAGSQGETLPGARD KSMSTSEAEATAEDEAYAKPEAEA MPTSESEGGSGTQACRKTQPNIH DY YWNGIGVEDWIAAERWIKFRFQTM DGDWENSVSWADDENEASIGSWSG ASDKAGIIRSWAVACDETSVKSWA GARAENVVGIGTWARAGEQASGGL |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | WAGGQTSEGTWAGDKASGGAWT GAENQASGGSWALAGNQAIGELW AAGQASDGSWPGGQASGVSWVGE EAIGGSWTGAENQASEGSWAGAGA GNMSSVSYWAGVVDQAGGGSWA GTSDQSGGGSKPRFEDQASGEGSW AGAGGQASGGSM LGPEDQSSGRSW ADTADQASGGSR LGHVDQSSGGA WAGTLDQSGGGSKPRFENQTTEEG SWAGAGGQAGGGSKVGPEDQSSG RSWANS GDQISGGFLVGIVDQANG GSWTGAGHPASVGP KPIFEDQVSGR GSWADAREQVVGD SRLGLRDQSSG DSWAGTGDQASGWFCVCPGSQTN GGSWGGASGQDVGGSRPGPTNQSS AGSWDSPGSQVSGSCWTGAGAVD QAGGCSKPGFEDQAIGGGFWPGAG DQTGGGSRPGSEDQSSGIGSWGVA GGQVLGGARPGPADQSSGGSWAGT GNQSSGRSWIGPGDQAVDCSKPEFE DQACGGGSWAGAGSQASGESWAG SRPGNEAIGGSRMGSEDQATGGSW ARSEDQASGRFQVSFEVEANEGFW FGPGAEAVIGSWCWTEEKADIVSRP DDKDEATTASRSGAGEEAMICSRIE AENKAKSRLGAGEEAGVESWTLAR NVGEDELSRESSPDIEEISLRS LFWA ESENSNTFRSKSGKDASFESGAGDN TSIKDKFEAAGGVDIGSWFCAGNEN TSEDKSAPKAKAKKSSES RGIYPYM VPGAGMGSWD GAMIWSETKFAHQ SEASFPVEDESRKQTRTGEKTRPWS CRCKHEANMDPRDLEKLCMIEMT EDPSVHEIANNALYNSADYSYSHEV VRNVGGISVIESLLNPNPYSVRQKA LNALNNISVAAENHRKV KTYLNQV CEDTVTYPLNSNVQLAGLRLIRHLT ITSEYQHMTNYISEFLRLLTVGSGE TKDHVLG*EQRQSQCHD*SRGQ GK LEGQFPG |
| 3307 | 8804 | A | 3570 | 1 | 611 | YAALGADVTRVSLPTPRCPALGAL ASGPGESGPTLLQDCGAKCPG/GPQ PRGENREKEETTRIGPGVMESKEKR AVNSLSMENANQENEEKEQVANK GEPLALPLDAGEYCVPRGKS*GGSA FRAAHP\EYRWDMMPWRPWRTHRP DEEKRIMEKDWGGGETADGKKLE GEKPVGVISLRGESGTDPPSPMTHH D*VFALLPLNP |
| 3308 | 8805 | A | 3571 | 1 | 379 | EMESHSVTRLECS/GTILVHCNLCL LGSSDSPASAFQVAGITGVHYNA*V IFVFLVETGFCYVGQAGLEFLTSTD PPASGFQNCWNYRDEKPHPAETVS KTTTTKNYICVSTINYKKKNLGLSNI L |
| 3309 | 8806 | A | 3572 | 6 | 222 | DRVSRSAAQAGV/QWC/NLSSLQPL PPRFK*FSCLSLPSTWDYRHTPPRPA NFCIFSRDRVSPCWAGWSQSLDLK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3310 | 8807 | A | 3573 | 1 | 445 | |
| 3311 | 8808 | A | 3574 | 1 | 3212 | DSINNLAELNKFALRKQLEQDVL SYQNLKRTLEEQISEIRREESFSL YSDQTSYLSICLEENNRFQVEHFSQ EELKKKVSDLIQLVKELYTDNQHL KKTIFDLSCMGFQGNFPDRLASTE QTEIMKDLKGGCKNGYLRTESKI SDCDGAHAPGCLEEGAFINLLAPLF NEKATLLESRPDLLKVVRELLGQ LFLTEQEVSGEHLDGKTEKTPKQKG ELVHFVQTNFSKPHDELKLSCEAQ LVKAGEVPKVGLKDasVQTVATEG DLLRFKHEATREAWEEKPINTALSA EHRPENLHGVPGWQAALLSLPGITN REAKKSRLPILIKPSRSLGNMYRLPA TQEVVTQLQSQILELQGELKEFKTC NKQLHQKLILAEAVMEGRPTPKT LLNAQPPVGAAYQDSPGEQKGIKTT SSVWRDKEMDSQQRSYEIDSEICP PDDLASLPCKENPEDVLSPTSVAT YLSSKSQPSAKVSMGTDQSESINT SNETEYLKQKIHDLETELEGYQNFIF QLQKHSQCSEAITVLCGTEGAQDG LSKPKNGSDGEEMTFSSLHQVRYV KHVKILGPLAPEMIDSRVLENLKQQ LEEQEYKLQKEQNLNMQLFSEIHNL QNKFRDLSPPRYDSLVSQARELSL QRQKIDGHGICVISRQHMTMIKA FEELLQASDVDCVAEGFQEQNLNQ CAELLEKLEKLFLNGKSVGVEMNT QNELMERIEEDNLTYQHLLPESPEPS ASHALSDYETSEKSFFSRDQKQDNE TEKTSVMVNSFSQDLLMEHIQEIRT LRKRLEESIKTNEKLRKQLERQGSE FVQGSTSIFASGSELHSSLTSEIHFLR KQNQALNAMLIGSRDKQKENDKL RESLSRKTVSLEHLQREYASVKEEN ERLQKECSEKERHNQQLIQEVRC GQELSRVQEELKLRQQLSNDKL LQSLRVELKAYEKLDEEHRLREAS GEGWKGGQDPFRDLHSLMEIQALR LQLERSIETSSTLQSR/LKEQLARGA EKAQEGALTLAVQAVSIPEVPLQPD KHDGDKYPMESDNSFDLFDSSQAV TPKSVSETPPLSGNDTDSLSCDSGSS ATSTPCVSRLVTGHHLWASKNGRH VLGLIEDYEALLKQISQGGQRLAEM DIQTQEAPSSTSQELG\TKGPHPA LSKFVSSVSTAKLTAAEAYR/RGLK LLWRVSLPEDGQLPLHCEQIWRNE RQRVPKLHKKLFEQEKKFAKTP*RF LQLSK\RQEKVIFDQ/LVVTHKILRK ARGNLELRPGGAHSRTCSPSR/PGS ALATRKEHRNQHSAEQASRNSWQ GGQRRHRKEPSLWLSKPCPSLRCPF SLTNTMTVNIPWKVIIHLICLIPPRQ |
| 3312 | 8809 | A | 3575 | 1 | 1362 | SGNIKVLERFLYIDTKFSQNRQCKA LPMASAYQSNLPHNYTMTVHNN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QLAQALRVYSQHAIGAVLYKYSMQ VHEDCYKFWWSNG\MQLCEERSLTD QHCVHKFHSPLPKSGEKPEADRNPPV LYHNSRARSTGACNCGRKQAPRDD PFDIKAANYDFYQ\FWEEKCCGKIG SVYSISQYLEPSTPGSWLLA*KWNP/ RPAPPDSADKLKEKEPQTQGESTS LSLALSLGQSTDLSLTYPADPQ/DRR R*SRSSWSSRSSEN/SRRDQTSIDRH/ LTVEYLPGLHNSNCPKGLLPTFSSW VFVKLPG*SYNFHTRFR/NQQGFIP GNKLSYALGTLSSRARSW*RRLR HKLLACSK*SYSWKEKCGCNGKRK TAR*H\TRAFVGFEYEDSRGRFMC SGALTK**K*WGSGA/IRDSAFKSP*I VDMPLY\NRHPLKVEGLKTLITLQL MRLFVVVPDASFA |
| 3313 | 8810 | A | 3576 | 1 | 673 | EGGW MEDYDYVHLQKKEEFEMTH IELLDKGSITRQGMSQL*LEQLKLFV RLEQEVSRPIDHDLAIWTPAQPLAP GRSGG\LGPSDRQLLLFYLEQCEAN LTTLTNAVDAFFTA\ATNQPPKILV GASKVLL\SAHKL VFIGDLSRQA K\AADVR\SQVTHYSNLL\CDLL\QGI VATTK\AAALQYPIAFPGPKDMV/E KRVKELGHSTQ\QFPPRS*GQLGSPP EGW |
| 3314 | 8811 | A | 3577 | 3 | 531 | FFLLQSL/DSAGQARVQWCDLGSLO PLPPRFMRVSCLSLSSWDYRHLPP RLAMIFVFLVE\QGFTVLARLFSNS* PQ/CDPPTSASQSAGITGMSHHA\RL FLFETGSGSIAQGGVQ*CNLGSLOP LPPRLKPSSHLSSLSS*DYRRVPTCP SNFCIFGRDGVSPCCPDWSGTPGLK |
| 3315 | 8812 | A | 3578 | 1 | 223 | GSGGIHRLPLSSRPEQPIVWLWAPG CFSHLSRLQVTV*/GEIKQRCRELHH SLAQHPRHQAGNHISHPILHLKIL |
| 3316 | 8813 | A | 3579 | 3 | 341 | FFETESCSVSQAGVQWRDLGSLQA LPPGFTPFSCSLSPSSWDYRHLPPHP ANF/SVFLVETGFHRVSHDGLDLT RDPPTSASQSAGITGVSHRARPIVAI FMFCEYPLFSSH |
| 3317 | 8814 | C | 3580 | 168 | 347 | MTYGLLLFLGNNPHLNLYXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXSTIV* |
| 3318 | 8815 | A | 3581 | 852 | 1216 | GFLINGNTDFFFETESRSVAQGGV QWRDLGSLQPLPPGFKRFSCSLPSS WDYRHLPPQYPS*IFVFLVETGCSSY STIL**RPAHVGQAGLELLTPGDPPAS TSQNAGITGLSHRTWSAI |
| 3319 | 8816 | A | 3582 | 2 | 238 | |
| 3320 | 8817 | A | 3583 | 680 | 891 | |
| 3321 | 8818 | A | 3584 | 697 | 979 | IFGV SQGYKILWKMNSLPGVSFES KRSF*QK*LQILSS*FAKKIFYWHEN NRCKWRPNIPKCIYSITSQKLFYPS LLFFLLPTFLGVGGAR |
| 3322 | 8819 | A | 3585 | 2 | 518 | GRGYQNPRQCTSDRLSEHVSEGES |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PPDSQEDSFQGRQKSKDKAATPRK DGPKRSVLSKSVPGYKPKVIPNAIC GICLKGRESNKERKG*IHFIHCSQCE NSG\HPSCLDMTNGACFYD*DLTPW QCMECKTCHICG\NPHHEEEMMFC\ DMCDRGYHTFCGGPGSNPTRPLNL |
| 3323 | 8820 | A | 3586 | 1 | 165 | SLEDRVLLCHPGTAYCSLELLGSISP PALTLTSEAS\LPGRDYREIPGSPCQL FL |
| 3324 | 8821 | A | 3587 | 1 | 249 | LVDRVLLCHPGTA/VLQP*TPGINQS SCLSLPSS*D\YRYVPPCLVYCFIFLA EMGLTVLPRLISNSWPQAILPSQPPK VLGLQT |
| 3325 | 8822 | A | 3588 | 3 | 282 | NSWDYRHPLSCLANFCIFSRDGGFT ILTKLVLNS*PRDPAASASQSVGITG VSTHGLASWN\FNKLKNSYTQVD*L GSQEWPLKVCLAKPRTAS |
| 3326 | 8823 | A | 3589 | 1 | 714 | |
| 3327 | 8824 | A | 3590 | 1 | 726 | MAEGETESPGPKKCGPYISSVTSQS VNLMIKGVVLFFIGVFLALVLNLLQI QRNVTLFPPDVIAIFSSAWVPPC CGTASAVIGLLYPCIDRHLGEPHKF KREWSSVMRCVAVFVGINHASAK VDFDNNIQLSLTLAALSIGLWWTFD RSRSGFGLGVGMLFLATVVTHL*V YNGVYQYTSPDFLY\RSWLPACIFF AGGITMGNIGR\QLAMYECKVIAEK I/LIRNEEGKK\YLLYRKAR |
| 3328 | 8825 | A | 3591 | 469 | 537 | PGLARRAMASGRSHGWP*IPPLRST FQGGRTLDAAFRINCHGKTYLFKG SQHWRFEEDGVLDPDYPRNISDGFD GIPDNVDAGLALPAHIYSGRERVYF FKGKQYWEYQFQHQPNIIEEREGSS LSAVFEHFAMMQRDSWEDIFELLF WGKTSAGTRQPFINLDWHGEPWQ ADAAMAGRIYISG |
| 3329 | 8826 | A | 3592 | 193 | 384 | |
| 3330 | 8827 | A | 3593 | 96 | 1635 | ARSPAMAPLRPLLILALLAWVALA DQESCKGRCTEGFNVDKCKQRDEL CS\YYQSCCTDYAECKPQVTRGDV FTMPEDYTVYERLGEKNNATVH EQVGGPSLTSDLQAQSKG\NPEQTP VLKPEEEAPAEVGAASKPEGIDSRPE TLHPG\RPQPPAEELCSGKPFDAFT DLKNGSLFAFRGQYCYELDEKAVR PG\YPKLI\RDVWGIEGPIDAAFTRI NLFRGRPYLFKG*\QYW\RAFEDGV\ LGPWIYPRNISWTAFDGHSPGQTW D\AALGLPCPLAYSGRERVYFFQRG KQYW/ESYQFPGTSPVQEECEGSSL\ SAVF\EHFAMMQRDSWEDIFELLF \WGAERSGWVTR\QPQFHLAGEWH GVPG\QVD\AAMG\GRILHLQGMAT RPLLWPKKK\RFRR\NRN\KGYRS\Q R\AHSRGR*PETPRRP\SRAMWLSF VLPSEESNLGA\NNY\DDYRMD\WL VA\ATCEPIQECFFFSFGDKYYRVNL RTRRVDTVDPPYP\RSIAQYWLGC |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | APGHL |
| 3331 | 8828 | A | 3594 | 44 | 166 | |
| 3332 | 8829 | A | 3595 | 3 | 1173 | SSAPEAAKKPTPCHRCRGLVDKFN QGMVDTAKKNFGGNTAWECKTL SKYESSEIRLLEILEGLCESSDFECNQ MLEAQEEHLEAWWLQKSEYPDLF EWFCVKTLKVCCVPGTYGPDCLA CQGSQRP\CSGNGHCS\GDGSRQG DGSCRCHMGYQGPLC\IDCMDRL QLRSRNETHS\CTAVRTGLSDSYPP CCLSLGCWRGVGHAWIRGRNTHQ PGYSSRVWIAAFSPACDESKTCSG LTNRDCGECEVGWV\RTAPCVDV EKCAAQTPPCSAAQFCKNANGSYT CE\ECDS\CVGCTGEGPGNCKQCIS GYAREHGO\CADVERVPH*PEKTL EEKTKTCYNTPG\SYVVCVCPDGFE T/RRCLCAAGRRLKPQKGESPTQLP LP |
| 3333 | 8830 | C | 3596 | 1 | 300 | MRSFGQLTLCPRNGTVTGKWRGSH VVGLLTTLNFGDGPDRNKTRTFQA TVLGSQMGLKGGAGSVWLQAAGL GLLPASLLWPSLLCHCYVLPPAGV PLV* |
| 3334 | 8831 | A | 3597 | 359 | 1229 | MPQPPTLGQEMTGPSQPWTGKGGL PGP*QLRAKAQEVDSHLGRKKIKQ QNRSKSC |
| 3335 | 8832 | A | 3598 | 2 | 311 | VRWNSAAPLVTSRGAPASARPRGQ ALPGGSAPSAPHGQLPGRAQPAPVS GPPPTSGLCHFDPAAPWP\GLGLG MLPPHPQDWPAQP*HPPGLGLFFEIF SAS |
| 3336 | 8833 | A | 3599 | 1 | 426 | |
| 3337 | 8834 | A | 3600 | 18 | 738 | |
| 3338 | 8835 | A | 3601 | 65 | 425 | RLPQPPGAAVGGSTRPCPSWKAVR VDLVVAPVSQFPFALLGWTGSKLF QRELRRFSRKEKGLWLNHGLFD/R GAGKQQWQDS*VTEVLLLLQKTF QAASEEDIFRHLGLEYLPEQRNA |
| 3339 | 8836 | A | 3602 | 3 | 233 | FFFFFKTLQIPLLSPPPPGPCRVQSL LPNPFPEKGA\PPFQTDERGQDFRLD PPLGSPSPRV*SLNCYVPVPPKEK |
| 3340 | 8837 | A | 3603 | 7 | 510 | THAPAPSPRAQAP*PLFIHCP*APRV TPPPPPQPVKCVVPAEVI/SPPPPGPCR VQSLIPLTRFPEKGAYLLSRQMKRG QDFKAGIQPLGLSLPQPGSTGRGRV TAGD |
| 3341 | 8838 | C | 3604 | 846 | 989 | MKSYNGMREMGDQASRRKLIKWN TDSKFLDMENGEQKKITPRPGVKI* |
| 3342 | 8839 | A | 3605 | 3 | 232 | KSLLREGLESAMLVLKSLLPFSYFV SSMSSGNWSALHNHLGPEDTGTAS PYNRCS*RGDRHLGKRSSTRGTTLG PN |
| 3343 | 8840 | A | 3606 | 303 | 400 | |
| 3344 | 8841 | A | 3607 | 3 | 404 | LRQRLTVTQAGVQ*HRLSSLQPLPP RLKRFSCSLPSSWDYRRVPPHMA NFLY/FLVETGFHHVQGAGLKLLISS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DLPALASQSAGTTGMRHRAQPKSF QLEQKWKTEPHKLIYVVTNLKRM YKLKTYHIPYYF |
| 3345 | 8842 | A | 3608 | 2838 | 3122 | FFFFFFETKSCSVARLECSGTISAHC NLHLPGSSDSPASAS*AAGITGACH HTRLVFLYF**RRGFHHVSQAGLEL LT*VIHPPQPPKVLGLQA |
| 3346 | 8843 | A | 3609 | 1 | 325 | RLFFFFFFETVSHSVTRLECT*AILAHC NLCFPRSSNSLASASQVAEITGACY YTQLIFVFSVETGFHHVQGAGLELL T*VIHPPPPPKVLGLQVSATVPGLI GTFSL |
| 3347 | 8844 | A | 3610 | 3 | 398 | GSLQPPPPRLK*FSCLSIPSSWDYKR LPPCPANFCIF\TELGFHQVQGAGLE LLTSGDPPASTSQTVGITGISHHAWP PEILSKGTMGKQMVNMLLASSCR EMGHSAPAHLGQCLPMILPKDLAVI IINPV |
| 3348 | 8845 | A | 3611 | 3 | 311 | AQTGMQW\DLCSVKPPPPRFERFSC LSLLSC*DYKRTPTCPANFC/DFVVE TEFHVHGQAGLELLTSSDLPASASE NPQITGMNYCIWPEWYYYIHSLTNT IHK |
| 3349 | 8846 | A | 3612 | 310 | 415 | SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRL/DSVAQAGVQWRDLGS LQRPFGFTPFSCSLPSSWDYRRPP PRLANFFVFSVETGF\VSARMVSIS *PRDPPASASQSAGDTGVSQAPV |
| 3350 | 8847 | A | 3613 | 1 | 114 | ARAEMLIVQYILPRLTHCAIFTILFIF SLLT*VMLLSS |
| 3351 | 8848 | A | 3614 | 335 | 477 | TPASLKIPVE**NTLLAKMVSIS*PR DLPASASQSAGITGVSHRARC |
| 3352 | 8849 | A | 3615 | 135 | 804 | GIDTILTLNQN*SLKTRQ*FTLIH/IFF FFLRWSLALSPRPDCGLQWRDLGSL QAPLPGFTPFSCSLPSSWDYRCPPP RPANFFCNFFFSRDGGFTVLARMVS IS*PQ/CDPPTLASQRAGMTGLSHCT RLFFF*WMESPSVTQAGIQWHDLGS LQPMPPQFR*FSWLSLPSSQDYRCM PPCQANF\CIFSRDEVSPC*PGWSGS PDLVIHLPWPPKVLGLHA |
| 3353 | 8850 | A | 3616 | 3 | 285 | HEIIVLRVRVSPCCPGWSA\TVD*SW FIAASYS*VKRLSCLSLRLIWGCRQ VPPWLSFKLFWRQGLAVLPKLVSN SWPKMTLLPQLRLGLQE |
| 3354 | 8851 | A | 3617 | 3 | 575 | PSLRHASHEAGWQCPLHGQPLPGY TELRTLPQ*GDGYGRPGVSAASQR R/GLAGQCVEGRDWVEGKAG*CSG GHGEGKGPLD*GALLPGPQNR\S GAGDPC*AVESVGCQ*PGECHFQR DPPGSGAAPGAPPAVP*LHRQPD AAGGTAGPSLPHLPPPLGLRVERS KPGGAAEEQGHPHLEHGP GD |
| 3355 | 8852 | A | 3618 | 3 | 379 | FFETESCSFTQAGVQWHDLGTL*SP PPGFK*FSLSLSSWDYRRPPRTA/ NYIYIVFLVETGFYVVGAGQKLLT |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SCNLPALVSQSARITGVSHCAQLCN FLLTVKHFKPLTLRLEARTPQSFL |
| 3356 | 8853 | A | 3622 | 1 | 214 | ETESRSV/SQAGVQWRDLGSL*PPPP PGFQRFSCSLSPSSWDYRRAPPLPH NFCIFSRDGVSPCWPGWSQIS |
| 3357 | 8854 | A | 3623 | 2 | 309 | WCVFFETETHSAAQAGVQWCNLS LQPPPGVKQFSCSLSPSSWDYRCA SPCLASFCIFSRA*GFTMLTCLLELT SGNPPTSASQSAGIQGVSHHTWPSI F |
| 3358 | 8855 | A | 3624 | 1 | 294 | FFFFFFLRQGLTSLARLECSGMISAH CSLDLPG\SGDPPTSAS*VAGTTGTC HHAWLIFLFLVETGFHHVAQAGTLS KHRNHIQPVQVRATCSKDGO |
| 3359 | 8856 | A | 3625 | 23 | 282 | ASTGKPLSPQVQSES/CLALQLP*RS WN*TRVMSTTPWPNFFGIFVEMGF RHIGQAGLELLTSSNPILASQSAGI TGLSHRVQPTSS |
| 3360 | 8857 | A | 3626 | 37 | 289 | QWHDLGSLQPLPPGF\RRLSCLSLTS SWDCR/QPALRPANFFCIFK*RWGF TVLAQDGLDLLTSSDLPASAS*SAGI TGVSHRAWA |
| 3361 | 8858 | A | 3627 | 70 | 362 | KLHFKAIEGISSLGEQMKPSMWML LCPQIKIKLTLPIQIKQAKTCRQIPKV QGSQ*KNVGPSSFPVPW/EHGSAMI EAPWALNPYLGLGPVQILETQK |
| 3362 | 8859 | A | 3628 | 60 | 303 | KLKNHHHHHHQQQQKQQQQKQK QMDPRVSFSFFKKKKSSTPKPSQ*FP *SSRNS/HPR*ISESDTLRPTEAIPGL KMKLPL |
| 3363 | 8860 | C | 3629 | 193 | 285 | MLLVSYPRNSNRCQIQYHEAFCPIIF LRVL* |
| 3364 | 8861 | A | 3630 | 159 | 483 | DPTSFGHGYLVFPTPCFKGFYFF*DR VSFCCSGML/IGSLQAQPSGFKPKPS SHLRLSSEDCRHTPPRLANLFFYFF L*RWDLTMLPRLVSNS*AQVILPSW PPIMLG |
| 3365 | 8862 | A | 3631 | 6 | 244 | DRVLLVTQAGVQWHDLGSLKPPPP GFK*VSCLSLPSSWNYRRLPPRPAN F*FLVETGFLHVCQAGLKLPTSGDP PASA |
| 3366 | 8863 | A | 3632 | 2 | 262 | NDLGSLK\PPPPGFK*VSCLSLP/RVS WNYRRLPPRPSLIFVFLVETGFL/HV CQAGLKLPTSGDPPPSASQSTWITG VNHRARPQIGF |
| 3367 | 8864 | A | 3633 | 1 | 1149 | |
| 3368 | 8865 | A | 3634 | 280 | 602 | TDFFFFFFLRWSFTLVAQAGV*LHD PE*LQPPPPGFKRFSCSLSPSSWDYR HPPWPANF*FLVETGFHHVGGQAG LELLTSGDPPASASQSVGITGVSHR ARPELNF |
| 3369 | 8866 | A | 3635 | 3 | 679 | SLHQSGRSNPTCCFPSSKGTGTNGH PTPSQSPPGTRDGPLFFPHSASTPP PTGASQPLTGTGRPPSPVEPVSHAC ASL*FSEGLRSEHPAVACGKTLQSP TGSKEACSGEQGNCVLAIEIVVLGT QDPSAH*GGAGARGGGALWVTEG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VKGPGPVSGQCRKSQPHACGEIPCR APPTMGTSGLPLGLPKLCPHFHCSR ASPAPSNSPFCFWSPTSGGPNPFPC |
| 3370 | 8867 | A | 3636 | 1 | 334 | EMESRSVAQAGVQWHDGLSLQPLP PGFKRFSCSLPSSWDYMRAP/PRP G*FFVFLVEMGFHLVGQAGLKLLTS /S/DLPTSASQSAGITGMSHRTRPNSL LVIQSGRFNTKITR |
| 3371 | 8868 | A | 3637 | 2 | 309 | FFFFETRFRFVAQAGV*WHAYGSPQ PRPPGPKPSSQLSLPS*DYRHTLLCL ANF\DFLVETGFYHVAQTGLELLSV RDPPALASQSAGIAGVSHRARPGCI F |
| 3372 | 8869 | A | 3640 | 19 | 458 | KHLFYSSNLYFRSTFRHTRRRSPCEP SLALR/WCVLEPGSSRV**RLHPNTV GFQDASAKPRERTTSFHAFANF*K QYIFQC*LPPLTWLEIFSPFSRETGST KRCRLQDPGPSHFWRVVLGCLLWG QDRAPSWAPLQMQCLCHCLYL |
| 3373 | 8870 | A | 3641 | 1 | 322 | FLRRSLALVTQARVQWHDPGSLQP SPSGFKRFSCSLPSTRDYRHPPRL ANFF/VFFLYL**GFATLAWLVNLSH L/CDPPASASQSARTTGASHHAQPP VSFFKTRI |
| 3374 | 8871 | A | 3642 | 333 | 438 | |
| 3375 | 8872 | A | 3643 | 391 | 492 | |
| 3376 | 8873 | A | 3644 | 598 | 699 | |
| 3377 | 8874 | C | 3645 | 176 | 319 | MCSAQPAFSVDIIKSRHLGILGFYK PRILCQKHMLRLLHSFQNFQR* |
| 3378 | 8875 | A | 3646 | 2 | 50 | QLLGTGTMHHYA*LIF |
| 3379 | 8876 | A | 3647 | 3147 | 3308 | FFKKNLCASAHYY/TWCVPLPFFFF LRQGL/NSIGQAGVQWCNHSSLQPC PPQDLE |
| 3380 | 8877 | A | 3648 | 1554 | 3041 | GTRERRAPDPCAGKCRNHVAGGRL KLSLHLSLPSSWDHRHAPL/PHD*FF KYLR/RSPCVTQAGLKLLGSSDPPI LASQSIGITDMSHCT/WPSSPTPCFH LRDSFAPSPRPGMQ*CDHSSL*PQTL GLKQFSHQPPFYFFVQMG\FAMLPK LVLNWPQ/DNPSALAPQSAGIVGM SCCAQPPCFNINSHS*IQE |
| 3381 | 8878 | A | 3649 | 280 | 444 | |
| 3382 | 8879 | C | 3650 | 135 | 377 | MAGSWGAGQVQWLMSVIPILWEA KMGGSLRSLRPAWVTQGDVSN RLFHSSASVLWLQATLGTIPKSLEYI TLAFRAK* |
| 3383 | 8880 | A | 3651 | 1791 | 6596 | CPKDTQILIFQKNNFSIRRFTQHLAD FLKEFCLTFKKKGRSLL*FCCFVYI IF*KKFVCFCSLHWCVPLPFFFFLR Q/RHSIGQAGVQWCNHSSLQPCPP RLK\HPCTSASQVAGTTGMHHYA*L IF*IFETGSPCVTQAGLK/PPGLK*SS HLGLPEYWDYRHEPLHLPSSPTPCH FLRDSFAPSPRPGMQ*CDHSSL*PQT LGLKQFSHQPPFYFFVQMGSCYVA QAGLK/PPGLKQSFCLGPPKCWDCG HELLCPASMF*YQHPHMYTLKTTV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TFSTQNYIRYSLNCRKIKTIPKSDCR VDFFLQNT |
| 3384 | 8881 | A | 3652 | 3 | 332 | ETESHVAQDGVQWRHLSSLQPPLL GFK*FSCSLSPSSWDYSCPSPT/P*LI CFFFFFLIEPGFHHFGLAGLELQTSG DLPASAFQDAGITGMSH*TRPELLS LDHTPFT |
| 3385 | 8882 | A | 3653 | 3 | 272 | FETESH/VSPRLECSGVIFAHCSFCL PGSSDSPASAS*VSGMIGTRNHAQLI FVFLVEVRFHVQGAGLELLA*VI HPPQPPKVLGLHV |
| 3386 | 8883 | A | 3654 | 1 | 272 | ETGSRSTRLLECSGAITAHCSLDLPG RSNPPTSAS*/RIAGASGECRHTQL/I* KFIFFVNTGCRYVVQAGLKLLASGA KQSSCLGLSKCWD |
| 3387 | 8884 | A | 3655 | 249 | 906 | RIHFPRVSGPSQSNPKFAVASRGFFS LSLSSAQPDPLPPPLGEALALSLHPV PRRSTETVAGDSSELQLGLRSPQQP LAGLAFLARLFLFPPP*RCKSKPN* NDRRRSSVDSQIHLVGRESAHPLAG LRVCVSLPLLARCFGQVLQGVPG WIPSPGGS/AGVSGRRREERHMGVV VMRVRVEARVSS*ESKI/SRALR*ST HLGLPKCWDYRREPPCPAH |
| 3388 | 8885 | A | 3656 | 1 | 514 | FFFFSRSL/NSVIQAGAQRDLGSLQ P/LLPPGLKQFSCSLSSWDYRCPP PRLANFYIF/M*RRGFTILARLVLS* TQ/CDPPTSASQSAGITGVSHPTQ/LL FSF/CLKESGSSLMVSATLRFHK*RH SGPSRAALSSSP*LEPRKLKFGTASL QNKWAMQQTRQHWAGRGSKPM |
| 3389 | 8886 | A | 3657 | 2 | 307 | FFFFFFETESYSVTQAGVQWHDGLL LQPLPPGLKQFSSLSLPE*L/DVTGSP PPCPVNFCTFGKGLGFTMVGQAGS GTSCLKVICPPGLPKVLGITGCEPRR L |
| 3390 | 8887 | A | 3658 | 79 | 91 | NTFW*RRGFTVLARMVLIS*PHDLM TC/PASASQSARITGMSHCARLVLYF SRDGVSLCWPGWSQTADLR*STCL GLPKCWDYRYEPPCPASLHHFLIYA TSIIKYL |
| 3391 | 8888 | A | 3659 | 162 | 493 | DGSSPPVAQAGVQWRDLGSLQAPP PGFTPFSCSLSRSDYRRPPRPA NF/SCIFIVETGFHRVSQDGLDLLTS* S/VPASASQSAGITGVSHRARPRSCIS FDSTVTLAQ |
| 3392 | 8889 | A | 3660 | 3 | 251 | GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSLI LPSSWDYRH |
| 3393 | 8890 | A | 3661 | 3 | 251 | GGALRLHQVPPALPLRGAVSGAAA VQGMSDCTPCCEVHLLQD*VPAGE ARVQWHDGLGSLQPPPPRFKRFSLI LPSSWDYRH |
| 3394 | 8891 | A | 3662 | 17 | 287 | KYHRIQCPNSGICEAVYSSVSGLKA HLGSCTLGNFVAGKYKCLLCQKEF VSESGVKYHINSVHAEVRL*SCGP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DM*ATREVDVPIVMD |
| 3395 | 8892 | A | 3663 | 3 | 567 | DRKLYTRPGLPTFSQEV LHKWKT DIKYYHRIQCPNQGCEAVYSSVSGL KAHLGSC TLGNFVAGKYKCLLCQK EFVSESGVKYHINSVHAEDW FVVN PTTTSFEKLMKIKQPAARRRKA EA AAQEQKVSKKGGSSLGIELPETEPS LRVGKDQRRNNE DW*QPPCKEP/ GAGASASTVPESKAPKD |
| 3396 | 8893 | A | 3664 | 1 | 184 | SSRDILLCTDIASRG LDSTGVELVVN YDFPPTLQD\ELAAARRRSLPGLASS VKEPLPQAT |
| 3397 | 8894 | A | 3665 | 2 | 1748 | HEARTKGNMALSAARLRLLPFFVN SVCFLAP\RRGL\TVRSPDE\LPVVR IPVASTSGKLEQRQ\SRRLNPEGR LVRPGPLLVSARRPELN\PARLTLG RWERAPLASQGWKSRRARRDHFS\I ERAQQEAPAVRKLSSKGSFADLGA WKPRVLHALQEAAPEVVQ\PTTVQ SSTIPSLLRGRHVVC AETGSGKTL YLLPLLQRLLGQPSLD\SLPIAPRGL VLVPSRELAQQVRAVAQPLGRSLG LLVRDLEGGHGMRRIRLQLSRQPSA DVLVATPGALWKALKSR LISLEQLS FLVLDEADTLLDES FLELV DYILEK KDLAVFLYHLRLEAEVEVVEMLGP HGQPCPQHNSDISAYTYERTLMME QRSQMLRQMRLTKTERERE AQLVK DRHSALRLESLSDEEDES AVGAD KIQMTWTRDKYMTETWDP SHAPD NFREL VHIKPDQSNVRRMHTAVKL NEVIVTRSHDARLVLLNMPGPPRNS WCTTSSRTEKRQWNC PAVRTEKNA QTRQTIIAETKTQKKDTEPRIPEADL AVQYDNHYTNTKYCLCQMLREQ ESPQGRLLHAAQSSREIW |
| 3398 | 8895 | A | 3666 | 1 | 1704 | MALTRPVRLFSLVTRLL LAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRLNLRPV LVRPGPLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAAPEV VQPTTVQSSTIPSLLRGRHVVC AAE TGSGKTL SYLLPLLQRLLG\HPSLDS LPIAPRGLVLVPSREFF\QHLRAVA QPLGRSLG LLVRDL\EGGHGMRRIR LQLSRQPSADVLVATPGALWKAL KSRLISL\EELSFLVLDEG\DTLLG*K ASWELVDYIL\EKSH\AEGPADLED PFNPKAQLVLVGATFPE\GVGQLLN KVASPD AVTTITSSKLHCIMPHVKQ TFLRLKGADKVAEL\VHILAKHR\SR AEKGLGPSGTGFVFCNSSSTVNWL GYILDDHKIQHLRLQGQMPALMRV GIF\QSFQKSSRDILL\CTDIASRG LD STGVELVVNY\DFPPTLARLTFHRA GESGPVWGAEGPGTVISFVTHPW DVNPWFKKD*SLAARPKEEVL PGL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AIPR*KKPFAPQSNPDFEQNLIK M |
| 3399 | 8896 | A | 3667 | 2 | 222 | RWSLTLFQAGMQWPNLSSLQPPPP RFKQF*CLSLPSSWDYWYTPPRLAN FCIFSRDGVSPCWSGWSRTPDLR |
| 3400 | 8897 | A | 3668 | 1 | 29 | |
| 3401 | 8898 | A | 3669 | 2 | 206 | VTQAGVQWLALSSSLQPLPPG/LK*F YCLSLPSSWEYRHTPPHPTKFCIFFL VEGVSPYWP GWSQTPGLR |
| 3402 | 8899 | A | 3670 | 3 | 139 | TSHMWWCRHVVSATREAEVGEPL EPRQSRLQ*AMTAP\CTPAWATK |
| 3403 | 8900 | A | 3671 | 86 | 384 | |
| 3404 | 8901 | A | 3672 | 3 | 746 | RQEEGLPPVVDAIDDASVEEDLAVA VAGGRLEEVSFLOPYPARRRRALLR ASGVRRIDREKRELQALRQSREDC GCHCDRICDPETCSCSLAGIKCQMD HTAFPCGCCREGCENPMGRVEFNQ ARVQTHFIHTLTRLQLEQEAESF/QG AGGPCPGQPTQPW*GGPGPYFPTGQ APHEQ*AGRQQLQQRHD\YSSTASS SASGTSEAPDCPTHPLPGPGFQPG VDDDSLARILSFSDSDFGEEEEED |
| 3405 | 8902 | A | 3673 | 72 | 332 | LPALETPRAQSKCSPPPQSWVSRDY RCVPTHALANF*IFGEMGS/LLCCPR LISNS\WPQGILPPPPKVLGLQGSYS AKITTGFFLK |
| 3406 | 8903 | A | 3674 | 33 | 396 | RVWYLHRVTGRPASCLREVGP GDS LETASLREIWRSRRCRAT/ECSQQL NHRLARQREHEARLRQQREQNSRY FTDV*HL\RSKQAEWSSKTTYQRSM HAYHREKMKEEKRRSLWARLEKL M |
| 3407 | 8904 | A | 3675 | 217 | 935 | QRQREKEDQIRQQWEQNSRYFRMS DICSSKQAEWSSKTSYQORMHAYQ REKMKEEKRRSLEARREKLRLQMQ EEQDLLARELEELR/REHELAKKN PGAAREAEISQRAEETDC*TTFVR TLEKEQPETSRDGAGPSPEACRLL GNAE/MKKKKKQAEASAEQGNKRYE NEYERARREALERMKAEEERRQLE DKLQAEALLQOMEELKLKEVEVGT SPSQP*PPPQLLVSMRWALERLP |
| 3408 | 8905 | A | 3676 | 1 | 382 | EMEPCFVS*TGV*WHDLSLQPPPLP KFKRFSLKIPEASWDYRRTP/PMP/V LTGFHHVDQAGFELLTSSDPPTSAS QSVGITGMGDHTWPTLHTLTKPCE VDENAVMRELKLTGQGPLRKWQF EHLNPA |
| 3409 | 8906 | A | 3677 | 1 | 2456 | MPTYPKLEKTDQSTSYTKFNDLSPD SSRERYTSLEIKSVCYTALPEQGQK QLQLWYNCVKTQCKTTQECSLKWI FTMNETSDREDGLPKGHVTDSEN DEPLNLNASDSESEELHRQKDS DSE SEERAEPASDSENEDEVNQHGS DSE SEETRKLPGSDSENEELNGHASDS ENEDVGKHPASDSEIEELQKSPASD SETEDALKPQISDSESEEP RHQASD SENEPPKPRMSDSESEELPKPQVSD |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SESEPPRHQASDSENEELPKPRISD SESEDPPRHQASDSENEELPKPRISD SESEDPPRNQASDSENEELPKPRVS DSESEGPQKGPASDSETEDASRHKQ KPESDDSDRENKGEDTEMQNDSF HSDSHMDRKKFHSSDSEEEHKKQ KMDSDEDEKEGEEKVAKRKA VLSDESEEEKASAKSRVSDADDS DSDAVSDKSGK\KRRTIASDSEEEA GKELSDKKNEEKDLFGSDSESGNEE ENLIAD\NLENLVMKRK*NLQVLT KIWEEKGETQVKEAEDSDSDDN IKRGKHMDFLSDFEMMLQRKKS MSGKRRRNRDGGTFISDADDVVS AMIVKMNEAAEDLKETFIDSGV MSAIKEWLSPLPDRSLPALKI REGVLKILQELPSVSQETLK HSGIGRAV MYLYKH PKESRSNKDMAGKLINEWSR PIFGLTSNYKGMTREEREQR DLEQMPQRRMNS/DLVVRH PERDLEKVL TGEEK ALRPGDPGFVPRARVPMP SNKDYVVRPKWNVEMESSR PGILKKGLSRLEKHKRRFAE QKRLSKVHRAVKFSIEG NRMPL |
| 3410 | 8907 | A | 3678 | 1 | 564 | TLKQVGLTEHVMYLYNDPKESRSN KDMAGKLINEWSRPIFGLTSNYKG MTREEREQRDLEQMPQRRRN DSTGGQTPRRDLEKVL TG KEKALRPGDSLNLV/PRAR VPMPSNKDYGVPRPKMKCG NGVIQVSGDPPQKGIQSDWI NQMRKFHRY*GKKADLAHA VENPAIEGNKMPIGDPCPGM CPPILL |
| 3411 | 8908 | A | 3679 | 63 | 361 | |
| 3412 | 8909 | A | 3680 | 151 | 384 | |
| 3413 | 8910 | B | 3681 | 385 | 479 | MAGAFRRRFASEVRAQGLES LLEHGLRCAGSLRGGQSLPT TMWSPVKVGFE* |
| 3414 | 8911 | A | 3682 | 3 | 698 | VFFFFFFSGCTRGPLFESDF HRAPHRCGQGLAAP*AAGAP QPRAPGETRGPEPAPHWRS ASGDKPPGQAAPPALVP GEGPSWSDPRGHRCSQATL PRVLAGPLQP*LS*LSL* DPPELRSL*PPL*LRL** SLEPP*PPLLDNRFPP*PR SPPLENPRPRPRPRPKKPR PPAEPPRYPTESVSDDLPA WSTRISVHLQTSHSWPSWA SLASSMFFKVTKPNSRELW SS |
| 3415 | 8912 | A | 3683 | 138 | 550 | FCCCFTSSEHSLLAYGSCS PRRTEVLCAQQNPSETQAAP LAS\YMWK*PCNSRLKGP GPGLGEGWPES\RMTSGV TVPGGTSPGTRAGGSPCP GGLSPEALRQ*GAGSGPRV SPGA/PGCGAPAA YGAAS PCPQRCGAL |
| 3416 | 8913 | A | 3684 | 2 | 555 | FFFFFFLGAHVALYSNPTFT GLHIVVGKDWPPP*AAGAP QPRAPGETRGPEPAPHWRS ASGDKPPGASGCLQLLF QGEVPPGDS*PQRSSLALR PPFPRVLGPGPFQPAKAKQ RYSQRPPQGSQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | APP/GPPRKQPQPLRKVSG*SGGCDLRLRHRPACGRVCTLAQLEPATRMGWSYVGQCGL |
| 3417 | 8914 | B | 3685 | 95 | 371 | MASDEGKLFVGGLSFDTNEQSLEQVFSKYGQISEVVVKDRETQSRGFGFVTFENIDDAKDAMMAMNGKSV DGRQIRVDQAGKSSDNPIPW* |
| 3418 | 8915 | A | 3686 | 314 | 1055 | SKCFHLHQVWKQKGEEYRVGTGYG GWSWISKTHVYRFVFKLHGNTNVN YRKSLEGTKNNMDENMDES DKRCSRSPKKIKIEPDSEKDEVKGS DAAKGADQNEMDISKITEKKDQDV KELLDSDSDKPCRKTNGSRR*HENRVTCKLSGEFSSRCGQC**GFSSKD*LQKENKIIQTRWTS*KEN*TVYTGRKTA TRKNQVGGWN*GYRKD\STNSSKN LSESPVITKAKEGCQSDSDETRTEPKCK |
| 3419 | 8916 | A | 3687 | 11 | 345 | DSLTVASQSGVQWHNLISLQPLPPGVK*LFCLSLPSS*DYRRAPHPANFSF LVEMGFYHVGQAGLELLISSDLTSL ASQSAGITSVSHWAWPENVYLN LQ QTEKSLMVSG |
| 3420 | 8917 | A | 3688 | 1 | 521 | NPTKSCMLEG*NPHVHCKVREGAQA ITGMPI*KATKYLKYFLLQKLCVPF QS/YESGVGRCTQDRHWGWTHHQ WPRKGTEICLQVQSYAELKGIDVDS LVIEHIQ/V/NKAPIMYHLTYRTHGQ MNP/YHKLPCHIOMMLSEKKHLVP KAEKEDARKKKIPQKKHKLKRQTN SAKRKCK |
| 3421 | 8918 | A | 3689 | 1 | 281 | ETGSHSDAQAGVQWHDLGPMQPLP PGFKRFSHLSLLSSWDYRHAP/PRPGLFL*RWGFHQVGQVDLELLNSSDP ASTSQSAGITSASHRAWPN |
| 3422 | 8919 | A | 3690 | 3 | 314 | HAEHEITELTATFTKFDNRDGNRILDE KEQEKMRQDLEER\LTRVLQLET VLERVVAQIDALSSKLEMLEKKGVSLSLFTSFNIRAFKSLFSHYSSVTPINYL |
| 3423 | 8920 | A | 3691 | 61 | 400 | LVTGIWSATCLWVLLLLLFEKGCPS VQRLQCS\NVITACCSNL\RGSDNPPTSASRVPGDHRCCHYTWANFLIF LWEMRSHCVGFRLGLGTPVLKLQT ILQPQPPKVLGLQA |
| 3424 | 8921 | A | 3692 | 33 | 436 | REQEL/CKGKQKDGTSFGEYGGWY KACKVDSPTVTITLKNLALYRRQ GKFEAAETLEEAAMRSRKQGLDNV HKQRVAEVLNDPENMEKRRSRESL NVDVVKYESGPDGGGEGVSGRASFCGKRQQQWPGRHR |
| 3425 | 8922 | A | 3693 | 37 | 355 | NSEYGGWYKACKVDSPTVTITL\K NLGALYRRQKGFEAAETLEEAAMRSRKQGLDNVHKQRVAEVLNDPEN MEKRRSRESLNVDVVKYESGPDGG EEDGTGSLKRS |
| 3426 | 8923 | A | 3694 | 229 | 2000 | QRERARPSGARMYDTMSTMVYIK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EDKLEKLTQDEIISKTKQVIQGLEAL KNEHNSILQSLLETCLKKKDDSN LVEEKSNMIRKSLEMLELGLSEAQV MMALSNHLNAVESEKQKLRAQVR RLCQENQWLRDELANTQKQLQKSE QSV AQLEEEKKHLEFMNQLKKYDD DISPSEDKDTDSTKEPLDDLFPNDED DPGQGIQQQHSSAAAAAQGGYEI PARLRTLHNLVIQYASQGRYEVAVP LCKQALEDELEKTSBGHDHPDVATML NILALVYRDQNKYKDAANLLNDAL AIREKTLGKDHPAVAATLNNLAVL YGKRGKYKEAEPLCKRALEIREKV LGKDHPDVAKQLNNLALLCQNQG KYEEVEYYYQRFLEIFQTKLGPDDP NVGKTKNNLASCYLKQGKFKQAET LYKEILTRAHEREFGSVDDEANKPI WMHAEERECKGQKDGTSFGEY GGWYK\ACTVDSPTVTTTLNLGAL YRRQGFEEAETLEEAAMRSRKQG LDNVHKQ\RVAEVLN*PLRTLEKPQ EPVESL\NV\DVVKYESGPDG\GEEV SMSVEWNGGVSGRASFCGKRQQQ QWPGRHR |
| 3427 | 8924 | A | 3695 | 1 | 314 | KVDSPTVTTTLKNLGALYRRQKGF EAAETLEEAAMRSRKQGLDNFTKQ RLPEVLNDP\ENMEKRRSRESLNV VVKYESGPDGGEEVSMSVKWNGM RKMMLGAG |
| 3428 | 8925 | A | 3696 | 2 | 450 | VNKAGGLIYQLDSYAP\RAEAEKTF SYPLDLLLKLHDERVLVAFGQRDGI RVGHAVLAINGMDVNGRYTADGK EVLEYLGNPANYPVSI RFGPRLTS NEKLMLASMFHS\IKFVVLADP\ RQ AGIDSLLRKIYEIYSDFALKNP FYSL EMP |
| 3429 | 8926 | A | 3697 | 2 | 823 | FGTRGKAAMAIFS VYV VNKAGGLI YQLDSYAPRAEAEKTF SYPLDLLLKL LHDERVLVAFGQRDGI RVGHAVLA INGMDVNGRYTADGKEVLEYLGNP ANYPVSI RFGPRLTS NEKLMLAS MFHSLFAIG\SQLSPE\QGSSG\IGCLE TDPFQFH\CSRTLTGIKF\VV LADP\ RQ QAGIDSLLRKDFMEILLQTLPLKNPI PIPLEMP\IRCEPL*PQNPEA*SLEVA\ EKAG\TFGPRVHRLNPVMGPPQNPE SSLQQEYCLLTLPVEIPAALVSAP |
| 3430 | 8927 | A | 3698 | 165 | 354 | ENFGGKITNFAKLFGYILPYSHYFW CLEKNRNR/SLTLLPRLVSNWAQA FLLWPPKVLRLQA |
| 3431 | 8928 | A | 3699 | 3 | 166 | SETGFCHVAQAGLELLVSRSPASV SQS\TGISHQARPSISYFYDHSAPITH TDH |
| 3432 | 8929 | A | 3700 | 1 | 421 | ETKSHSVTKTEVEWRDPSSLQPLSP GFKQFSCRSLPNASWDYR/PSPANFV FLVETGFYLVGQAGLELLTSNDPPA SASQSAGITGVSHCAQPRITNSLTTA SFIQPRKHSEFPVMTCPSSNATESK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VGGRGPHGAIARLM |
| 3433 | 8930 | A | 3701 | 2 | 205 | APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ |
| 3434 | 8931 | A | 3702 | 2 | 205 | APVTSW/IQPKVGSCPFSESTKTISLY ISSEQQFHLPRPSESDDFIEDTADMLA VSFSGYSSAPKNQEQ |
| 3435 | 8932 | C | 3703 | 282 | 445 | MISAHCNLLPPEAGELLEPGGRRFS EPLHSSLMTEQDSVSKINKNKTSIS NPE* |
| 3436 | 8933 | A | 3704 | 170 | 607 | WPSG*FQR*SMRLKYYKIHLNVSRR PQLAPGKELYFSF*LLFYFYFYFIHHI FEMESHSVTRLECSGTISAHCNHL PGSSDSPASAPVAGTLIDACHHTW \LIFYNF*VEMGFHHVQGAGLKLTT *VTHPPRPSKVLGLQA |
| 3437 | 8934 | A | 3705 | 3 | 231 | FETESLFPRLECSGTISAHCNLRSLG SSNFWLIFCILVEMGFHHVGQTSLE LLTSSHPTSAFQSARITGVSHRTW |
| 3438 | 8935 | A | 3706 | 4 | 144 | |
| 3439 | 8936 | A | 3707 | 333 | 416 | FTGLPCLFSPQNNVSLQSCIDLKFN NN |
| 3440 | 8937 | A | 3708 | 1 | 1219 | MAAVPELLQQQEEDRSKLRSVSVD LNVDPQLQIDIPDALSERDKVKFTV HTKTTLPFQSPEFSVTRQHEDFVW LHDTLIETTDYAGLIIPPAPTKPDFD GPREKMQKLGEGECSMTKEEFAK MKQELEAEYLAVFKKTVSSHEVFL QRLSSHPVLSKDRNFHVFLDYDQDL SVRRKNTKEMFGGFFKSUVKSADE VLFTGVKEVDFFEQEKNFLLNYN RIKDSCVKADKMTRSHKNVADDYI HTAACLHSLALEEPTVIKYLKVA ELFEKLRKVEGRVSSDEDLKLTLL RYYMLNIEAAKDLLYRRTQS/ALI DYENSNKALDKARLKSVDVKLAEA HQQECCQKFEQLSESAKEELINFK \RKRVA\AFRKNLIEMSELEIKHARN NVSLQSCIDLFEF |
| 3441 | 8938 | A | 3709 | 527 | 724 | TMKIGLGFSLVSINIFSPVELINFKR KRVA\AFRKNLIEMSELEIKHARN NVSLQSCIDLKNN |
| 3442 | 8939 | A | 3710 | 1 | 1220 | QEGGSAGSAGSGADGTGLRQSLAG HVGRPGRGQWGQRSGDLPGRHP PARSEHRCVAEG/NLSLYVFGGYNP DYDESGPDNEDYPLFRELWRYHF ATGVWHQMGTG\YMPRELASMS LVLHGNLLVFGDTGIPFGESNGND VHVCNVKYKRWALLSCRGKKSRI YGQAMAHNGSLYVFGGTTGYIYST DLHKLDLNTREWTQLKPNLSCDL PEERYRHEIAHDGQRIYILGDGTW TAYSLNKIHA\YNLET\NAWEEIATK PHEKIGFPAARRCHSCVQIKNDVFIC GGYNGEVILGDIWKLNLQTFQWVK LPATMPEPVYFHCAAVTTA\GCMYI HG\GVVNIH\ENKRTG\SLFKI\WLVV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PSLLELAWEKLLGAFNLANL\SR QLLH\LGFTQGLIERLK |
| 3443 | 8940 | A | 3711 | 2 | 266 | FLMESRSVTRLECSSTITAHCNLC LPVSSDSAVSASQVAGTTGMRHHA QLIFVFLVETGFHHVQGQDGLHLL /NIVIHLPRPPKVLGLQA |
| 3444 | 8941 | A | 3712 | 1 | 453 | FKRAMDLVQEEFLQRLDFSQHSWL PARALVEEALAQRFQVDPSPGEIV ELAKGACPWKEHLYHLESGLSPPVA IFVVIYTDQ/RWTVANIAGCPLPEPW RGLRDEALDQVSGIPGCIFVHASGFI GHRREGALSMARATLAQRSFLPQI S |
| 3445 | 8942 | A | 3713 | 20 | 891 | RWNSRYDHHQRSFTETMSSLSPGK PWQTKLSSAGLIYLFHGAQVLAQL LGTSEEDSMVGTLYDKMYENFVEE VDAVDNGISQWAEGERPYALTTL SARVARLNPTWNHPDQDTEAGFK RAMDLVQKEVSCRD*IFYQHSWLP ARGLGGKSHLPQRIPRWNPSPGK\VE LAKRCHVPWKEHLLPPGNLGLSPS KWPIFFVIYTD/SRL/EQWRIQCVAQ/ VSPTHSQSRAALPEPWRGLRGTRP WT*FSGIPGCIFVHASGFI/SAVNATR EGALSMARATLAQRLIPTNLLV |
| 3446 | 8943 | A | 3714 | 176 | 450 | |
| 3447 | 8944 | A | 3715 | 1 | 472 | |
| 3448 | 8945 | A | 3716 | 418 | 1354 | AAARRATCLGCRSCSGATARRASS WRTAPRVHSAWKL\DGRRLASGS FDKTASRLLAWRRTFRGQKKTIIGG HGG*C/VTSFCWHPSNPEPICYGV/Y GDKTIRIWECEYKNALPLVNIKGE NINICWSPDWQTIAVGNKDDVVTFI *CQDTPFQSRRAVQVPRSTKSPWNH DHNMFLLTNGNGCINILSYPELKA\ VQSINAHPSN\ICINQV*PHGESTLP QASCKMLLVSLWDVG*VSVCFGAF SRLDWAC*EPFSFSDGKMLASASE DHFIDIAEVETGDKLWEVQCESPT\ SQVAWAPQKASAGHLPR |
| 3449 | 8946 | A | 3717 | 1 | 296 | LWDV/EELVCVGAFLRDWP/VRTSV SAHDGKMLASASEDHFIDIAEVKTG DKLWEVQCESPTFTVAWHPKRPLL AFACDDQKTANMTSSREAGTVKPV GAS |
| 3450 | 8947 | A | 3718 | 2 | 276 | RSTFALVAPAGVQWHDNRSLOPLL PRFKQLSCLSLSSWDYRCPPPSPA NF/SLFLVETGFRHAGQAGLQLLTS GDLPTSASKSAGITGMGLQ |
| 3451 | 8948 | A | 3719 | 3 | 613 | GLRALRRGQGLPGL*CCSRPQPSPR AQGHPSMGGPMQRTVTPRGMASV GPQSYGGGMRPPPNLAGPGLPAM NMGPGVRGPWASPSGNSIPYSSSSP GSYTGPPGGGGPPGTPIMPSPGDST NSENMYTIMNPIGQAGRANFPLG PGPEGMAAMSAEPHHVNGSLGS GDMDGLPKSSPGAVALSNAPGTP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RDDGEMAA |
| 3452 | 8949 | B | 3720 | 134 | 471 | MYAKGGKGSAPSDSQAREKLALY VYEYLLHIGAQKSAQTFLEIRWEK NIMPSPGDSTNSENMYTIMNPIGQ GAGRANFPLGPGPEGPMAAMSAME PHHVNGSLGSGDMDG* |
| 3453 | 8950 | B | 3721 | 223 | 692 | MEPSPRAQGHPSMGGXMQRVTPPR GMASVGPQSYGGGMRPPPNLGLP GLPAMNMGPGVVRGPWASPSGNSIP YSSSSPGSYTGPPGGGGPPGTPI PGDSTNSENMYTIMNPIGQAGRA NFPLGPGPEGPMAAMSAMEPHHV GSLGSGDMDG* |
| 3454 | 8951 | B | 3722 | 228 | 292 | XLARDDHERVMGRQPRASLRA* |
| 3455 | 8952 | A | 3723 | 1 | 1753 | MYAKGGKGSAPSDSQARENLSAF QAATELTSLDRLALYVYEYLLHIGA QKSAQTFLEIRWEKNITLGEPPGFL HSWWWYGLGCCGVFWDLYCAAP DRREACEHSGEAKAFQDYETPERP AHRHGNAGRAGSSSGMIDVGGSSD PQILRPPTTPVCSLTNASSLSHGAGHL QRGGGTPQSAAAAPSPVMGSMAPG DTMAAGSMAAGFFQGPSPSPH NPNAPMMGPHGQPFMSRFPGGPR PTLRD\GSQPPAGPPWVSPSSPG\A MEPSPRAQGHPEHGRPNARGVTPP RG/MGPAWGPWAYGGGMRPPPNL TRPRACLPMNMGPRKFVGPWAQPP VEYSIP\YSSSSPGSYTG\PPGGGGPP GTP\IMPSPGDS\TNSENMYTIMNPI GQGADRANFPLGPGPEGPMAAYG \GMEPHHVNGSLGSGDMDGLPREF PQAPVAGLSNAPGVTPRDDGEMAA AGTFHAPSSQSE\NYS\GMTMSRV NWAAAPGALCGPRLPRRCLRAK GLKVTPSGTLDLANQGLPMLGGP TRKTLTILLKTQGPRETFFSVWTLPA ICILVPERKALWGGPSSPGRQGGGA H |
| 3456 | 8953 | A | 3725 | 65 | 210 | ATRAGLIFDDSEHDVWQDASSFRL IFIVDGWHPELTPQQRSLPAI |
| 3457 | 8954 | A | 3726 | 2548 | 3800 | NSLILLFFFFRQRSLTLECSGVISAH HNLHLPSSSNS/P/ASAS*VAGITGM HRHAWPICIFLVETGFRHVQGAGLE LLTSGDPPAPTSQSM*ATTSGLILL SKILFPFHSTKVFK*SCPS*KILKEEN CSVINEWFNSESYTSKEKNLVPN AC*EITM*VATNCDFT/SLL*RSENY PKLFHNNETTSQKIHLKIKISRPATS GQWILFSLVWWRARKG*GILMIHN GILY*TIC*IKLHRLP*GMDYPNQPD/ MKSGWDKRMSHTL*F*GKEIVDFD QNQQNKLSTLYLSVQE**HEEFFFR DLKYNKPGSTIKSLVSF/HSLTLFFFF FFEARSHSASQAGVQWGNIGSLQPA PPGLKRSSYLSLLSSWDYRRVPPHP ANFCIFCR/GWGFGVSPCCPGSSGTP VLKWRAHLSLPNC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3458 | 8955 | A | 3727 | 2 | 217 | SSPSPPHPPASPPSSPSPAPASPPPSLP LPSPDFPPLSPCSSLSPFSSFSPPPSPP SPFFSRGSPSPDNFH |
| 3459 | 8956 | A | 3728 | 25 | 396 | ISGRSTFSLFSRQGLSALSPRLEVCV AISAHCNLRPLPGSSN\GTTGA*HHTR LILYF/LAEMGFHHVVGQAGFEVLTS SNPPASASTSARITGMSNRT\GHLFN FHP*MCYKYRCGSLAGRGSSRW |
| 3460 | 8957 | A | 3729 | 80 | 460 | YISLNVTTHLIFFFFFFLRQGL\CSVTQ AGV\QWCNLSLQPLPPRFK\NWDY RCVTPHLANFVFLVEMGF/LPASAS QSAGITGVSHCTQLGVFICICYGSSH GVRQSWHQFCSSKLLVKSGRVGVG LLG |
| 3461 | 8958 | A | 3730 | 1 | 316 | FFFFFETESHIVQAGVQWRDLSSL QPPPPRFKRFSSLSLPSSWDYRHVPP RPA\NFAFLVEMGFHHVVGQAGLELL TPGDPPSSASQSAGMTGVTHCAWP RCLMF |
| 3462 | 8959 | A | 3731 | 3 | 1717 | RPQTLKGHQEKIRQRQSILPPPQGPA PIP\SSTAAGIPRRPRIAWARR/WPLS EPGFRRRESQEEPRAVLAQKIEKET QILNCALDDIEWFVARLQKAAEF KQLNQRKKGKKKGKKKAPAEGVLT LRARPP\PEGEFIDCFQIKLAINLL AKLQKHIQNPQRR\DVVHFLFGPLD LIVNTCSGPDARSVSCPLFSRDAVD FLRGHLVPKEMSLWESLGESWMRP RSEWPREPQVPLYVPKFHSGWEPPV DVLQEAPWEVEGLASAPIEEVSPVS RQSIRNSQKH/RPHFRAHPPGGCPY HQSAPHILTRGYQPTPAMAKYVKIL YDFTARNANELSVLKDEVLEVLED GRQWWKLRSRSGQAGYVP\GNILG EARPEDAGAPFEQAGQKYLGTQP DPQATPKLPGGT/IDELMQHMDENV DELIRK\NTTSRAQPQRHFRVERSQP VSQPLTYESG\PDEVRA\FLEAKAFS PRIVENLGILTGPQLFSLNKEELKKV CGEEGFRVYSQTMQKAFLEKQQS GSELEELMNKFHSMNQRRGEDQLG PAALGWGLRRGSPPTMHGVFLYV YVFCIK |
| 3463 | 8960 | A | 3732 | 1 | 324 | |
| 3464 | 8961 | A | 3733 | 1 | 581 | MDKLETTYSLQRLSQEEIESLNRTI MSFKTKSVINTIPTKKSPGPDRLTAN FYQMCKEELADIIHGLCIRHEMTPV NPGVGQCCTSSYANRRPCFSSLVVD ETYVPPAFSDDKFIFHKDLCQAQGV ALQTMKQEFNLVKQKPQITEEQL EAVIADFSGLLEKCCQGQ\NQEVCF AEEGQKLISKTRAALGV |
| 3465 | 8962 | A | 3734 | 39 | 1935 | LATMKWVESIFLIFLLNFTESRTLHR NEYGIASILDSYQCTAEISLADLATIF FAQFVQEATYKEVSKMVKDALTAI EKPTGDEQSSGCLENQLPAFLEELC HEKEILEKYGHSDCCSQSEGRHNC FLAHKKPTPASIPLFQVPEPVTSCEA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YEEDRETFMKNKFIYEIARRHPFLYA PTILLWAARYDKIIPSCCKAENAVE CFQTKAATVTKELRESSLLNQHAC AVMKNFGTRTFQAITVTKLSQKFTK VNFTEIQKLVLDVAHVHEHCCRGD VLDCLQDGEKIMSYICSQQDTLSNK ITECKLTTLERGQCIIHAENDEKPE GLSPNLNRFLGDRDFNQFSSGEKNI FLASFVHEYSRRHPQLAVSVILRVA KGYQELLEKCFQTEPLECQDKGE EELQKYIRE\GQPWAKGSSGFSKK* GEYYLQTGSSLSLQQ*RPPQLTSSSEL MAITRKMAATAATCCQLEDKLLA\ CGEGAADIIIGHLCIRHEMTPGKPL VFGQVPAPPSICPNRRPHASSTWVV DGNIWSPPCISLMTKFHFSP*RDPGG PSLQGW*ALAKPMKAKRFPSLTLV KAKGPQIPGGNNSEAVIARFPQAWL EK\CCQ/GPQEQEVCF AQEGTK\LSK TRALGV |
| 3466 | 8963 | A | 3735 | 95 | 272 | RALQPDTTWE*GSQRRPWLPQVTN KPV*SKTSKS |
| 3467 | 8964 | B | 3736 | 344 | 1420 | MLLKTVLLLGHVAQVLMLDNGLL QTPPMGWLAWERFCNINCEDEPK NCISEQLFMEMADRMAQDQWRDM GYTYLNIDDCWIGGRDASGRLMPD PKRFPHGIPFLADYVHSLGLKLGIIY ADMGNFTCMGYPGTTLDKVVQDA QTFAEWKVDMLKLDGCFSTPEEAA QGYPKMAAGLNATGRPIAFSCSWP AYEGGLPPRVNYSLOADICNLWRN YDDIQDSWRSVLSILNWFVEHQDIL QPVAGPGHWNDPDMLLIGNFGLSL EQSRAQMALWTVLAAPLLMSTDRL TISAQNMDILQNPLMIKINQDPLGIQ GRRHKGSWMPKGSVCVPGCLRDPG TQDSQGKISHRSVHAASVQQG* |
| 3468 | 8965 | B | 3737 | 49 | 2119 | MALWTVLAAPLLMSTDRLTISAQN MDILQNPLMIKINQDPLGIQGRRIHK EKSLIEVYMRPLSNKASALVFFSCR TELCLIATTSCGLQLNFTGSVIYEAQ DVLLS* |
| 3469 | 8966 | A | 3738 | 139 | 536 | QSLGFIPFRKRQRISISYTFYFETGS YSVAQAGVQWHNLGSLQPRPPGFK QSSCLSPPGSWDHWRAAPHQANFA LLVETGSPHAAQASLKLSSSDPSA LASQSTGITGVSHHGQPYISHTLIIFI GKFI |
| 3470 | 8967 | A | 3739 | 1 | 213 | QFSCLSLPSSRDYRHEQP/PLIFVFLV ETGFYHVGQAGLELLTSGDPPALAS QSAEITGVSPRTRPNNLKS |
| 3471 | 8968 | B | 3740 | 75 | 729 | MEGTAGGERPSVVNGDSGKSGGVG DPREPLSCLQEGSGCHPTTESFEKSV REDASPLPHVCCCKQDALILQRLH HEDGSQHIGLLHPGDRGPDHEYLLV EEAERAMSEREARPNEESVQRNRLI CRTNPYRIFEYLP\SL\EEAFFLVYAL GCLSIYYEKEPLTIVKLWKAFTVVQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PTFRTTYMAYHYFRSKGWVPKVG KYGTDLLLYRKGPFFYHAX* |
| 3472 | 8969 | A | 3741 | 1 | 2649 | |
| 3473 | 8970 | A | 3742 | 41 | 656 | PVPRPCCGLRARSWPSSPRAARAAL PHGESALSRLLRALLAARASLDLCL FAFSSPQLGRAVQLLHQRGVVRV VTDCDYMALNGSQIGLLRKAGIQV RHDQDPGYMHKFA\VDRRVLITG SLNWTQTQAIQNNRENVLITEDDEYV RLFLEEFERIWEQFNPTKYTFPPKK SHGSCAPPVSRAGGRLLSWHRTCG TSSESQT |
| 3474 | 8971 | A | 3743 | 3 | 267 | FNMESQSLASLKCSGAVSAHCNLCF LGSSNSPASASRVSGITGVLYHTWLI FVFLVQTGFHHVQAGLELL/NLVI HPPRPPKVLGLQA |
| 3475 | 8972 | A | 3744 | 2 | 430 | FFFETGGAFVTQAGVQWPNLSSLPQ SPPGFKPSSHLSLPSTWDYRYTPPCP ASFCIF\TDTGCHVDQAGLELLASC NLPASASRSAGITGVSHHACPFLLFS FFKSGITSPNYPISHHEIIESNVAPVF LFEDSTAIYVYYF |
| 3476 | 8973 | A | 3745 | 2 | 316 | EFLFFETEFCSVTRLECSGAISAHCK LCLLGSRHSPASASRVARTTGTRHH AQRI\FVFSVETGFHRVS\RDGLDLL/ NLVIHPPQPPKVLGIRGREPPCPACF FAF |
| 3477 | 8974 | A | 3746 | 1 | 1053 | |
| 3478 | 8975 | A | 3747 | 1 | 3011 | SLQRLPGLMHNLTQFLLDGNFLQSL PAELENMKQLSYLGLSFNEFTDIPE VLEKLTAVDKLCMSGNCVETLRQ ALRKMPHIKHVDLRLNVIRKLIAD VDFLQHVTQLDLRDNKLGDLAMI FNNIEVLHCERNQLVTLDICGYFLK ALYASSNELVQLDVYPVPNYLSYM DVSRRNL\ENVPEWV\CESRKLSF GILGHN\QIC\ELPARLFCM\SSLRKLL GQGHN\QLARLPERLERTSVEVLDV QHNQLELPPNLLMKADSLRFLNAS ANKLESPPATLSEETNSILQELYLT NNSLTDKCVPLLTGHPHLKILHMA YNRLQSFPASKMAKLEELLEEIDLSG NKLKAIPTTIMNCRRMHTVIAHSNC HRGPFPEVM\QLP\EIKCVD\LSCNE\ LSEVTLP\ENLPSNCRSLDLTGNPR PCPLITKPLELLNNIRCFKID\QPSTG DG\SGAPAVW\SHG\YTEA\SGVKNK LCV\VALSVNNFCDNREALYGVFD GDRNVEVPYLLQCTMSDILAEELQ KKTKEEEYMVNTFIVMQRKLGT GQKLGGAAVLCHIKHDPVDPGGSF TLTSANVGKCQTVLCRNGKPLPLSR SYIMSCEEELKRIKQHKAITEDGKV NGVTESTRILGYTFLHPSVVP QSVLLTPQDEFFILGSKGLWDSLSV EEAVEAVRNVPDALAAAKKLCTLA QSYGCHDSISAVVQVLSVTEDSFCC CELSAGGAVPPSPGIFPPSVNMVIK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DRPSDGLGVPSSSSGMA\SEISSELST SEMSSEVGSTASDEPPPGVALSENSP AYPSEQRCMLHPIWLSNSFQRQLSS ATFSSAFSDNGLDSDDEEPIEGVFTN GRRVEVEVDIHCSRATEKEKQQHL LQVPSEASDEGIVISANEDEPGLPRK ADFSAVGTIGRRRANGSVAPQERSH NVIEVATDAPLRKPGGYFAAPAQPD PDDQFIIPPELEEEVKEIMKHHQEQQ QQQQPPPPQLQPQLPRHYQLDQLP DYYDTPL |
| 3479 | 8976 | A | 3748 | 1 | 246 | LPTLECSGMISAHCNLR LPGSSDSP ASASQVAGITSAHHYA WL VFVFSV EMGFHHVGQGWSRSLDLVIRPPQPP KMLGLQA |
| 3480 | 8977 | A | 3749 | 153 | 527 | LLVFYLP T PSLKGGRLQ L DMSLLCQ LYSLYESIQEYKGACQAASSPNWTY ALENGFFDEEEYFPEQNSLH DRRD RGPPRDLSL\APPSPAATGFWSPSR GSWEGCDCWEALPTGHA V I C C F S |
| 3481 | 8978 | A | 3750 | 2 | 377 | IPAASTFFCFLRQSLTLWPHAGVQW CGLSSLHPPPPGFM L F S C L S P S S W D YRRPPRP AKFSVFLVETGFHRVSQ DGLDLMTSDPPALASQSAGITGVS HCTRPKEA Y F Y F L A L D P R C K D G V R |
| 3482 | 8979 | A | 3751 | 2 | 294 | LFLHADRLEYSGMTISHLQ P Q T P G A QGDPLTSSLPREVGLQ/CVCHHTQL FFF/CIFVETESHHLA\RAGL K L L G S S DPTASPSQSDGITGMSHSCPSTF |
| 3483 | 8980 | A | 3752 | 80 | 267 | RQGLTILPRLVLNSC/RLKLSSHLSLP KYWDYRQEPPLAISIFFKKS LIYY LNLAILYFKCK |
| 3484 | 8981 | A | 3753 | 1 | 972 | |
| 3485 | 8982 | A | 3754 | 1 | 283 | PKPQEIELPEAKNR\PWIFNKILGTTV KLMELKPNTCYCLSVRAANTAGVG KWCKPYKVSPGKRGALGVERS PKP REPGLWRLGTPLCPHDSSG |
| 3486 | 8983 | B | 3755 | 346 | 472 | XRNMN ILQYCPSSDMWTLFETCDV HIRKQQMVSV EETIYIVGG* |
| 3487 | 8984 | A | 3756 | 1 | 1346 | MSAEEMVQIRLEDRCYPVSKRKLIE QSDYFRALYRSGMREALS QEAGGP EVQQLRGLSAPGLRLV L D F I N A G G A REGWLLGPRGEKGGGVDEDEEMD EVSLSELVEAASFLQVTSLLQLLS QVRLNNCLEMYRLAQVYGLPDLQE ACLRFMVVHFHEVLCKPQFHLLGS PPQAPGDVSLKQRLREARMTGTPV LVALGDFLGGPLAPHYPYQGEPPSML RYEEMTERWFPLANNLPDLVNVR GYGSAILDNYLFIVGGYRITSQEISA AHFLQGP/RTNEWLQVASMNQKRS NFKLVAVNSKLYAIGGQAVSNVEC YNPEQDAWNFVAPLPNPLAEFSAC ECKGKIYVIGGYSTRDRNMN ILQY C PSSDMWTLFETCDVHIRKQQMVSV EETIYIVGGCLHEIRGPNRRSSQSED MLTVQSYNTVTRQWLYLKENTSKS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GLNFDLCAP |
| 3488 | 8985 | A | 3757 | 3 | 358 | TNSMPPMMSMSYRICAMLKGE/DV QALRRAHQRNVKHMROQLMDRGL PCHPLPPANINPIRV/DPHPCPIALS HPIYSWSLTLPNKPTSVAVFNYLLS CLTIPFIASFVSLFEKLSAILD |
| 3489 | 8986 | A | 3758 | 1 | 164 | GSTTPAMEFASLFFKILLIDCRD/RG LALLPRLVLSSWPQVIFLPWPPKFL GLRT |
| 3490 | 8987 | A | 3759 | 3 | 280 | FFFETESHSAVARLEYRGITLAHCILC RQGSSNSPASDPQVAGTTGTRHRA QLTFV\FLVQMGFFHFGQAGLELPN LGIHPTSASPKCWDLPA |
| 3491 | 8988 | A | 3760 | 3 | 516 | AQHQPMMNIFPYPVGVHAPLMNIQR NPFNIHPQLPLHLHTGVPLMQVATP TSVSQGLPPPPPPPPSQQVNYIASQ PRWKRNCTKLQIQEKAAQEVKLAI KPFYQNKDITKEEYKEIVRKAVDKV CHSKSGEVNSTKVGNL\VKAYVDQ YEYSRKGSRKLEWGPVSTGKN |
| 3492 | 8989 | A | 3761 | 173 | 411 | |
| 3493 | 8990 | A | 3762 | 438 | 789 | LTWSTPVLPAAPGKYGNFGQ PSSGNTSSSSHSQRPLMAAVKLAES KVSVAVEASADSSKTDKKLQIQEK AAQEVKLAIKPFYQNKDITKEEYKE IVRKAVDKCVLLECSIQKM |
| 3494 | 8991 | A | 3763 | 1097 | 4669 | ILLGTSCGYALAHTQEGEEKKQTS GTSNTRGSRKPAMTTPTRRSTRNT RAETASQSQRSPISDMSGCDAPGNS NPSLSVPSSAESEKQTRQAPKRKSV RRGRKPPLKKKLRSSVAAPEKSSS NDSVDEETAESDTPVLEKEHQPDV DSSNICTVQTHVENQSANCLKSCNE QIEESEKHTANYDTEERVGSSSSESC AQDLPVLVGEEGEVKKLENTGIEA NVLCLESEISENILEKGGDPLEKQDQ ISGLSQSEVKTDVCTVHLPNDFPTC LTSESKVYQPVSCPLSDLSENVESV VNEEKITESSLVEITEHKDFTLKTEE LIESPKLESSEGEIITVDRQSVKSPE VQLLGHVETEDVEIATCDTFGNE FNNIQDSENNLLKNNLLNTKLEKSL EEKNESLTEHPRSTELPKTHIEQIQK HFSEDNNEMIPMECDSECDQNESE VEPSVNADLKQMNENSVTHCSENN MPSSDLADEKVETVSQSPESPKDTI DKTKKPRTRRSRFSPTTWSPNKD TPQEKKRQSPSPRRETGKESRKSQ SPSPKNESARGRKKRSQSPKKDIA RERRQSQRSPKRDTTRESRRSELS PRRETSRENKRSQPRVKDSSPGEKS RSQSRERESDRDQRRERERRTRK WSRSRSHSRSPSRCRTKSKSSSFGR DRDSYSPRWKGRWANDGWRCPRG NDRYRKNDPEKQENENTRKEKNDIH LDADDPNSADKHNDCPNWITEKI NSGPDPRTRNPEKLKESHWENRN ENSGNSWNKNFGSGWVSNRGRGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GNRGRGTYRSSFAYKDQENNRWQ NRKPLSGNSNSSGSESKFVEQQSY KRKSEQEFSFDTPADRSWTSASSW AVRKTLPADVQNYYSRRGRNSSGP QSGWMKQEEETSGQDSSLKDQTNQ QVDGSQLPINMMQPMNVMQQQM NAQHQP MNIFYPVGVHAPLMNIQ RNP FNHPQLPLHLHTGVPLMQVAT PTSVSQGLPPPPPPPPSQQVNYIAS QPDGKQLQGIPSSSHVSNMSTPVL PAPTAAPGNTGMVQGPSSGNTSSSS HSKASNAACKNWQKGKVSVAVEA SAIYSSKTDKKFAKFQEKAAQVVKI WANKPFYQNKDITKEEYKEIVRKA VDKVCHSKSGEVNSTKAAANLVKA YVDKYKYSRKGSLLKKTLEPRVTE KDLG |
| 3495 | 8992 | A | 3764 | 108 | 253 | |
| 3496 | 8993 | A | 3765 | 2 | 283 | RRLFFFETESRSVSRLCSGNSIAHC NLH/LPGSSNSPGSASRVAGITGACH HAQLIFVFLVETGFHHVGGAGLEL L/NLMICPPQPPKVLGLQA |
| 3497 | 8994 | A | 3766 | 1 | 290 | RSTFFFFLERVYCSVTRLCSGTNIS AHCNLR L PGSSGSHASVSQVAGITG AHHHTQPIFVFLVETGFHHIGQAGL ELL/NLMIHPPRPPKVLGLQV |
| 3498 | 8995 | A | 3767 | 234 | 1449 | EPGTHDPHLFLQGLLFWQAGGGEG GDGTGPAGGRQICVPPAALAHVRV PGEFLAQVAAAA*AIHDEQRPGKLH HPPG/ELMQRGVASESYMIVAPPMP SSWSSSGTNGPPSPTNLT*PIVHFIFS APTP/TKKTTTNTAMKTATHIPDVQ SAFCSPHSGTQRGDGLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNACLEAAAGAAAE DSGAARGSLQPAPAPPPGDPAAQA SVSNGEDAGGGAGRELVDLKIWN KTKHDVKFPLDSTGSELKQKHSIT GIPDESRRRGPPAPYQQSQRLEL YAQATEALLKTGAAYPCFCSPQRLE LLKKEALRNHQTPR |
| 3499 | 8996 | A | 3768 | 1 | 8157 | |
| 3500 | 8997 | A | 3769 | 1126 | 1355 | |
| 3501 | 8998 | A | 3770 | 1 | 1611 | MGSRC LNPPPPAHSDTTGKDSFGNI RGAETGQGASACSVTSARVTCGAG SEPHSHRNPGISAQVGLAPSYGAAR GRRRPLALQQSPQERRHVGWNSTR GLLPASLPGTASSQSASATASAALP LKVTGPLARNPTPPWTAAALATR GQRPEKGLFPGPAPFSLGKRKRGRG RTWERRRRVSIETSTCFRPGCERLG AAAGANLSQLASSQRPLRERWVLY TIIMAAAGAPDGMEEPGMDTEAET VATEAPARPVNACLEAAAGAAAE DSGAARGSLQPAPAPPPGDPAAQA SVSNGEDAGGGAGRELVDLKIWN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KTKHDKFPLDSTGSELKQKIHSIT GLPPAMQKVMYKGLVPEDKTLREI KVTSGAKIMVVGSTINDVLAVENTP KDAAQQDAKAEENKKEPLCRQKQ HRKVLDKGKPEDVMPSVKGQERL PTVPLSGMYNKS GGK VRLTFKLEQ DQLWIGTKNGTEKLPMGSIK\NVV\S DPI\EGHEDYHNDGRFQLAPTEA\SY YWVYVWPTQYVDAIK\DTVLGKW QYF |
| 3502 | 8999 | A | 3771 | 482 | 631 | AGGWGPQAPDTPWVGPAQAGRL HPLRSTKRS/MSVPATRTTVPLTVM Q*RRVCRWCWGPLGHWEAHGFLV SGDVNHFGGPAALLL |
| 3503 | 9000 | A | 3772 | 1 | 1579 | |
| 3504 | 9001 | A | 3773 | 3 | 486 | DRYMLTRDYLTVKVWDLNMEARP IETYQVHDYLRSKLCSLYENDCIFD KFECAWNGSDSVIMTGAYNNFFRM FDRNTKRDVTL\EASRESSKPRAVL K\PRRVCVGG\KRRRDDISVGQLGTF TKKIL\HTAWHPAE\NIHLPFAATNN LLHLSRGKVNSDMH |
| 3505 | 9002 | A | 3774 | 72 | 1317 | KLLPAPRQPPRPTNGSPRDPTPAQV* VEAPAGSSQ*TAP/ARRPLRAARTLP AAEAAGLTLRGCFHGDGRACAAL RRWPWRQLRGWGFVPAPPLL RTP AELVG/RSPEPRCPGKVSMAEFLTEF LEIPPFNKQYTESQLRAGAGYILED NEAQVDVLESQFSQLLHQINSTRDF ESIRLAHDHFLSNLLAQSFILLKPS VEEKSEPQDFQEADSWGDTKRTPG VGKEDAAEETVKPGPEEGTLEKEE KVPPPRSPQAQEA PVNIDEGLTGCTI QLLPAQDKAIVFEIMEAGEPTGPILG AEALPGGLRTL PQEPGKPKDEVLR YPDRSLSPEDAESLSVSPSPDTAN QEPTPKSPCGLTEQYLHKDRWPEVS PEDTQSLSLSEESPSKETSLDVSSKQ LSPKALAPFQLGN |
| 3506 | 9003 | A | 3775 | 1 | 350 | FGTRKPGAVGAGEFVSPCESGDNT GEPsALEEQRGPLPLNKLTLFLGYAF LLTMATTSDKLASRSKLPDGPTGSS EEEEEFLEINPPFNKQYQESQLRAGA GYILKEFKEAQVRSFFV |
| 3507 | 9004 | A | 3776 | 3 | 318 | RRGLTLSSRLEYSGLIKTHWNHLHL GSSNPPTSASQVAGTTGTCHHAQLN FF/CLTFLVATRSHDIAQAGLELLDS SHPPASASHSAGTTGVNHHAWPAV ALLWIN |
| 3508 | 9005 | A | 3777 | 4 | 378 | ARNHHDLCFKKAILFFEMESCSVSQ AGVQWRVFGSLQAPPPGFLPFS/CY RCQPPSPANFFLYFLVETGFLF**RQ GFTVLDRMVSI*PRDPPALASQSA GITGVSPRTRQEGHS*R*EENGIG |
| 3509 | 9006 | A | 3778 | 19 | 418 | VEMGFCQADQAGLELLTSGDPPAS VSQSTGITVLSLFFFETESRSVAQA GVQWRDLGSLQRPPPGFTPFSCSL PSSWDYRRPPRLANFFVFSVETGF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HRVSQDGLDLLT/S/GDPPASASQSA GDTGVSQAPV |
| 3510 | 9007 | A | 3779 | 3 | 331 | CFIFYFILFYFETESRSVAQAGVQWR HLDSLQAPPPGFTPFSCSLPSSWDY RRP/PPRPANFFVLLVQTGFHRVSQD GLDLLT/S/GDPLASASQSAGITGLSH RARPAQVS |
| 3511 | 9008 | A | 3780 | 659 | 1092 | AYNIFQFANRTNTGENLPKTLVIKYY SSTFRSFFFFFFLQRQSRVAQAGVQ WRNLGSLQPPPGFTPFSCSLPSSW DYGRPPRPANF/SVFLVETGFHRVS QDGLDLLT/S/GDPPTSASQSAGITG VSHCARPHSVLIKEITQT |
| 3512 | 9009 | A | 3781 | 8 | 295 | GRVSLRHQAGVQWRSLGSLQAPPP RFTPFSCSLRLRSWDHRRPPRPANL LYFLVETGFHRVRQDGLDLLT/S/GD PPALASQSAGITGVSHRAHPTY |
| 3513 | 9010 | A | 3782 | 1474 | 1870 | SARGITGVSHCTRPFSEFFFFFFFETE SHSIAQAGVQWRYLGSLQPLPPGFK QFACLSLSSSWDCRHAPRPANFLAF LVEMGFHHL*LELLISSDPPASAFKS ARITGVSHRAWPIRFFLLKNIFKFLN FC |
| 3514 | 9011 | A | 3783 | 60 | 560 | SDNYEKSHNIQEMTGLQSTLLVNN RVQLNFKWELNFFLSFLKQSSTLVA QAGVQWHDLGSLQPPPGVKRFSC LSLPSSWDYRHVPPCLANFVFLFFL VETGFLHVGQAGPELLTSGGPPASA SQSAGITSVTHRPLPEDSAFYQCRL NLWQRSPLECRCSLVLKT |
| 3515 | 9012 | A | 3784 | 3 | 230 | FFFKTESRSVTRLECSGAVLAHCNL QLPGSSNSPASASRVAGITRHVPPH RLIFVFLVETGFHHVQGQDGLDLLTL |
| 3516 | 9013 | A | 3785 | 3 | 4117 | |
| 3517 | 9014 | A | 3786 | 1 | 457 | FPVRNLDLSTYICIGQKEEQLPSEY YADINHYGGMIGGHYTACAPLPND RSSQRNDVGWRLFDDSTLTTRDQS QAVTRYAYVLFYRRRNSPVERPPK AGHSEHHPDLGPAAEAAASQ/ATRP WPGPRGG/APRGQPLNASPPLWIGQ TPPLKQT |
| 3518 | 9015 | A | 3787 | 1 | 298 | NNQESCSVTEAGVQWHDLGSLQPP PSGFKQFS/CAQLLSSQDHRHMPPCP ANFYVFLIAEMGFYHVSQAGLELL TSSDLPALASQSAGIIGVSHRAWAK |
| 3519 | 9016 | A | 3788 | 3 | 286 | FFFFLFETQSHSHIRLECSGVISDYC NLCLPSSDSLVLASGVAGTMGVR HNARLIFVFLVKMRFHVHGPRLGP QIPWTGIWIPSHFGPPQSA |
| 3520 | 9017 | A | 3789 | 1 | 1422 | |
| 3521 | 9018 | A | 3790 | 353 | 470 | IPGVSLYSLFSLQ/NIPQSTEILKKL MTTNEIQSNIYT |
| 3522 | 9019 | A | 3791 | 1328 | 1615 | VSLFHAGVQWCDLSSLPAPPPGFKR FS/RLNLLSSWDYRRPLPHPSTFCKF VEMGFHHIGQAGLKLLTSGDPPASA SQSARITGVSHRARNCFYVT |
| 3523 | 9020 | A | 3792 | 2 | 114 | CQPGFVMKGPPHVRVQCQALNKWE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TELPSCSR/VCLPEA |
| 3524 | 9021 | A | 3794 | 1940 | 2062 | |
| 3525 | 9022 | A | 3795 | 785 | 892 | |
| 3526 | 9023 | A | 3796 | 1 | 2745 | |
| 3527 | 9024 | A | 3797 | 1 | 3297 | |
| 3528 | 9025 | A | 3798 | 1 | 2202 | |
| 3529 | 9026 | A | 3799 | 1 | 2868 | |
| 3530 | 9027 | A | 3800 | 1 | 3237 | |
| 3531 | 9028 | A | 3801 | 1 | 2001 | |
| 3532 | 9029 | A | 3802 | 1 | 2982 | |
| 3533 | 9030 | A | 3803 | 1169 | 3269 | VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPTVSAQNLLK LMSNFSKVSQYKINVQKSQAFLYT NNRQTESQIMSGLPFTITSKRITYLGI QLTRDVKDLFKENYKPLLKEIKEDT NKWKNIPCSWVGGRINLVKMAILP KVIYRFNAIPIKLPMTFFTELEKTTL KFIWNQKRALIAKSSLSQKNKTGGI TLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNYLIFDK PDKNKQWQKDSL FNKWCWENWL AICRKLKLDPFLTPYTKINSRWIKDL HVRPKTIKTLEENLGNTIQDIGMGK DFMSKTPKAMATKAKIDKWDLIK KSFCTAKETTIRVNRQPTWEKIFA TYSSDKGLISRIYNELKQIYKKKTN NPIKKWAKDMNRHFSEEDIYAACK HMKKCSSSLAIREMQIKTTMRYHLT PVRMVIIKSGNNRCWRGCGEIGTL LHCWWDCCLVQPLWKS VWQFLRD LELEIPFDPAIPLGIYPEDYKPCCYK DTCTRMFIAALFTIAKTWNQPKCPT MIDGIKKMWHIYTM EYYAAIKKDE FMSFAGTWMKLETIILRKLSQGQK TKHRMYSLIGGNLTMRTFGHSAGS HHTPGPIMRCGAGGGIALGEIPNVN DELMGTANQHGT CIPMQQNCTLCT CTLKLV |
| 3534 | 9031 | A | 3804 | 2821 | 5793 | |
| 3535 | 9032 | A | 3805 | 2 | 256 | KRSLSLPSRLECSGVILAHCKLRLLG SRHSPPSDSGAAGTAGARH HARLFF LYFLVFHRVCLDGLDLL/NLVIHLPR SPKVWGLQA |
| 3536 | 9033 | A | 3806 | 1 | 2406 | |
| 3537 | 9034 | A | 3807 | 139 | 6503 | |
| 3538 | 9035 | A | 3808 | 1 | 3204 | |
| 3539 | 9036 | A | 3809 | 77 | 277 | PHPTPCSCFPW SASSPLT*TH\QALT EEDEW*QAKNSGQAAQGQTPALPL GNLGQVTAPLCPRFIC |
| 3540 | 9037 | B | 3810 | 21 | 219 | MMPRSSRTKSCRSSCVAWSSCMKE NKLRAEAERLGHELQQA GLKTKE AEQTCRH LTAQVRS LGGTX* |
| 3541 | 9038 | A | 3811 | 1 | 6359 | MTLHATRG AALLSWVNSLHVADP VEAVLQLQDCSIFIKIIDRIHGT EEGQ QILKQPVSERLDFVCSFLQKNR KHP SSPECLVSAQKVLEGSELELAKMT |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | MLLYHSTMSSKSPRDWEQFEYKI QAELAVILKFVLDHEDGLNLEDLE NFLQKAPVPSTCSSTFPEELSPPSHQ AKREIRFLELQKVASSSSGNNFLSGS PASPMGDILQTPQFQMRRLKKQLA DERSNRDELELELAENRKLLETEKDA QIAMMQQRIDRLALLNEKQAASPL EPKELEELRDKNESLTMRLETLLKQ CQDLKTEKSQMDRKINQLSEENGD LSFKLREFASHLQQLQDALNELTEE HSKATQEWLEKQAQLEKELSAALQ DKKCLEEKNEILQGKLSQLEEHLSSQ LQDNPPQEKGEVLGDVLQLETLLKQ EAATLAANNTQLQARVEMLETERG QQEAKLLAERGHFEEEEKQQLSSLIT DLQSSISNLSQAKEELEQASQAHA RLTAQVASLTSELTTLNATIQQQDQ ELAGLKQQAQEKQAQLAQTLLQQE QASQGLRHQVEQLSSSLKQKEQQL KEVAEKQEATRQDHAQQLATAAEE REASLRERDAALKQLEALEKEKAA KLEILQQQLQVANEARDSAQTSVT QAQREKAELSRKVEELQACVETAR QEQHEAQAQVAEELQLRSEQQKA TEKERVAQEKDQLQEQLQALKESL KVTKGSLEEEKRRAADALEEQQRCI SELKAETRSLVEQHKRERKELEER AGRKGLEARLQQLGEAHQAETEVL RRELAEAMAAQHTAESECEQLVKE VAAWRERYEDSQEEAQYGAMFQ EQLMTLKEECEKARQELQEAKKV AGIESHSELQISRQQNELAELHANL ARALQQVQEKEVRAQKLADDLSTL QEKMAATSKEVARLETIVRKAGEQ QETASRELVKEPARAGDRQPEWLE EQQGRQFCSTQAALQAMEREAEQ MGNELERLRAALMESQGQQQEERG QQEREVARLTQERGRAQADLALAK AARAELEMRLQNALNEQRVEFATL QEALAHALTEKEGKDQELAKLRGL EAAQIKELEELRQTVKQLKEQLAK KEKEHASGSGAQSEAAGRTEPTGP KLEALRAEVSKLEQQCQKQQEQAD SLERSLEAERASRAERDSALETLOG QLEEKQELGHSQSALASARELA AFRTKVQDHKAEDWKAQVARG RQEAERKNSLISSLEEEVSILNRQVL EKEGESKELKRLVMAESEKSQKLEE RLRLAQAETASNSARAAERSSALR EEVQSLREEAEKQRVASENLRQELT SQAERAEELGQELKAWQEKFFQKE QALSTLQLEHTSTQALVSELLSAKH LCQQLQAEQAAAEKRHREELEHSK QAAGGLRAELLRAQRELGELIPLRQ KVAEQERTAQQLRAEKASYAEQLS MLKKAHGLLAENRWLGERANLG RQFLEVELDQAREKYVQELAAVRA DADTRLAEVQREAQSTARELEVMT |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | AKYEGAKVKVLEERQRFQEERQKL TAQVEQLEVFQREQTKQVEELSKK LADSDQASKVQQQKLKAVQAQGG ESQQEAQRLQAQLNELQAQLSQKE QAAEHYKLQMEKAKTHYDAKKQQ NQELQEQLRSLEQLQKENKELRAE AERLGHELQQAGLKTKEVAEQVTCR HLYLPRLRSLEVAQVAHARPSSFRD LGKFQVATDALKSREPQAKPQLDL SIDSLLDSCEEGTPLSITSLPRTQPD GTSVPGEPASPISQRLPPKVESLESL YFTPIPARSQAPLESSLDSLGDVFDQ SGRKTRSARRRTTQINITMTKKLD VEEPDSANSSFYSTRSAPASQASLR ATSTQSLARLGSPDYGNSALLSLP GYRPTTRSSARRSQAGVSSGAPPGR NSFYMGTCQDEPEQLDDWNRIAE QQRNRVCPHLKTCYPLESRPSLSL GTITDEEMKTGDPQETLRRASMQUI QIAEGTGITTRQQRKRVSLPHQGP GTPESKKATSCFPRPMTPRDRHEGR KQSTTEAQKKAAPASTKQADRRQS MAFSILNTPKKLGNSLLRRGASKKA LSKASPNTRSGTRRSPRIATTTASAA TAAAGATPRAKGKAKH |
| 3542 | 9039 | A | 3812 | 241 | 6884 | LSGITKMTLHATRGAALLSWVNSL HVADPVEAVLQLQDCSIFIKIIDRIH GTEEGQQILKQPVSERLDFVCSFLQ KNRKHPSSPECLVSAQKVLEGSELE LAKMTMLLLYHSTMSSKSPRDWEQ FEYKIQAEALAVILKFVLDHEDGLNL NEDLENFLQKAPVPSTCSSTFPEELS PPSHQAKREIRFLELQKVASSSSGN NFLSGSPASPMGDILQTPQFQMRRL KKQLADERSNRDELELELAENRKL LTEKDAQIAMMQQRIDRLALLNEK QAASPLEPKELEELRDKNESLTMRL HETLKQCQDLKTEKSQMDRKINQL SEENGDLSEKREFASHLQQLQDAL NELTEEHSKATQEWLEKQAQLEKE LSAALQDKKCLEEKNEILQGKLSQL EEHLSQLQDNPPQEKGEVLGDVLQ LETLKQEAATLAANNTQLQARVEM LETERGQQEAKLLAERGHFEEEEKQ QLSSLITDLQSSISNLSQAKEELEQA SQAHGARLTAQVASLTSELTTLNAT IQQQDQELAGLKQQAQKEKQAQLAQ TLQQQEQASQGLRHQVEQLSSSLK QKEQQLKEVAEKQEATRQDHAQQ LATAAEEREASLRERDAALKQLEA LEKEKAAKLEILQQQLQVANEARD SAQTSVTQAQREKAELSRKVEELQ ACVETARQEQHEAQAQVAEELQL RSEQQKATEKERVAKEDQLQEQL QALKESLKVTKGSLEEEKRRAADA LEEQQRCISELKAETRSLVEQHKRE RKELEERAGRKGLEARLLQLGEA HQAETEVLRLRELAEMAAQHTAES |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | ECEQLVKEVAAWRDGYEDSQEE AQYGAMFQEQLMTLKEECEKARQ ELQEAKEKVAGIESHSELQISRQQN KLAELHANLARALQQVQEKEVRAQ KLADDLSTLQEKMAATSKEVARLE TLVRKAGEQQETASRELVKEPARA GDRQPEWLEEQQGRQFCSTQAALQ AMERAEQMGNELERLRAALMES QGQQQEERGQQEREVARLTQERGR AQADLALEKAARAELEMRLQNAL NEQRVEFATLQEALAHALTEKEGK DQELAKLRGLEAAQIKELEELRQTV KQLKEQLAKKEKEHASGSGAQSEA AGRTEPTGPKLEALRAEVSKLEQQC QKQQEQADSLERSLEAERASRAER DSALETLGGQLEEKAEQELGHSQSAL ASAQRELAAFRTKVQDHSKAEDW KAQVARGRQEAERKNSLISSLEEEV SILNRQVLEKEGESKELKRLVMAES EKSQKLEE/RLRLLQAETASNSARA AERSSALREEVQSLREVEAEKQ RVA SENLRQELTSQAERAEEELGQELKA WQEKFFQKEQALSTLQLEHTSTQA LVSELLPAKHLCQQQLAEQAAAEEK RHREELEQSKQAAGGLRAELLRAQ RELGELIPLRQKVAEQERTAQQRLA EKASYAEQLSMLKKAHGLLAENR GLGERANLGRQFLEVELDQAREKY VQELAAVRADAETRLAEVQREAQS TARELEVMTAKYEGAKVKVLEERQ RFQERQKLTAQVEELSKKLADSD QASKVQQQKLKAVQAQGGESQQE AQRFQAQLNELQAQLSQKEQAAEH YKLQMEKAKTHYDAKKQQNQELQ EQLRSLEQLQKENKELRAEAERLG HELQQAGLKTKEAEQTCRHLTAQV RSLEAQVAHADQQLRDLGKFQVAT DALKSREPQAK\PQLDLSIDSLDLSC EEG\TPL\SITSKLPRTQPDGTSVPGE PASPISQRLPPKVESLESYFTPIPAR SQAP\LESSLDSLGDVFLDSGRKTR SARRRTTQIINI\TMTKK\LDVVEPD/ SAPNLSFYS\TRSAPASQASLRATSS TQSLARLGSPDYGNSALLSLPGYRP TTRSSARRSQAGVSSGAPPGRNSFY MGTCQDEPEQLDDWNRIAELQQRN RVCPPHLKTCTPLESRPSLSLGTITD EEMKTGDPQETLRRASMQPIQIAE GT\GITTRQQRKRVSLPHQGGPGTPE SKKATS\CFPRPMTPRDRHEGRKQS TTEAQK\KAAPASTKQA\DRROSM/ AFS\LNTPKKLGNSLLRTG*PQRKA LSK\ASPNTSRG\TRRSRPNJATTTASA ATA\AAIGCHPSRPRGKGKALKGPV PVSGPHLCSPMVAVTWSSAYCPSQ CLLSAPRPTVAKPLETVMPARTLA WSLVLHWRLLGAGPGGLEHGQCG RSPYLASFLLKAKSLLHHNQI |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me- thod | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|-------------|-------------------------------------|---|--|---|
| 3543 | 9040 | A | 3813 | 1 | 3466 | EKEKAAKLEILQQQLQVANEARDS AQTSVTQAQREKAELSRKVEELQA CVETARQEQHEAQAQVAEELQLR SEQQKATEKERV AQEKDQLQEQQLQ ALKESLKVTKGSLEEEKRRAADAL EEQQRCISELKAETRSLVEQHKRER KELEEERAGRKGLEARLQQLGEAH QAETEVLRLRELAEAMAAQHTAESE CEQLVKEVAAWRERYEDSQQEAAQ YGAMFQEQLMTLKEECEKARQELQ EAKEKVAGIESHSELQISRQQNELA ELHANLALALQQVQKEVRAQKLA DDLSTLQEKMAATSKEVARLETLV RKAGEQQETASRELVKEPARAGDR QPEWLEEQQGRQFCSTQAALQAME REAEQMGNELERLRAALMESQGGQ QEERGQQEREVARLTQERGRAQAD LALEKAAARAELEMRLQNALNEQRV EFATLQEALAHALTEKEGKDQELA KLRGLEAAQIKELEELRQTVKQLKE QLAKKEKEHASGSGAQSEAAGRTE PTGPKLEALRAEVSKLEQQCQKQQ EQADSLERSLEAERASRAERDSALE TLQGQLEEKAAQELGHSQSALASQA RELAAFRTKVQDHSTAEDWKAQV ARRRQEAERKNSLITILEEEVSILNR QVLEKEGESKELKRLVMAESEKSQ KLEERLRLQLAETASNSARAAERSS ALREEVQSLREEAEKQRVASENLR QELTSQAERAELGQELKAWQEF FQKEQALSTLQLEHTSTQALVSELL PAKHLCCQLQAEQAAAEKRHREEL EQSKQAAGGLRAELLRAQRELGELI PLRQKVA\EQERTAQQLR AEKASYA EQLSMLKKAHGLLAEENRGLGERA NLGRQFLEVELDQAREKYVQELAA VRADAETRLAEVQREAQSTARELE VMTAKYEGAKVKVLEERQRFQEER QKLTAQVEQLEVFQREQTKQVEEL SKKLADSDQASKVQQQKLKAVQA QGGESQQEAQRLQAQLNELQAQLS QKEQAAEHYKLQMEKAKTHYDAK KQQNQELQEQLRTLEQLQKENKEL RAEAERLGHELQQAGLKTKEAEQT CRHLTAQVRTLEAQVAHADQQQLRD LGKFQVATDALKSREPQAKPQLDL SIDSLDLSCEEGLPLSITRSGGSLPPY VCLWSACCLSGCILVR |
| 3544 | 9041 | A | 3814 | 35 | 266 | |
| 3545 | 9042 | C | 3815 | 383 | 628 | MDPSAGVTIVTCLASLFSGRLVRFR CSHDWRNYTERVLLFQWVELKTKC WRHTEAGLKPSHYFLEKMKKTLRE SQATYDRI* |
| 3546 | 9043 | A | 3816 | 2 | 513 | DIYGGDYERFGLQGS AVASSFGNM MSKEKRDSISKEDLARATLVITITNNI GSTA\WLCALNENIDRVVFGNFLR INMVSMKLLAYAMDFWSKGQLKA LFF\VEHQGYLGAVGALLGTVQND |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LMTSRRRGSGRETASQKGQRTKKL LLEKVKVALGRKPSHLWQMNLLGFC |
| 3547 | 9044 | A | 3817 | 29 | 175 | KSRPGTVAHACNPSTLGSRGGRIPAE QEFKTSLGNTVSEPCLYLRKNN |
| 3548 | 9045 | A | 3818 | 171 | 419 | KFFPFQSLWWERRAFPLKGEDMAA LLCQDEKKDQVERSSTAFHGEIFGT SVPENG\HHPKKQSDGMEEYKTFGL GLTNVKKNR |
| 3549 | 9046 | A | 3819 | 2 | 1209 | WPSKETAF\NTTQMPC\QSASTWS SYEHNSESYLLREHVSELDSSFHVS LSLPSDVPLHFHFETLLKKTEIKGNL AENKFVDEYIISPSPVHSTLNQWRN GYSPICKPQIRSESSAQLLQGRKKRH LSETALGERTKL\KEFDFHHTESGSH SNFTAVSNVNVLSRIQNSSRNRTARR R\LRSESSYD\DNIVIPMSL\VAPAK LEKLQYKEILTPSWRMVVLQPLDE YNLGKEEIEDLSDEVFSLRHKKYEE REQARWSLWEQSKWHRNSRAYS KNVEGQDLLLKEYPNFSSSQCA AASPPGLPSNQDLCA\GLPSLNQS QETKSLWWERRAFPLKGEDMAALL CQDEKKDQVERSSTAFHGEIFGTSV PENGHHPKKQSDGMEEYKTFGLGL TNVKKNR |
| 3550 | 9047 | A | 3820 | 7 | 447 | |
| 3551 | 9048 | A | 3821 | 1 | 373 | EQQVLRSTCLGVGAKV/L/VEGMVL QYSTQKGILT/ENHIQEINAQ/TTGLR /KTMLLLDILPSRGPKAFDT/FLDSLQ EFPWVREKLKKAREEAMTDLPAGL EEKGRTGRRMGWGAGEEKGQKCCQ TVGMRT |
| 3552 | 9049 | A | 3822 | 1 | 708 | TPVWWNSLWGRFPNSQDSGCSFSP PPQRYVVADGEMEARDKQVLRSLR LELGAEVLVEGLVLQYLYQEGILTE NHIQEINAQTTGLRKTMLLLDILPSR GPKAFDTFLDSLQEFPPWREKLKK AREEAMTRPCLAVDRLTGIPSHILN SSPSDRQINQLAQLGPEWEPMVLS LGLSQTDIYRCKANHPHNVQSQVV EAFIRWRQRFGKQATFRTLDNGLR AVEVDPSLLLHMLE |
| 3553 | 9050 | A | 3823 | 791 | 1090 | HFLHGPLAQEDKSERERWQ\HLAD\ LADFALA\MKDTLTNNNQSFNNFM LRIGEHTPAGLPSRLPSHAGAWPP TRRDMRLRTTEAIRVGRFTHSQGKE T |
| 3554 | 9051 | C | 3824 | 172 | 243 | MRPSHGPSEQLCSTLSPPIKPRPT* |
| 3555 | 9052 | A | 3825 | 1 | 615 | |
| 3556 | 9053 | A | 3826 | 1 | 596 | PGWEKRMSRSSVVNTQEALPTAAIP RDAKGRVYYFNHITNASQWERPSG\ NS\SSGGKNGQGEP\AV\RC\SHLLV KHSQSR\RPSSWRQ\EKITRTKGGGP GSLINGLHPEDSSSGEEDFESLASQF SDCK/SSAKARG\DLGAFQ\QKVR\Q KPFLKTPRFAL\RTGGDERGPCFTD\ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SGIHILPHLSEGGEPRPGLGAGQGG |
| 3557 | 9054 | A | 3827 | 1 | 295 | ETVFHSVTQSGMQWHNLASLQRLP LRLKQTSLSLLSSWDCRHMPPNL A/NF/CVLRDKISPFPCPGWASNPPG LKQCIGILKYPQALTPYELINIWEGI |
| 3558 | 9055 | A | 3828 | 131 | 771 | MGVILEPSGTTVPLVSSV*LLVWDH GPTRIVGLIIRLGPR/YPLVSSSSKSG RTMPNILDIIASAVENKIPPSKTSKI NVKPELKEEPEESIISAVDENNKLYS DIPHSWICDALQKAFTDKEELLKQQ ASNLHEQKKAGVIFEAEVITLLTS VLKTSSASRTSLSSRHQFAPGATVL YKGDKMVLNLDNRVPTCEKIEA ILKELEKPAP |
| 3559 | 9056 | A | 3829 | 1 | 655 | MPVNAGGKVQESQKPPTLIPEPKDS QANFKSSSEQSLTEWRPNNNLSK EKTEWHVEKSSGKLQAAMASVIVR PSSSTKTDSMPAMQLASKDRVSERS SAGAHKTDCLKLAAGETGRILPN VNSDSVHTKSEKNFQAVSQGSVPSS VMSAVNTMCNTKTDVITSAADTTS VSSWGGSEVISS/CIKYHFLYIIRM CIFKKCQSASGSKTRMQGYLE |
| 3560 | 9057 | A | 3830 | 1 | 515 | LTLENQIKEEREQDNSESPNGRTSPL VSQNNEQGSLRDLLTTTAGKLRV GSTDAGIAFAPVYAMGAPSSKSGRT MPNILDIIASVVENKIPPSKTSKINV KPELKEEPEESIISAVDENNKLYSDIP HSWICEKHILWLRIIIIVIGSFKNV GNKDSLQWFLVCIRK |
| 3561 | 9058 | A | 3831 | 6 | 226 | RKGGFFVDFVRVSNQVAVNMYK QLGYSVYRTVIEYYASNGEPDEDA YGKLPSMAVSPRSRNSYILSTDCSI |
| 3562 | 9059 | A | 3832 | 37 | 611 | SGGGAMTTLRAFTCDDLFRV/FNNI NLDPLTETYGIPFYLAHWPEYF IVAEAPGGELMGYIMGKAEGSVAR EEWHGHVTALSVAPEFRRLGLAA KLMELLEISERKGGIFLVDLFVRV SNQVA\VNMYK\QLGYSVYR\TVIE YYFGPATGEP**GTLIDMRESTFPRD TGERNPIIPLPHPGGGLEDH |
| 3563 | 9060 | A | 3833 | 1 | 191 | MQK*ITAWAPAPMKIKIIASPERKYS VWIGGSIWPQLST/FQQMWISKQEY DESGPSIVHRKCF |
| 3564 | 9061 | A | 3834 | 2 | 1203 | LSRRCQLSHSVLPPLRRRVSLPVAM EEEIAALVIDNGSGMCKAGFAGDD APRAVFPSIVGRPRHQGMVGMGQ KDSYVGDEAQSKRGILTLKYPHIG IVTNWDDMEKIWHHTFYNELRVAP EEHPVLLTEAPLNPKANREKMTQIM FETFNTPAMYVAIQAVLSLYASGRT TGIVMDSGDGVTHTVPIYEGYALPH AILRLDLAGRDLTDYLMKILTERGY SFTTTAEREIVRDIKEKLCYVALDFE QEMATAASSSSLEKSYELPDGQVITI GNERFRCPEALFQPSFLGMESCGIH ETTFNSIMKCDVDIRKDLYANTVLS GGTMYPGIADRMQKEITALAPST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MKIKIIPPERKYSVWIGGSILASLST FQQMWISKQEYDESGPS\VHRKCF |
| 3565 | 9062 | A | 3835 | 3 | 412 | SRFPEGLFQPPFPGMKSCGIHETTF HSH/IKFDVAIR\KDLYANTLLPGGN HQVSGALLTGMQKEIHAPAAQATL RFKIIAPPGSASTRW/VGSGVGSILASL STFQ\QMWISKQEYDESGPLHSSTA KCFLNGLSQIA |
| 3566 | 9063 | A | 3837 | 3 | 480 | SHITVLTNLVNGLNAPVKRHRLAN WIKSQDPPVCFIQETHLTCRDTHRL KIKGWRKIYQANGK/QKKAGVAIL VSDKTDFKPTKI/KRQGHYIMVKGS MQQEEQVLRDPQRDLDSHTMIMGD FNTLLSILDRSTRQKVNKDIQELKSA LHQADLIDIYRTLH |
| 3567 | 9064 | A | 3838 | 1 | 834 | MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNLDYWKYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP T/KKSPGPDGFTAIFYQ\MLEVLAR AIRQEKEIKGIQLVKEEVKLSLFADD MIVYLENPIVSAQNLLKLIGNFSKVS GYKI/NVQKSQAFLYTNNRQTESQI M |
| 3568 | 9065 | B | 3839 | 1 | 543 | MGDFNTPLSTLDRSTRQKVNKDIQE LNSALYQVDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHIVGSKALLSKCK RTEITNCLSDHSAIKLELTIKKLTQN RSTTWKLNLLNLDYWKYKQPSN KHL YANKLENLEEMDKFLDTYTL RLNQEEVESLNRPIRSEIEAITNSLP TKK* |
| 3569 | 9066 | A | 3840 | 1 | 1470 | MEQSWVENDFDELREEGFRRSNFS EVKEESRTQPKEAKNLARRDTHRL KIKGWRKIYEENGKQKKAGVPILVS DKTDFKPTKIKRDKEGHYTMVKGSI QQEELTILNIYAPNTGAPRFIKQVLR DLQRDLDSHTIIMEDFNTPLSTLDRS TRQKVNKDIQELNSALQQVDLIDIC RMLHPKSTEYTFFSAPHHTYSKIDH RVGSKALLSKCKRTEITNCLSDHSA IKLELRIKKLTENRSTAYNLNLL NDYGVHNEMKSEIKMFFETNENKD TTYQNLWDTFKAVEIQTIREYYKH LYRNKLENLEEMDKFLDTYTLPRV NQEEVESLNRPIRSEIEAITNSLP KSPGPDGFTAIFYQRYKEELVPFLL KLFQSIEKEGILPNSFYDASIILPKPG KDTTKKENFRPISLMNIDAKIMNKIL ANQIQQHIKKLIHHDQVGFIPGMQV WFNIGKSINVIQHINRTKDQK\NHRII SIDAEKAF |
| 3570 | 9067 | A | 3841 | 2807 | 4148 | |
| 3571 | 9068 | A | 3842 | 2 | 1516 | WRKIYQANGK/QKKAGVAILVSDK TDFKPIKIKRDKEGHYIMVKGSIQQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EELTILNIHAPNTEAPRFIKQVLSDL QRDLDSHTIIMGDFNTPLSTLDRSTR RKVNKDTQELNSALHQVDLIDIYRT LHPKSTEYTFLSAPHHTYSKTDHIV GSKALLSKCKRSDIITNCLSDHSAIR LELRICKLTQNRSTTWKLNLLND YVWHNEMKAEIKMFFQTENKDT TYQNLWDTFKAEEVKSLNRPITGSE IVAIINSLPTKRSPGPDGFTVEFYQR CRKAFDKIQRPF TLKTLNKL AIDGM YLKIIRAIYDKPTANVILNGQKLEVF PLKTGTGRQGCPLSPLLFNIVLEVLAR AIRQEKEIKGIQLRKEKVKLSLFVD DMIVCLENPIISVQKLLKLISNFSKV SGYKINVQKSQAFLYNNRQTESQI MSELPFTIASKRIKYLGIQLTRDVKG LFKENYKPLLNKIKEGTNKWKNVP CSWIGKINIMKMAILPKETPSHMQR HT |
| 3572 | 9069 | A | 3843 | 3 | 120 | FIIDKKQKQLKSPSIDEWIK\KMWYI HKIEYHSAIKGIKF |
| 3573 | 9070 | A | 3844 | 2 | 244 | SRLSFPSSWDYICAPPHLANFCIFLV ERSVAMLPRLVSSSWAQAILPPWP PKAQGFTGMGHHHAQSAAGLYIFSG LGSNAI |
| 3574 | 9071 | A | 3845 | 1 | 2616 | |
| 3575 | 9072 | A | 3846 | 1 | 773 | QTSPMIPSIVVHCVNEIEQRGLTETG LYRISGCDRTVKELKEKFLRVKTPV LLSKVDDIHAICSLKDFLRNLKEPL LTFRLNRAFMEAAEITDEDNSIAAM YQAVGELPQANRDTLAFLMIHLQR VAQSPHTKMDVANLAKVFGPTIVA HAVPNPDPVTMLQGHQGVQPKVV E\RLFLGLWEYWEFSFMDGWEQG GTFDPLHVIENSNAFSTPQTPDIKAV PGGGLCVHFTAGEAEIQKGPSCGQ NKSTAAFNY |
| 3576 | 9073 | A | 3847 | 1 | 422 | CGRVRACGRVREPSSQIHNNMANL FIRKMVNPLLYLSRHTVKPRALSTF LFG\SIR\SAAPRGCGNPGA\VR\SL SPGLPA\HHL PACGWGFKKQDCPLR KRCKDCYLVK\RRGRWYVYCKT\H PRHKQKTRCRTLFPPESTR |
| 3577 | 9074 | A | 3848 | 1959 | 4060 | RFFSFFFFFETESHVAQAGVQWCN LGSLQAPPPG\SRHSPASASRVAGTT GAHHHARLIFVFLVETGFHRISQDG LDLLTS*SARLGIPKCWDYRCEPPH LASI |
| 3578 | 9075 | A | 3849 | 1 | 1320 | |
| 3579 | 9076 | A | 3850 | 1239 | 1733 | ALFFSFFFFFETESRSVAQAGVQW RDLGSLQAPP\PGSRRSPASASRVAG TTGARHRIFFVFLVEMGFHRDLDFP TS*SA\QGLQA*ATAPGPFLFFFFFFF LRRSLTLLPRLECNGAILARCNLYL LGSSNSPASASRVAGIAGMHHR LIFCILVEMGFHHL |
| 3580 | 9077 | A | 3851 | 131 | 436 | VTHLHQKKGSVFFFFFFFETESCPV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AQAGVQWRDLRSLQAPPPG\SRHSP ASASRVARTTGAHHYTRLIFVCLV ETGFHHVSQDGLDLQDQFPWSLFLF CPP |
| 3581 | 9078 | A | 3852 | 56 | 192 | KFLFSPKALNSVRKFFQYFPPPKKR/ CPSQNSQVG/CLKSPP*GEKF |
| 3582 | 9079 | A | 3853 | 1 | 230 | FQLHQHLLNPKHDYRGWAKWNR NSLYEKMKEGERRK\RRSAIPYLQG QRLDNVVAKKSVQFFPLRVRDPG VKSSC |
| 3583 | 9080 | A | 3854 | 3 | 126 | SCCGVGNQFKGPGGGGGG/RGGG/RR NVSGGGAGGRGWKNERKER |
| 3584 | 9081 | A | 3855 | 1 | 1021 | MPRLEAFVNNQTCPKKECGAASEG DTIGKQSELSFGKAKMARETHWPK KVGKLRSTVVKQLPKTFQAISSTET KDQGPVVPAPVKGEPIVPAPVKDE GPMVSAPIKDQDPMVPEHPKDESA MATAPIKNQGS MVSEP VKNQGLSG\ PGPVKDQDVVPEH*KGHDSALV APW*RIKGPVVPRSPVKNQDPILPV LVKDQGPTVLQPPKNQGRIVPEPLK NQVPIVPVPLKDQDPLVPVPAKDQE P/TLPG/PLGSETAAPVPAHSHSPPPA GSSPAPPRAPGSGRLRLPCSLAPRDLG TRDRAGTVSGALRTMRHPTGGLCQ KGPCWVPPPPLLQIQHFGPP |
| 3585 | 9082 | A | 3856 | 1 | 448 | SSRKDQGLVVS GPVKDQDVVPEH QRSRFSCQV VAPVKNQGPVVPESV KNQDPILPVLVKDQGPTVLQPPKNQ GRIVPEPLKNQVPIVPVPLKDQDPL VPVPAKDQGPVPEPLKTQGP/KGT LSLPTVSPLPRVMIPTAPHTYEIESSP |
| 3586 | 9083 | A | 3857 | 1 | 573 | DPQFISGSPESPIRLWCVGLGNTKVT FTNPKNPVRAVVIHPRHYTFASGSP DNIKQWKFPDGSFIQNLSGHNAINT LAVNFDGGLVFGAANGPMHLWDW ETWAPIFKRVHA\AVQPG\SLDSESG IFACAFDQ\SESRL\TAEADKPIKV YREDDTATEETHPVSWKPEIKRKR FLMNVEFFLSLFFSF |
| 3587 | 9084 | A | 3858 | 1 | 589 | EDLRKCTFIFIIGGPGSGKGTQCEKL VEKYGFTHLSTGELLREELASESER SKLIRDIMERGDLVPSGIVLELLKEA MVASLG DTRGFLIDGYPREVKQGE EFGRRIGDP\QLVIGKE\CSPDT\MTN RL\LQRSRSLPVDDTTK\TMAKRLE AYYR\ASIPVIAYYETKTQLHKINAE GTPEDVFLQLCTAIDSIIF |
| 3588 | 9085 | A | 3859 | 1 | 557 | KLLSPKQPLLRAQLKTLVRLLCFSH AFVGLSKITTWYQYGFVQTQGPKA NILVSGNEIRQFARFMTEKLNVSHT GVPLGEEYILVFSRTQNRLILNEAEL LLALAHEFQMKTVTVPWRTPPLTD VVRLVSNASMLVSMHGAQLVTTLF LPRGATVVELFPYAVNPDHYTPYK TLAMLPGHGTSSM |
| 3589 | 9086 | A | 3860 | 323 | 656 | NEELMPKGRLYPPLANIQEV SINIAI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KVTEYLYANKMGFPDQTQEPEDKA KYVK/EKGTWAEWNMDSLLPDVY EWPEICNQAPPVNTEIEALPLINTFV CSRGTPFFQTRKR |
| 3590 | 9087 | A | 3861 | 1411 | 1799 | GYLQFSFSFFLFFFFFFFLRWSLTLS PRLECSSVISTHCNLRPGSSDSRAS ASQVAGTTGAHHHARLIVCVLVER VFHHVGGAGLEVLTSGGPPTSASQS ARITGMSHHTRPVICSFQFSDDLPEHY F |
| 3591 | 9088 | A | 3862 | 1 | 1007 | MDGGHLFSNLTGKEEVHKGAKLH PNGYRMAQGSETLVARGGPCRSVE PSAASPQELRGWWEAQALKRWGL MGGVWVMEVDPSWLGAISAIWSSS ASRLKSVWHIPCPHFLLRPQLKE AQRKKQLEERCVEESIGNAVLT WNNEILPNWETMWCSRKVRDLWW QGIPPSVRGKVWSLAIGNELNITHEL FDICLARAHERWRSLSLGGSEVENE GLCVAVCAQQGHVGVMGFGSDEP SAVSPCEKGKSLAAWVLIFVDFRVG LQKSFQKRKERESTKLQQLWSWCL MLTYFAAFEVFFEENLPKLFHFHKK NNLTPDIYLID/W*FRLLVGC |
| 3592 | 9089 | A | 3863 | 1 | 1857 | |
| 3593 | 9090 | A | 3864 | 1 | 840 | GIPAADR/EASLELIKLDISRTFPNLCI FQQGGPYHMLHSILGAYTCYRPD VGIVVQGMFIAAVLILNLDTADAFI AFSNLLNKPCQMAFFRVHDHGLMLT YFAAFEVFFEENLPKLFHFHKKNNL TPDIYLIDWIFTLYSKSLPLDLACRI WDVFCRDGEEFLFRTALGILKLFED ILTKMDFIHMAQFLTRLPELPAEE LFGPSIATIQMSRNKKWAQVLTAL QKDSREMREGKSVPTLRLQREFAL GTNQSPMPRLCCFRLTPGQPRRTD AL |
| 3594 | 9091 | A | 3865 | 3 | 288 | FFFEMESLYVTRLNCSGTITISVHC NLCFPGSSDPASASQIAGITGRHH AQLILVFLVEMGFC/HISTKQMEVIH PPWPPKVLGLQVVTHDVL |
| 3595 | 9092 | A | 3866 | 285 | 489 | |
| 3596 | 9093 | A | 3867 | 3 | 425 | GSSDPPASAFQVAGSISVCHHTQLIF VFLVEVEFHVSQASLQL/RDLSLPS SWDYRRPPRPANFFVFLVEMGFH HLNKAIKSFACNEIQPLSAVSVARA GWGVFEYVSVYFLCSNSDYFSSNPS IANWMREWPLRLSLF |
| 3597 | 9094 | A | 3868 | 1 | 156 | APHPAN/FAFLVEMEFHDVGQGD QLLASSDLPASASQSAGITGVSHCN WI |
| 3598 | 9095 | A | 3869 | 1 | 526 | LAESGEGVLVSGGSLRLPCIASRFIF SSYYMSGVRQAPGKGLEWVSFIRA TSVRGRFTMSRDESKNITYLQMKSL RRGMFRGDLG/DWPGGDGHWGAL RIWEPLWIFRCLWKMGLRLGASDG VTEPGGLGSHIWTRCLNKPGLVLM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AEECVSGAVSVGLQDRCTAANRAI FSLEL |
| 3599 | 9096 | A | 3870 | 2 | 353 | |
| 3600 | 9097 | A | 3871 | 136 | 315 | FKYVLSFLFLASGDGESLDEDESEFTL ARDFEIGHFFRERIVPRAVLYFTGE AIEDDDNV |
| 3601 | 9098 | A | 3872 | 132 | 1552 | GDKNIQMADHSFSDGVPSDSVEAA KNASNTEKLTQVMQNPVLAALQ ERLDNVPHTPSSYIETLPKAVKRRIN ALKQLQVRCAHIEAKFYEEVHDL RKYAALYQPLFDKRREFITGDVEPT DAESEWHSENEEEKLAGDMKSKV VVTEKAAATAEPPDPKGIPEFWFTIF RNVDMSELVQEYDEPILKHLQDIK VKFSDPGQPMFVLEFHFEPNDYFT NSVLTKTYKMKSEPDKADPFSFEGP EIVDCDGCTIDWKKGKNVTVKTIK KKQKHKGRTVRTITKQVPNESFFN FFNPLKGKSVASGDGESLDEDESEFT LASDFEIGHFFRERIVPRAVLYFTGE AIEDDDNFEEGEEGEEEGLEGDEEG EEDDDAEFNPVKVLIFFLLIHTFSRR DPSQPAECKQQYAEAGAWQTGCR DSRPVGGASVLAQAQSRGQSLHL TRFQVHDFHFHSFFLLILNLYSGN |
| 3602 | 9099 | A | 3873 | 171 | 324 | |
| 3603 | 9100 | A | 3874 | 3 | 383 | |
| 3604 | 9101 | A | 3875 | 2 | 314 | FFFFISALKALFAFLQILLFQVNVLR TAHIVISFINLLSVTPSKAFLLAFIF CREDYSFTAYATISYLKIGPKANLL NNEAYVITMQVTKSTQNSFRVNG Y |
| 3605 | 9102 | A | 3876 | 3 | 319 | TESRSVPQLGVQWRDLGSLQPPPPG FTRFSCSLPSSWDYRHTPPRPANFL VFLVETGFRHVGQTGLELLTSGDPP ASASQSAGILCVLCTSTLGNHREHI YRMV |
| 3606 | 9103 | A | 3877 | 118 | 1341 | |
| 3607 | 9104 | A | 3878 | 1 | 214 | GFTSSLACMQMGEMFMGFTCQTH LLALGCALFTAYLGVGMANFMAE GTCERRIVGKKKASITKDHOQRRI |
| 3608 | 9105 | A | 3879 | 1 | 176 | MRTFALLTAMLLVA/HAQAEPLQ ARADEAAAQEQPGADDQEMAHAF TWHESAALPLSA |
| 3609 | 9106 | A | 3880 | 3 | 125 | AASTFLFPNLKNSLRGSLRTFSSVT NVRKTALTWLNSQDI |
| 3610 | 9107 | A | 3881 | 1169 | 1512 | YTQKNWHLFCFIFLRWSFVLVAQP GVQWCNLSLQPLPPRFR*FSCLSLL SSWDYRCAPPRPANF/SVFLVETGF HHVGQADLELLTSGDLPTSASQSAG ITGVSHCTWPDILYEI |
| 3611 | 9108 | A | 3882 | 43 | 347 | AGVQ*CDLG*LQLPLGFK*FSCLSL PSSWDYRRLPPRPANF*FLVETGFH HVGQADLELLTSGDSPASASQSAGI TGMSHRAGPI*KSFLKYSTNKLRTT |
| 3612 | 9109 | A | 3883 | 10900 | 11295 | KPWVNETGKLFQDSYSSISHILSGF SFPSFFSETESCSVTQAGVQWHDLS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SLKPLPPGFKQFSCSLPSSWDYRR VPTRPANF/SVFLLETEFHRVSQDGL DRLT/S/GDPPSSASQSAGITGVSHRA RPHSPHF |
| 3613 | 9110 | A | 3884 | 3 | 227 | RFSCSLSSSWDYRAPPPRLANFCI LVETGFHHAGQTGLELLTSGDPPAS ASEIAGITGMSHHTQPGQLLWECC |
| 3614 | 9111 | A | 3885 | 2 | 296 | KWSSALVAYAGVTWHHLGSLRSP PGFKRFCCLSLPSSWDYRHAPPPA/ NFFVFLVKTGFLHVGQAGLELPISG DPPALAPKQSAWIRGVSHRAQPQN |
| 3615 | 9112 | A | 3886 | 1 | 162 | LGGLVFPSEVVCK/RKLDGMQLIKV HLDKAQQNNVENKAETFSGVCKK HRDLMA |
| 3616 | 9113 | A | 3887 | 2 | 474 | |
| 3617 | 9114 | A | 3888 | 2 | 592 | STGKFSQEKAMFSSSAKIVKPNGEK PDEFESGISQALLELEMNSDLKAQL RELNITAAKEIEVGGGRKAIHFVPVP QLKSFQKIQVRLVRELEKKFQWES MSVFIAQRRILP/KPTRKSRTKNKQ KRPRSRTLTAVHDAILEDLVFPSEIV GKRIRVKLDGSRLIKVHLDKAQQN NVEHKVETFSGVYKKHRDLMA |
| 3618 | 9115 | A | 3889 | 1 | 93 | GFTMLP/RLVLNSWVQMCLPWP MLSLQA |
| 3619 | 9116 | A | 3890 | 1 | 252 | PTLEQYAMRAFADALEVIPMALSE NSGMNPIQTMTEVRAR/QDMKQQH VIETLIGKKQQISLATQMVRMILKID DIRKPGSEEE |
| 3620 | 9117 | B | 3891 | 18 | 1121 | MASMGTLAFDEYGRPFLIKDQDRK SRLMGLEALKSHIMAAKAVANTMR TSLGPNGLDKMMVDKGDVTVTN DGATILSMMDVDHQIAKLMVELSK SQDDEIGDGTGTVVVLGALLEEA EQLLDRGIHPRIADGYEQAAARVAIE HLDKISDSVLVDIKDTEPLIQTAKTT LGSKVVNSCHRQMAEIAVNAVLT ADMERRDVFELIKVEGKVGGRLE DTKLIKGVIVDKDFSHQPMPKKVED AKIAILTCPFEPKPKTKHKLDVTSV EDYKALQKYKEKFEEMIQQIKETG ANLAICQWGFDDANHLLQNNLP AVRWVGGEIELIAIATGGRIVPRFS ELTAEKLGFAGLDKRISFGDT* |
| 3621 | 9118 | A | 3892 | 1 | 282 | LPSSHTIPGYP/NPLHPRFPSSRLPP GIIGGEYDQRPTLPYVGDPISLIPGP GETPSQFPPLRPRFDPV/GPNDRFPF RPSRGRPTDGRLSFM |
| 3622 | 9119 | A | 3893 | 3 | 166 | PRPFPKSRLPPGIIGGEYDQRPNPILP /GRGGPNDRFPFARPSRGRPTDGRLS FM |
| 3623 | 9120 | A | 3894 | 101 | 1926 | SPVRGRRRLGRELLGPAAVPVAAS GSRPLGPPAAVMRLRVRLKRTWP LEVPEPETLGHLSHLRQSLCTW GYSSNTRFTITLNYKDPLTGDEETL ASYGIVSGDLICLILQDDIPAPNIPSS TDSEHSSLQNNQPSLATSSNQTSM |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | QDEQPSDSFQGQAAQSGVWNDDS MLGPSQNFEAESIQDNAHMAEGTG FYPSEPMCLCESVEGQVPHSLETLY QSADCS DANDALIVLIHLLMLESgy IPQGTEAKALSMPEKWKLSGVYKL QYMHPLCEGSSATLTCVPLGNLIVV NATLKINNEIRSVKRLQLLPESFICK EKLGENVANIYKDLQKLSRLFKDQ LVYPLLAFTRQALNLPDVFGLVVLP LELKLRIFRLLDVRSVLSLSAVCRDL FTASNDPLLWRFLYLDRDNRDNTVR GQD TDWKEL YRKRHIQRKESPKGR VFM LLLPSSTHTIPFYFNP LHP R PFP SSRL\PPG\NGGEYDPK T NTFPMLGD PISSLIPWVLGETPQPSFPPTETHALN PSWPPISRD PNPQSCPGAEGGPPN/R TRFPPLRPQPGGRANLMAGLVISCG LDLLIFISWSLPPVFCFLNYRCQRPW GADLRVLFS |
| 3624 | 9121 | A | 3895 | 2 | 442 | LSQLCGDPQRFDDFLRAYVEKYKF TSVVAQDLLDSFLSFFPELKEQSVD CRAGPPLAEPDLSQGSSLTRPVEAL FQL/WTAEPDQAAASASAI DISKW RTFQTALFLDRLLDGSPLPQEVVMS LSKCYSSLLDSMNAEIRIRWLQIV |
| 3625 | 9122 | A | 3896 | 1 | 1035 | GEFLVIDVIHEVAHSWFGNAV TNAT WEEMWLSEGLATYAQRITTETYG AAFTCLETAFRLDALHRQM KLLGE DSPVSKLQVKLEPGVNPSHLRNLT YEKG YCFVYLSQLCGDPQRFDDF LRA YVGE\YKFTSVVAQDLLDSFLS FFPELKEQSVD CRAGLEFERWLNAT GPPLAEPDLSQGSSLTRPVEALFQL WTAEPDQAAASASAI DISKWRTFQ TALFL\DRLLDGSPLPQEVVMSLSK CYSSLLDSMNAEIRIRWLQIVVRND YYSLT/FHRVRRFPGRARCHACYTIP LYEDLCTGALKSFALEV FYQTQGR L HPNLRRAIQQILSQGLGFQHRARP |
| 3626 | 9123 | A | 3897 | 2 | 912 | CSRSSRTGGW WPAPCSAASRRPTPG PAAAAAATTD/VVTAGCGFGKDFR KGLLKKGACYGDDACFVARHRS A DVLGVADGVGGWRDYGVDPSQFS GTL MRT CERLVKEGRFVPSNP I GILT TSYCELLQNKVPLLGSSTACIVLD RTSHRLHTANLGDSGFLVVRGGEV VHRSDEQQHYFNTPFQLSIAPPEAE GVVLSDSPDAADSTSFVQLGDIILT ATDGLFDNMPDYMILQELKKLKNS NYESIQQTARSIAEQAH E LAYDPNY MSPFAQFACDNLNVRGGKPDDIT VLLSIVA EYTD |
| 3627 | 9124 | A | 3898 | 2 | 220 | YMSKKFSALLQSQERNCLIIINWCSS LCLRVRLYL RQVTVIPRICKVSD\SP CAPEADAMFAFNADGVGDAKG |
| 3628 | 9125 | A | 3899 | 1 | 346 | SANATTKTSETNHTSRPRLKNVDRS TAQQLAVTVGNVTVIITDFK\EKTRS SS\TSSSTVTS\SAGS\EQQN\QSSSGV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QRAPDKGLPPRSLPTPKGDMSIAVN DEIFPEIATWNCEKL |
| 3629 | 9126 | A | 3900 | 76 | 368 | |
| 3630 | 9127 | A | 3901 | 1 | 1182 | MFAKGRGSAVPSDGGQAWEKLASV VVEYLLHVRVQKSAETFLSEIRWEK NITLGEPPGFLHSWWCVFGDLYCA APQRRDTCEHSSEAKAFHDYSAAA APSPVLGNIPPNDGMPGGPIPPGFFQ GPPGSQPSPHAQPPPHNPSSMMGPH SQPFMSPRYAGGPRPPURMGNQPPG GVPGITQPLL\NSMDPTRQQGH\N MGGSMQRMNPSRPLGPMGPRPHR ITGSGMRPPPNLSLGA\MP\GINMGP GAGRPWPNPNSANSIPYSSSSPGTY VGPPGGGGPPGTPIMPSPADSTNSS DNI\YTM\NPV\PPGGSRSNFQMGGP STGPMDSMGGMEPHHMIG\SLGSG DIDGLPKIFPNNISGISNPPGTPRDDG ELGGNFLHSFQNDNYSPTMTMSV |
| 3631 | 9128 | A | 3902 | 2 | 470 | IPTFGLPGSIQSDNGP\SFISQITQQVS QSLGIQWRLHIPCWPTSGKVERAN GILKAQLTKLTLEVQKPWDL\LLPH RHWESIRRP/GPKGTLLSFSSIWSLIY GTPFPLT\NRPPSNSQLGGIPSQQSSL MEVIFLWPTRPTRAFFPKPHGGGLPIP K |
| 3632 | 9129 | A | 3903 | 69 | 523 | PLGCASSQSIASRNTLCTTASSCCP QVLAHS\KAAEYMTRWKVQQMPH SQDRALQSVFCAPFHS**LVALPTG HR*MTPAQFSECFQATSGGSD*DPF LAPSFL\VPGLPVAPGLLLPLGPVHS RATMEEGQATHEELTVFIGLRPGVR GS |
| 3633 | 9130 | A | 3904 | 101 | 1469 | RTHPTFPHPGTGPTSAPPSGALEGTA GTITSNEWSSPTSPEGSTASGGSQAL DKPIDNDGEGVWSPDIEQSFQEALA IYPPCGRRKILSDEGKMYGRNELIA RYIKLRTGKTRTRKQVSSHQVRLAR RKAREIQAKLKDQAAKDQALQSM AAMSSAQIISATAFHSSMRLARGPG RPAVSGFWQGALPGQAETSHDVKP FSQQTYAVQPPLPLPGFESPAGPAPS PSAPPAPPWQGR\SVASSKLWMLEF SAFLEQQQDPDTYNKHLFVHIGQSS PSYLRPYLEAVDIRQIYDKFPEKKG GLKDLFERGPSNAFFLVKFWADLN TNIEDEGSSFYGVSSQYESPENMIIT CSTKVCSFGKQVVEKVETERYE NGHYSYRIHRSPLCEYMINFIHKLK HLPEKYYMMNSVLENFTILQVVTNR DTQETLLCIAVFEVSASEHGAQHH IYRLVKE |
| 3634 | 9131 | A | 3905 | 1 | 1290 | |
| 3635 | 9132 | A | 3906 | 2 | 270 | ISLADLKEGPHTHLKPPDYSVAVQR SKMMHNSLSRLPPASLSSNLVACVP SKIVTQPQRHNLQPFHPKLGDVTD DSEED\ENEQVSAV |
| 3636 | 9133 | A | 3907 | 2 | 288 | RWGLALSLR/AGAQWFHHGSLQPQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PPMLKSSSRSLPSSRNHRHTQPCPA NFFIFVEMGFHHVAQAGLELLSSLT VWASQSAGITGVSHRTHPLLS |
| 3637 | 9134 | A | 3908 | 3 | 222 | FFFETESRSVTRLECSGTISAHCKLH LPGSCHSPASASRVAGTTGAHCHTQ RIFVEMGFHRVSQDGLDLKNL |
| 3638 | 9135 | A | 3909 | 3 | 175 | GTSPKDCEVRDFCPSEGLYST*WGG SILPSLDT/FKKMWVSKKKYEEDGA RSIHRKTF |
| 3639 | 9136 | A | 3910 | 2 | 533 | RAAEFFEFETFNVPALFISMRAVLSLY ATGRTTGVVLDSEGDVTHAVPIYE GFAMPHSIMCIDIADRDVSRFLRL YLRK\EGYDFHSS\SEFEIVKAIKERA CYLSINP\QKDETLETEKAQYYLPD GSTIEISAPQERLYSTWIGGSILASLD TFKKMWVSKKEYEEDGARS IHRKT F |
| 3640 | 9137 | A | 3911 | 1 | 1213 | EFGALRRTRLGSSFPRRRDSSAMES YDVIANQPVIDNGSGVIKAGFAGD QIPKYCFPNYVGRPKHVRVMAGAL EGDIFIGPKAEHRGLLSIRYPMEHG IVKDWNMERIWQYVYSKD\QLQT F\SEHPVLLTEAPLNPRKNRERAAE VFFETFNVPALFISMQA VLSLYATG R\TTGVVLDSDGDVTHAVPIYEGFA MPHSIMRIDIAGRDVSRLRLYLRLK EGYDFHSSSE\FEIVKAIKERACYLF HKTPKRD\ETLETEKASVTTWLDGS TIEIGPFR\FRAP\ELLFGPRI*LEKESE G\HEVPGVRPFRKSDMGPAGARLF SNIVL/SQGGSTPVQKFSSLPISGFGD RLLC*VKKLAPKDVKIRISAPQERH VYPRGLGGSILASLDTFKKMWVLQ KGD MR*DGSTIEIGPFRIPGPLSCSSG PEFDWKRKVKASHEVPGVRPFRKS DMGPAGARLFSNIVLFREALPLFKS SPLCPFQVLVTGSFVIVKKLSSKRCE DQDICTSGETCISTWIGGLHPCLP GH HLRRCGCSKKEI |
| 3641 | 9138 | A | 3912 | 2 | 262 | LEKRSHSVTKLGYSGVIIAHCSLNF LSSSQPPTSASQTAGTTGICHSTQLIF KIFLVEMG/LHYVAQAGLDLLGSSN VEPPKVLLGL |
| 3642 | 9139 | A | 3913 | 1379 | 2175 | TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQEQRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPW CY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCV AHPHSW PWQVSLRTRSPRPSSYK VILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLSPNYVVA DRTECFITGWGETQEHFYFN |
| 3643 | 9140 | A | 3914 | 1 | 387 | TPEKEPPLWHAFTKEELVQKLSST TKSADQLNG\LLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKP GSERESLLPVINT |

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|---|---|-------------|-------------------------------------|---|--|--|
| | | | | | | MLQLSPEEKGKLAAVAQGLQETSIP KKK |
| 3644 | 9141 | A | 3915 | 360 | 885 | NV FV LLEA NQRTSTVTLATVSASGQ MPST EFGGLDSSI QKLI AIAH FILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQE QPRHFYFLNM RF/DDSL LGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRS AFQTLF |
| 3645 | 9142 | A | 3916 | 1669 | 4914 | |
| 3646 | 9143 | A | 3917 | 1379 | 2175 | TTAGIQMPIKAPGVLPQTPASGGST AT*KNAQE QKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPW CY TTNPRKLYDYCDVPQCAAPS FDCG KPQVEPKKCPGRVVGCV AHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN |
| 3647 | 9144 | A | 3918 | 1 | 387 | TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK |
| 3648 | 9145 | A | 3919 | 360 | 885 | NV FV LLEA NQRTSTVTLATVSASGQ MPST EFGGLDSSI QKLI AIAH FILNH RELGFLEKASSKSTLGFSPASDETFG PVSDHIIWGWQTSWDYFVSDDGRT A*L*QGNIFSCGLQE QPRHFYFLNM RF/DDSL LGVHPG*PCRMKALGTSP SSGQQSTPTLGISRCLHRS AFQTLF |
| 3649 | 9146 | A | 3920 | 1669 | 4914 | |
| 3650 | 9147 | A | 3921 | 1 | 246 | FLETEFHSAQAGVQWCHLGS LQP PPPGFKQLS\CLSLPSSWDYRGTPPY LANFCIFSRDGVSLCWP GWSQTPDL KQSSGNL |
| 3651 | 9148 | A | 3922 | 10 | 476 | DRVLLSVAQAGLQWRDLGSLQPPP P/GFKRFSCLSLPNSWDYRCVPPCLA NFFVFLVETGFHHVGQAGLELLTSG DPPLPQPPKVLGAGITGMSHTWLI SLIFYQTKWRQTAIASVGIPGSPLCH PLPLIRKGVAGKAVLCPRKDGHTH KTQLRP |
| 3652 | 9149 | A | 3923 | 2 | 465 | ARARADSARAARA EFEDIMKRNRA ISSSPISKAVSGASAGDYSDAIETLLT AIAVIKQSRVAK\DERCRLISS LKD CLHG\IEGQVPTVWGAQLGALS RKR HPFPGERSPASRSRETSRRHRDLLHN EDR\HDDYFQERNREHERHRDRER DRHH |
| 3653 | 9150 | A | 3924 | 3 | 218 | LPPPLSNIHSTLSTPFLPPAPL/SP/YP SRASPPSTYSPLPTPPPLPTS QPSTPT LPLPTPPCSTPSGQALFF |
| 3654 | 9151 | A | 3925 | 1379 | 2175 | TTAGIQMPIKAPGVLPQTPASGGST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AT*KNAQEQKRVL*HL/QPVVLLPD VETPSEEDCMFGNGKGYRGKRATT VTGTPCQDWAAQEPHRHSIFTPETN PRAGLEKNYCRNPDGDVGGPWYCY TTNPRKLYDYCDVPQCAAPSFDCG KPQVEPKKCPGRVVGCVAHPHSW PWQVSLRTRSPRPSSYKVILGAHQE VNLEPHVQEIEVSRLFLEPTRKDIAL LKLSSPAVITDKVIPACLPSPNYVVA DRTECFITGWGETQEHFYFN |
| 3655 | 9152 | A | 3926 | 1 | 387 | TPEKEPPLWHAFTKEELVQKLSST TKSADQLNGLLRETEATHAVLME QIKLLKSEIRRLERNQEESAANVEH LKNVLLQFIFLKPGSERESLLPVINT MLQLSPEEKGKLAAVAQGLQETSIP KKK |
| 3656 | 9153 | A | 3927 | 360 | 885 | NV FV L L E A N Q R T S T V T L A T V S A S G Q M P S T E F G G L D S S I Q K L I A I A H F I L N H R E L G F L E K A S S K S T L G F S P A S D E T F G P V S D H I I W G W Q T S W D Y F V S D D G R T A * L * Q G N I F S C G L Q E Q P R H F Y F L N M R F / D D S L L G V H P G * P C R M K A L G T S P S S G Q Q S T P T L G I S R C L H R S A F Q T L F |
| 3657 | 9154 | A | 3928 | 1669 | 4914 | |
| 3658 | 9155 | A | 3929 | 1 | 1542 | |
| 3659 | 9156 | A | 3930 | 3 | 1771 | |
| 3660 | 9157 | A | 3931 | 2 | 1869 | RLVVVEAKMAAAQAAAAQAAAA QAAQAEAADSWYLALLGFAEHFRT SSPPKIRLCVHCLQAVFPFKPPQRIE ARTHLQLGSLVLYHHTKNSEQARSH LEKAWLISQQIPQFEDVKFEAASLLS ELYCQENSVDAAKPLLKAIQISQQ TPYWHCRLLFQLAQLHTLEKDLVS ACDLLGVGAEYARVVGSEYTRALF LLSKGMLLLMERKLQEVHPLLTL GQIVENWQGNPIQKESLRVFFLVLQ VTHYLDAGQVKSVPCKLQQLQCCI QTISTLHDDEILPSNPADLFHWLPKE HMCVLVYLVTVMHSMQAGYLEKA QKYTDKALMQLEKLKMLDCSPILS SFQVILHEHIIMCRLVTGHKATALQE ISQVCQLCQQSPRLFSNHAAQLHTL LGLYCVSVNCMDNAEAQFTTALRL TNHQELWAFIVTNLASVYIREGNRH QEVVLYSLLERINPDHSFPVSSHCL RAAAFYVRGLFSFFQGRYNEAKRF LRETLKMSNAEDLNRLTACSLVLL GHIFYVLGNHRESNNMGG\PAMQL ASKIPDMSVQLWSSALLRDLNKAC GNAMDAHEAAQMHNFSQQLLQD HIEACSLPEHNLITWTDGPPPVFQFQ AQNGPNTSLASLL |
| 3661 | 9158 | A | 3932 | 2 | 614 | |
| 3662 | 9159 | A | 3933 | 1 | 4992 | VSSNNVLLNSQADDRVVINKPESAG FRDVGSEEIQDAENSAKTLKEIRTL MEAENMALKRCNFPAPLARFRDIS DISFIQSKKVVCFKEPSSTGVSNGDL LHRQPFTEESPSSRCIQKDIGHTQTNL |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|--|---|--|--|
| | | | | | | KCRRG IENWEFISSTTVRSPLQEAE KVSMALEETLRQYQAAKSVMRSEP EGCSGTIGNKIIIPMMTVIKSDSSSD ASDGNGSCSWDSNLPESLESVSDVL LNFFPYVSPKTSITDSREEEGVSESE DGGGSSVDSLAAHVKNLLQCESSL NHAKEILRNAEEEEESRVRAHAWNM KFNLAHDCGYSISELNEDDRRKVEE IKAELFGHGRTTDL SKGLQSPRGMG CKPEAVCSHIIIESHEKGCFTLTSE HPQLDRHPCAFRSAGPSEMTRGRQ NPSSCRAKHVNLSASLDQNNSHFK VWNLSQLKSHSPFQNFIPDEFKISKG LRMPFDEKMDPWLSELVEPAFVPP KEVDFHSSSQMPSPPEPMKKFTTSITF SSHRHSKCISNSSVVKVGVTESQC TGASVGVFNHFTEEQNPPRDLKQK TSSPSSFKMHSNSQDKEVTILAEGR RQSQKLPVDFERSFQEEKPLERSDF TGSHPSTRANC SNFKEIQISDNHT LISMGRPSSTLG VNRSSSRLGVKEK NVTITPDLPCIFLEQRELFEQSKAP RADDHVRKHHSPSPQH QDYVAPDL PSCIFLEQRELFEQCKAPYVDHQMR ENHSPLPQQQDSIASDLPSPISLEQC QSKAPGVDDQMNKHHFPLPQQGD CVVEKNNQHKPKSHISNINVEAKFN TVVSQSAPNHCTLAASASTPPSNRK ALSCVHITLCPKTSSKLD SGTLDERF HSLDAASKARMNSEFNFDLHTVSS RSLEPTSK\LLTSKPVAQDQESLGFL GPKSSLD FQVVQPSLPDSNTITQDL KTIPSQNSQIVTSRQIQVNISDFEGHS NPEGTPVFADRLPEKMKTPLSAFSE KLSSDAVTQITTESPEKTLFSSEIFIN AEDRGHEIIEPGNQKL RKAPVKFAS SSSVQQVTFSRGTDGQPLLLPYKPS GSTKMYYPQLRQIPSPDSKSDTT VESSHSGSNDIAIPDFPAQVLGTRD DDLSATVNIKHKEGIYSKRVTKAS LPVGEKPLQENADASVQVLITGDE NLSDKKQQEIHSTRAVTEAAQAKE KESLQKDTADSSAAAAAEHSAQVG DPEMKNLPDTKAITQKEEHRKKTIV PEEAWPNNKESLQINIEESECHSEFE NTTRS VFERSAKFYIHPVHLPSDQDI CHESLGKSVFMRHSWKDFFQHHPD KHREHMCLPLPYQNM DKTCTDYT RIKSLSINVLGNKEVMDTTKSQVR DYPKHNGQISDPQRDQKVTP EQTT QHTVSLNELWNKYRERORQQRQPE LGDRKELSLVDRLDRLAKILQNPIT HSLQVSESTHDDSRGERSVKESWG RQQQRNKLQKKRFRKSLEKSHKNT GELKKS KVLSHHRAGRSNQIKIEQI KFDKYILSKQPGFNYISNTSSDCRPS EESELLTDTTNNILSGTTSTVESDILT QTDREVALHERSSSVSTIDTARLIQA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FGHERVCLSPRIKLYASSITNQQR\RYLEKRSKH\SKESAGLTGHPLVTSEHTRRRHIQPPTSATACRQPLMTFCFYGFAYSGPFI |
| 3663 | 9160 | A | 3938 | 2 | 354 | NRILVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIFPEKPLALSGKSFLQLEALLPPRQKVITDDMDQVELKEFCPNEQNWRQHREAYEEDGDPQAGVQFQTA |
| 3664 | 9161 | A | 3939 | 204 | 374 | DHGFLIPLTQGDQKGP\RVHPL*ACYHWNQREKVISSCIGCICMSQIKDPLVKKKKK |
| 3665 | 9162 | A | 3940 | 39 | 385 | AGVQWRDLSSPQPPPPGFKRVSCSLPSSWDYRPQPRLANFC/DFLVEMGFCHVDQVAGLELLTSGDPPASASQSGITGVSHRTQPCLLFLKTKTWGKWEKDGMFWEMNGAQDQQE |
| 3666 | 9163 | A | 3941 | 1 | 200 | FETGSYSVT\RLVFSVQISAH\CNLCLPGSPDPPTSASEVVGTSVCHR\TQLIYIYPLQLPKLFRLOV |
| 3667 | 9164 | A | 3942 | 2 | 458 | LFYGVYFLFPLNSCILFVSFTVNH\LIQIFFFGGGMKSWSVRRLECSGVILAH\CNLRLPGSSDSPASASRVAGTTGTC\HR\ARLIFVFLVEMG\FHHVG/RRDGLGSPDLVIHPPR\TPKGVGG\LGQVSHCGPGPSPQGFY\KIKELGSSQGGEQFP |
| 3668 | 9165 | A | 3943 | 1 | 2499 | |
| 3669 | 9166 | A | 3944 | 855 | 2479 | PGGSGPGFPTLEGSSKAGRELIGYEPGSSGVGAPLTPHKMKKRKELNALIGLAGDSRRKKPKKGPSSHRLRTEPPDSSESSEEEEEFGVVGNRSRFAKGDYLRCCIKICYPLCGFVILAACVVACVGLVWMQV\ALKEDLDALKEKFR\TMESNQSS\FQEIPKLN\EELLSKQKLEKIESGEMGLNKVWINITEMNKQISLLTS\AVNHLKANV\KSAADLISLPTTVEGLQKSVASIGN\TLNSVHLAVEALQKTVD\EHKKTME\LLQSDMNQHFLKETPGSNQIIPSPSATSELDNKT\HSENLKQDILY\HNSLEE\VN\ALVGYQRQNDLKLEGMNETVSNLTQRVNLIESDVVAMSKVEKKANLSFSM\MGDRSATLKRQSLDQVTNRTDTVKIQSIQKEDSSNSQVSKLRE*LQLISALTNKVPESNRPPETAD\EEQVESCTSKPSALPKFSQFLGDPVEKGCPKLR\TYS P*QGVSKH*KIFQDLFR\KTGQD\VDGKLT\YQEIWTS\LG\SAMPEP\ESLRAF D\SDGDGRYSFLELRVALGI |
| 3670 | 9167 | A | 3945 | 336 | 519 | AALPCEPAFSP\LQEVQRLQDRGQ\NQ\TQRPFFL\NVVQA\VSQEG\ACV\YAVSELRK\EWGRPQ |
| 3671 | 9168 | A | 3946 | 252 | 2104 | LCASSCFICPPIRPSVCP\PAAPLLGCRAMARGYGATVSLVLLGLGLALAVIVLAVVLSRHQAPCGPQAF\AHAAVAADSKVCSDIGRAILQQQGS\PVDA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TIAALVCTSVVNPQSMGLGGGVIFT IYNVTTGKVEVINARETVPAHAPS LLDQCAQALPLGTGAQWIGVPGEL RGYAEARRHGRLPWAQLFQPTIA LLRGGHVVPVLSRFLHNSILRPSL QASTLRQLFFNGTEPLRPQDPLPWP ALATTLETVATEGVEVFYTGRLGQ MLVEDIAKEGSQLTLQDLAKFQPEV VDALEVPLGDYTLYSPPPPAGGAIL SFILNVLRGFNFSTESMARPEGRVN VYHHLVETLKFARGQRWRLGDPRS HPKLQNASRDLLGETLAQLIRQQID GRGDHQLSHYSLAEAWGHGTGTSH VSVLGEDGSAVAATSTINTPGAMV YSPRTGIILNNELLDLCERCPWGS TPSPVSGDRVGGAPGRCWPPVPG RSPSSMVPSILINKAQGSKLVIGGAG GELIISAVAQAISKLWLGFDLRAA IAAPILHVNSKGCVEYEPNFSQEVQ RGLQDRGQNQTQRPFFLNVVQAVS QEGACVYA\VSDLARKSGEAARS |
| 3672 | 9169 | A | 3947 | 2 | 97 | GLGRWLT/PVIPTLWEAKKGRSPEV RSSRPVKS |
| 3673 | 9170 | A | 3948 | 3 | 308 | PEDSDEKSLSSSVVHVRRPSRRVP RMPRGSRRTSRMAPPASRAPQMR AAPRPAPVAQPP\QPCLYEIKQFLEC AQNQGDIKLCEGFNEVLKQCRLAN GLA |
| 3674 | 9171 | C | 3949 | 38 | 154 | MXSNSFWSPRTRVTSSSVRVSMR CCYDFILCELIRIKS* |
| 3675 | 9172 | A | 3950 | 1 | 192 | GSNAEP/ARPDLT/Y/QEP/QGTQPAQ QQQPCLYEIKQFLECAQNQGDIKLC VGFNEVLKQCRLANGLA |
| 3676 | 9173 | A | 3951 | 1 | 254 | LMARMQTLKLAVLWASAIGHTWV HAFTGAFSGGSNAEPARP/DITYRSL YEIKQFLECAQNQGDIKLCEGFNEV LKQCRLANGLA |
| 3677 | 9174 | A | 3952 | 1 | 142 | |
| 3678 | 9175 | A | 3953 | 1 | 325 | FFFEMESCSVAHAGVRWA/DLSSLQ SPFPGFKRFSCGLLSSWDYRRLPP HPANFYFLVDTFHHVGGAGLELL T/S/GDPPASASQSAGITGTSHRAP VNTFNRPPAS |
| 3679 | 9176 | A | 3954 | 3 | 304 | HEGREKRRVLGAEAGGGRSCEIGV PLEWWRPLMRVRVMCC/LMLML RWGASFAWYCCFLSFCNWLASSET TGLMITFMLRISALLMRSLQNPEAM TLPW |
| 3680 | 9177 | A | 3955 | 3 | 961 | LLLLNSRPRRRDRLVTLESWANDPD YLKRQVGFCQWSLDNFLKEGRQ LTYEKNLSSIRAMLSNDVSEYK ISPHGLEARCDASSFESVCCSFCVD AGVWDYEVTVVTSGVMQIGWATR DSTFLNHEGYGIGDDEYSCAYDGC RQLIWYNARSKPHIHPCWKEGDTV GFLDLNEKQMIFFLNG/TPA/RPPEE QVFSSTVSGFFAAASFMSYQQCEFN |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | FGA\SPFKYPPSMKFSTFNDYAFLTA EEKIIL\PRHRLALLKQVSIRETAGS LCCDEVADTQLKPCGHS DLCMDCA LQLET CPLCRKEIVSRIRQISHIS |
| 3681 | 9178 | A | 3956 | 4 | 101 | RQSLAMLSRLA\LSNWPQVILLPWP PKVLGLQA |
| 3682 | 9179 | A | 3957 | 21 | 338 | HPVLAITLSIFIVAFAYAEELDEIQ P\CIMMKTNLKLGIEGMCLNSIKAIY \DKSNANFILNKEKLKAFFLRSGTRQ IRPNFQ\PLLFNIVLEVLAKEIRQEEI KV |
| 3683 | 9180 | A | 3958 | 90 | 360 | ALICLV DIESGENSTTRPFASHDQV CIALLRTA\GILCLET FIDSPSHGSRH FLFVLSSPPLTLFPLLHIYLLAVVPI VSPLLSLSDPP |
| 3684 | 9181 | A | 3959 | 1 | 424 | CGRRFSTRSDLT KHRRTDTG\EKPN RCELCGKRFTCVSNLNVHRRNHAG HKPHKCPECSKAFSVASKLALHRKT HLGERPAECARVGQVLQPQAPLS QHQRGPHAPPAPLPPLPSSPAVGHC PQSFEGGRLEQEKAKGSL |
| 3685 | 9182 | A | 3960 | 153 | 328 | SIASYFTLVCHLLRKCHPRLGTVAH TYNPSTLGGRGRWIMR\QEFETSLT NMVKPCRY |
| 3686 | 9183 | A | 3961 | 1 | 936 | |
| 3687 | 9184 | A | 3962 | 1 | 1023 | |
| 3688 | 9185 | A | 3963 | 15 | 337 | RINNTISWLIYVCKFCLSSFSIYLIIIII IIFFETESHVAQAGVQWRNLGSLQ PPPPRFKRFSCLSFPSSWDYRCPPPR PANFCIFSRDGVSPCWPGWFRTPDL R |
| 3689 | 9186 | A | 3964 | 3 | 1105 | HASALTPVVCMLSAIAFSNVFEHYL GDDMKRENPPVEDSSDEDDKRNQG NLYDKAGKVRKHATEQEKEEGLG PNIKSIVTMLMLMLLMFVHCTW VTSNAYSSPSVVLASYNHDGTRNIL DDFREAYFWLRQNTDEHARVMSW WDYGYHIAGMANRTTLVDNNTWA NNSHIALVGKAMSSNETAAYKIMR TLDVDYVLVIFGGVIGYSGDDINKF LWMVRIAEGEHPKDIRESDYFTPQG EFRVDKAGFPTLLNCLMYKMSYYR FGEMQLDFRTPPGFDRTRNAEIGNK DIKFKHLEEAFTSEHWLVRIYKVKA PDNRETLDHKPRVTNIFPKQKYLK KTTKRKRGYIKNLVFKKGKKISK KTV |
| 3690 | 9187 | A | 3965 | 1 | 181 | ANVVFTQLLIWYGVDVRSRDARGL TALAYARRAGSQECADILIQHGCS AEGCLSSTCY |
| 3691 | 9188 | A | 3966 | 640 | 961 | DGVSASCCPGLGVQWVRFLGSL\QP SASWGFKQFSCLSLPSSWDYRRALP PPRPANF/SVFLVKMGFLHVG\QAG LELLTSGHPAASASQSAGITGVSHR TRPAASILI |
| 3692 | 9189 | A | 3967 | 2 | 334 | VGLYGRIEASSPMGEGNRW*SGTPA NQG*QEQGIARPKPRGEPGLRNEGG |

| SEQ ID NO: of nucleo- tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | PGAILPGRWAGV*GPTGQEGR*RGSG QESCPCPAQSSCSHRVAGLDVGGSH GHSAAFPATP |
| 3693 | 9190 | A | 3968 | 1 | 361 | ARARLRHLRDLRAPAGPVGGLCAA GTACGWPGPGPLLGERVRAFLRR* RAQHLLHHHRVRAPLPGWREAAG GAPPFLGTYGPESQVRLRDAVVPEA GGQDSGSSGSASLRPRSSFSCSCS |
| 3694 | 9191 | C | 3969 | 151 | 373 | MPTAVXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXVLPFLV LEVMOCLCPVLLLYDPNSKTRYV FFKTR* |
| 3695 | 9192 | A | 3970 | 50 | 441 | IPSPPDGFFSNLGRKPFPCNFSCQ NILLTRKILLKSFLYPFFFLRWSLA LPPAVLSAHCNLCPPGSSDSLASAS* VAGITGVHHQAWPVLVLEVMQ CLCPVLLLYDPNSTPRYVFFKTRT FIA |
| 3696 | 9193 | A | 3971 | 3 | 224 | FLRWSLALPPAVLSAHCNLCPPGSS DSLASAS*VAGITGVHHQAWPVLV LVLEVMQCLCPVLLLYDPNSFV |
| 3697 | 9194 | A | 3972 | 1 | 214 | PIQFKQRLPFGFLFVVF*EGVLLCH PGWTAVTEDRSWLTATSTSWAQVI LQSSCLSLPGS*DYRQCLPGV |
| 3698 | 9195 | A | 3973 | 154 | 341 | KNFFRGQFWFVA*AGVQWGHFRSL QPQPSGVKQFFPLGLPKPLDCRCES HRVPFLFLGLETL |
| 3699 | 9196 | A | 3974 | 3 | 379 | FALVAQAGVQWCSFDSLQPPPGF K*FSCSLPSSWNYRHLPPRLANFV FLVEMGFHYVGQASLELLTSGDPPA SASQSAGIRGLSHCTWPHVSGFIMQ YEYTLCFMVFIMSFWRNCRKVAKY LK |
| 3700 | 9197 | A | 3975 | 2 | 35 | LKQAPCLCLPSS*DYRHLPPCLSNF* NFL*R*GLSLLPRLVSNS*PQAICPRR PPKVLRL*AQTSPLPLTK |
| 3701 | 9198 | A | 3976 | 1958 | 2316 | IHSSPTKATFFLRQSLALSPRLEYS AISAHCNLCFPGSSDSRALAS*AAG TTGACHHIRLIFLFFVFLVETGFHH VGQAGLELLVSSDLPLVLSARITG VSHHAQPPPKLLNALL |
| 3702 | 9199 | A | 3977 | 2 | 80 | SLCICMCVCACIRTHA*MYVCVCV HTHACMNATSPSWVF |
| 3703 | 9200 | A | 3978 | 123 | 452 | KTGSNFAPQLEAQGGNLG*LNPWP PG*KQFSGLTLLITWINGAPPPPRAN FGIFNKKGVTPCGQGGPKTRDLGIG PSKPPKGLEFRAQPPEPALMGKFYP MVNLSNVPPF |
| 3704 | 9201 | A | 3979 | 3 | 250 | AIAAH*NLHLLGSSNSSASVSRVAGI TGARHHTQLIFVFLVETGFHHVCQA GIEFLTSGDTSTSASQSARITGMSHH TWPQKQ |
| 3705 | 9202 | A | 3980 | 2 | 257 | PRSSPTCPACLCVQVNPPAQDPEDP APQLSPQPQDPAKPPQPYNPYPY PNLGCGL*PQNYCIIVCMVSIVYYH MGIETVKSQ |
| 3706 | 9203 | A | 3981 | 2 | 147 | LVEMGFHHVSQAGLKLLDSGNLSA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | S*RSAGITGISHRAHPPNSTNIYA |
| 3707 | 9204 | A | 3982 | 3 | 446 | QVVRGFGRVSKQMGIPANFPEQV VDNLPADISTGIYYGGASVGSQDVH KMOVSI*WNPYYKNTKKSMETHIM HTFKEDFYGEILNVAIGD*LRPDKN FDCLESISPVGQDGD*AKIRLELPE HLRI*EDTFFQVSLNRTMIVTDDK |
| 3708 | 9205 | A | 3983 | 1 | 162 | FFFRVKASICCPGWSTVAQ**LTAA SDSWAQKSSCSLWSSWDNRRLP HLANK |
| 3709 | 9206 | C | 3984 | 131 | 442 | MNIPLSMSLVVSNMQDVFWXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXX* |
| 3710 | 9207 | A | 3985 | 141 | 429 | TGSHFVAQAGMQWCNLWSMQLLP AGLR*FPYLSLPSSWDYRHAPPCST HFLYFFVEMGFCHVAQVGLELLAS SDVPTYASQSAGITGVSNHPRPF |
| 3711 | 9208 | A | 3986 | 1577 | 1879 | |
| 3712 | 9209 | A | 3987 | 1 | 219 | EM*SCRVTQAGVQWCNLSSLQLPS PGFKQFSCLSVPSGWGYRCMPHP ANFCIFSRDRASPRWPGWSQTPDLR |
| 3713 | 9210 | A | 3988 | 1 | 414 | FF*TGSCFVSQAGTQQQDHSSLQP* TPGLKPSSHLCLSSWDNRHLIFKFF VEMGSRHVAQAGLQLLGSNNPPTL AS*SARIISWSHRAQPTCTLCSWLC DSGAGTAESFLWQPALSRVANRGC CRRPGKLKEKQGT |
| 3714 | 9211 | A | 3989 | 3 | 666 | FFVETGFCHVGQAGLELLGSGNLPA AASQSAGITGMSHRVRQHS*YETHR KVFYS |
| 3715 | 9212 | A | 3990 | 1 | 436 | FFFFFLRQNLTLSPRL*CSGTILAH NLQHPGSSDSPAASQVAGITGVRH HIWLIFVFLVEMRFHHVQGASLELL NSGYLPTSASQSAEITGVSHCAQLQ PGILMHGLRRLTDLDDNVHHPRSRL KVTSSSAHPGAASSFLHL |
| 3716 | 9213 | A | 3991 | 167 | 563 | SESASEFSIFYLFIIIIIIIIETRSCSVA QTGVQWCDHGLLQPRPPWFRPSCH LSLLSSRDYR*APHPANTFNFFLE IGSHYVAWGSLELLGSSDPPASASQ SVEIIGVSHRGPDSQKSFIHLSRFP |
| 3717 | 9214 | A | 3992 | 3 | 456 | |
| 3718 | 9215 | A | 3993 | 78 | 129 | |
| 3719 | 9216 | A | 3994 | 96 | 251 | MDOYSRNSPLEVNGQQLLGWYQH ALRCKWNF*APLCYCSTVFNSQPT HTEE |
| 3720 | 9217 | C | 3995 | 94 | 351 | MKRISTTQYYHCQDYDLRHSKHM CLVSTAFQKVPLYKYLEILQENLD PQKDSRWFSVISSPRSQNVKQVWR HLQSCLTSHCKH* |
| 3721 | 9218 | B | 3996 | 1 | 431 | MAVASTKSRWETGEVQAQSAAKT LSCKDIVAGDMSNKSFEQKGGSK TSSTITAQIAFLQGERKGQENLKD LVRMIRMLEYALKQKRAKYHKLK YGTELNQGAMKPPSYDSDEAQQQA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MRSVHGPLHLSAPPASQQKRPTER* |
| 3722 | 9219 | A | 3997 | 772 | 1391 | IANNKDALRKTWNPKFTLRSHFDGI RALAFHPIEPVLITASEDHTLKMWN LQKTAPAKK*EYSTLTLEFYFK*HA |
| 3723 | 9220 | A | 3998 | 3215 | 3491 | SAKVLRPTEFFFFFFFFFAIESHCVT QAGVQWCNLAQLQSPTEFK*FSC GLPSSWDYRCVPPHPANFYIFSRDR VSPCWPGWSKTPDLK |
| 3724 | 9221 | A | 3999 | 1 | 779 | MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEK VPETTTTRFWAPGVEAPGDDAERRR REASGPATRHSPPLTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGGLK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF |
| 3725 | 9222 | A | 4000 | 1 | 1286 | MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGGPGLGLGV RPGMPPQPQGPAPLRRPDSSDRYV MTKHATITYPTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLLSRIAE NLPKQLAFISPEKYDIKCAVSEAAI LNSCVEPKMQVTITLTSPIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLOSCVHIR ILRDLQCRVP/TWS/DFPSWAMELLV EKAISSAS\SPQSPGDALRRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PDPASRED/LSTSQCHSLPLETS LAFPPRYHKVLGMDPITRK*AQR NI\HNRRKRRRD\SDGVDGFEEAGK KDKKDYDNF |
| 3726 | 9223 | A | 4001 | 2 | 379 | DLPASATQONAGITGVSHHIWPRJIFL LW*KTFTILTFLSVQYSSSNYIHPVC NRALELFKSYKTETKLNFPSPPPPI VNLHCIFFF*GLTFLLGFFSLPKYRG FTNFVSPCTVAMLTRGGGGGEF |
| 3727 | 9224 | A | 4002 | 229 | 445 | RPGPNFGLLETLTWGLKGTWLWNP PKNWELGAHPPTPGNFWIF*KGGF WNVSQGGSKTRGLRELPPFSWKKG |
| 3728 | 9225 | A | 4003 | 192 | 529 | HEVLNFLTSCVLTTLVFLIADIHWS CRTRSLPFVATTLEVLPLSLIGLCHH TILVFISNAFFI*KAYFVTSSFIMFP*S FFLFNISVLSYMYLTFSHLTSFVIAY FSYSHI |
| 3729 | 9226 | A | 4004 | 330 | 754 | SDLSQKESSSSLSKFLVTEKNSSLGS GGCDMANKENELACAGHLPEKLH HDSRTYLVNSSDSGSSQTESPSSKYS GFFSGGFLRDHETMAQVLFSDMR LNVALTFWRKRSISELVAYLLRIED LGVVVDCLPVLTNCLQE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 3730 | 9227 | A | 4005 | 296 | 861 | VSQDHETMAQVLF SRNMRLNVALT FWRKRSISELVAYLLRIEDLGVVVD CLPVL TNCLQEEKQYISLGCCVDLL PLVKSLLKSKFEE*CY*WVLTGLQA VIKRWWSSELSSKTEINDGNIQILKQ QLSGLWEQENHL TLVPGYTGNIAK DVDA YLFPVTIEGFHLLKSIWFFKTS LELYNLQKKKVS |
| 3731 | 9228 | A | 4006 | 2 | 265 | NNFFSFSETESHSVTQAEAQWYDNS SLQP*ILGLKQSFCLSLPSNWDHRC APHPQFSFLIPGLYVSQFILGNKPSS LPCQMFKSAV |
| 3732 | 9229 | A | 4007 | 3 | 295 | HFNLSHRSAQAKGNRYKEAEALTN AAVHVDDMPNALNALIDLRAHNLG QDPVNFKRLSHCLLVTLAAHLLAEL TPAVHA*LDKFLASVSTVLT SKYT |
| 3733 | 9230 | A | 4008 | 1 | 1077 | |
| 3734 | 9231 | A | 4009 | 3 | 285 | ETESRLATQAGVQCCDLGSLQPLSP GFK*FSCFSLPSSWDYRYPPSCQAN FCILVEMGFHHVQGASLELLTSGDP PASASQSARITGVSHRAQ |
| 3735 | 9232 | A | 4010 | 1 | 338 | VIATYHGGGLCTQKSQPPPPQALWSA STSTINLMVSTEPLALTETHICKLPK D*GTCRDFILPWDYDSNTKSCARF WYGRCSANENDFGSQSECEKVCAP VLCKPGVISEMAT |
| 3736 | 9233 | C | 4011 | 269 | 526 | MLARLVSNLSPQVIHHTQPRVGSPT RIPTLSLNLPLPLALTSLRWDRHQLR GQGHWGAQELRAITGFKDHQVWQ TLNCSLCV PKP* |
| 3737 | 9234 | A | 4012 | 2 | 51 | |
| 3738 | 9235 | A | 4013 | 83 | 5229 | |
| 3739 | 9236 | A | 4014 | 3 | 45 | EVVHALRCRWWWSWGLKLDLLTPEP EPICGPALLSRSSLRGSHPTAFLLPP QVSQ*RGELGPSTFRAFRAEFPTSRG SKDNKEKNQQEQDMAKPATGTGQ G*GADGGAGA |
| 3740 | 9237 | A | 4015 | 3 | 323 | LLWKVESSWRDQKDIMSWEWDKR RRRHHLTDRSQLCSKVQFQVDCDLI EWGTWIINLKQYNAYHCEGECHNP VG*KFHQSNHAYIQVGCQVLGEE AVIWHWGTGL |
| 3741 | 9238 | A | 4016 | 2 | 279 | FFF EAKSHSVTRMLECNGAISAPC NLHLP GSSDSPASASQVVGITGVYH HTQLIFISVETGFCHVGQDGLNLPD LMIHPPWPPKVLG*QA |
| 3742 | 9239 | A | 4017 | 166 | 939 | |
| 3743 | 9240 | A | 4018 | 2 | 225 | KELTGRRCAEPPHPRPSPQLL TEEPF TKGRFSGEWRGRNAASMKTGPF AE HSNQLWNISAVPSWSKVNQGLIRM YKAEP*EGADRKALCRASPPPIPPV TDRGAIYKRPI LWVERQERSVYED WPICRALQPAVEHQRRPFLVQSEPG SHPHV |
| 3744 | 9241 | A | 4019 | 142 | 1336 | KARGDCKHPGRCWPEQMAEGERQ PPPDSS EAPPATQNFIPKKEIHTVP DMGKWKRSQAYADYIGFILTLNEG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VKGKKLTFEYRVSEAIEKLLALLNT LDRWIDETPPVDQPSRFGNKAYRT WYAKLDEEAENLVATVVPHTLAA AVPEVAVYLKESVGNSTRIDYGTG HEAAFAAFLCCLCKIGVLRVDDQIA IVFKVFNRYLEV MRKLQKTYRMEP AGSQGVWGLDDFQFLPFIWGSSQLI DHPYLEPRHFVDEKAVNENHKDY MFLECILFITEMKTGPFAEHSNQLW NISAVPWSASKVNQGLIRMYKAEC \EKFPVIQH/FSKFGSLPIHPVHVGL GGAKPKEPPRGTVSCCLPFPPTAVA PPSPSPSVSSRLMRGCLLGLGGEMG LRGLRA |
| 3745 | 9242 | A | 4020 | 80 | 283 | |
| 3746 | 9243 | A | 4021 | 61 | 626 | DLICVIGVPEEEKETGAKNIFKEIMG ENSPHLVKDVIVHIEEIHSDEN*** Q*KSYK**QKGIIKLRVDLLETMEA KCSRTPSLKCLGKESFGESWESRILH PAEISHRNECHMKIILDFKSEKGPDA VAHTCNPSILGGHTAGGSLEARSFE TNLPETLSLLKKLNLKEKEFVASYP PLVEMLK |
| 3747 | 9244 | A | 4022 | 18 | 161 | TSFKNPPPPPPGGLKKIPSPPPKKK KFKDVS*PTYFYLNLASSVT |
| 3748 | 9245 | A | 4023 | 30 | 262 | NRRQAGPFPKALGRPSPKGGFPNFF KSSSSKSSF*KNPKGQGWGFPPLIPG FQGPQVGGSLGAPGLKPPWGTPQN PF |
| 3749 | 9246 | C | 4024 | 193 | 366 | MYNYRSIPKNKYTYTYTKSYPNKIF SRLILYIPLGTVSQISTLNCVPRFVLL TWKAL* |
| 3750 | 9247 | A | 4025 | 3 | 258 | TIDSLKGLPCKQNEPWHTIQCGYL GNSSKWN*YQSGKDFIRIAFCVCIC I/CYF*E*IYSCT*IPVRNTLNELNPLA KCPCPFH |
| 3751 | 9248 | C | 4026 | 164 | 313 | MEGTRIFGKWVKLIQSIPNRNSCTTI DLFLKINIIHTQKAILMKSFDP* |
| 3752 | 9249 | A | 4027 | 9 | 373 | DRVSLCRPTLEVQWRDLGSLQPPSP QVQSNPALSLPSSWDYRRVPPCPS *FFVFLSRRWRFRVVGQTALFLIKM MGKKILKIKSNYTLGLYVGPSYSER MIKPQEFESSLGQHCKTPSQK |
| 3753 | 9250 | A | 4028 | 1 | 336 | DRILLHRPCWSTLARS*LTIPSNHLG SVFPPSALLES*DCRHTPTTPD*FLKI FL*RRGLTVFPRVLNVAWTQAIHQPL PLKALGLQDTFFKNINCDRLKVSEY YSDTEIEI |
| 3754 | 9251 | A | 4029 | 514 | 742 | LPKC*DHRHEPPHQAFFNFVEMG SCHVPQSGQLQLLGSSDLPASAFYSA GIAGMSHHTWPPYLFKSRHKSFRCP S |
| 3755 | 9252 | A | 4030 | 1 | 264 | QAQGKHGSGFGPPFAGLKGFPGGLGF PRTGNSGGFPQGGKYKGLIKNGVP PSFQGGF*IPGPGSHQRLGFRG*VGR AL*TPGFRATLF |
| 3756 | 9253 | A | 4031 | 7 | 417 | RQDLALSPRLECSDTIIAHCISIKLLG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SNGAPSAAS*VAGTTGTRHHAQLIF LKIFVETRSLYVAQASCVFPASSNPP TSASQSTGITGMSCCARPTSYVPGS DLSVLCILTHLILKIPLYRRYYYFVS LTYSKAEVQ |
| 3757 | 9254 | A | 4032 | 123 | 376 | KTGSNFVPQAEAQGGNSG*LNPLPP G*KQFSGLTLLITWINRAPPPPRANF GIFKKKGVSPPCC*GGLKTPNSGFSPF KPPKGLE |
| 3758 | 9255 | A | 4033 | 3 | 292 | QWHKHGLLQPQPPGLK*SSHLSLPR SWDHRHVSPCLTNFF*FSVSMGSCY VAQAGLKHLASSDPPASASVGTIG MSTT*SKTTLYTEKLANIILTK |
| 3759 | 9256 | A | 4034 | 1 | 230 | FFF*TDSCSVAQAGLQWRDYRPEPP CPANFITIKVQNKSVTFPARNLNK MRGASIMLYPIGLSLNDLMQLLSEGF |
| 3760 | 9257 | A | 4035 | 3 | 189 | SWDYRRRLPHARLIFVFLVGTGFHHV VQAGLELLTS*FTRLGLPRCWDYRR EHIAPGHIWY |
| 3761 | 9258 | A | 4036 | 2 | 148 | PGSSNPPTSASQLAGTAGTHHHA*LI FVCLVETGFCHVA*AGV*VKFF |
| 3762 | 9259 | A | 4037 | 348 | 696 | AEEQDKKGRQ*ERGKEWERETETK IYSRIKGNREGQAKKKWGHGELIH KTKDEKRKKSEEDKKLRWRKR*TN SQKD*IRKRLHKETANSER*EEKHK ERKQWRRGPKARRAISRG |
| 3763 | 9260 | A | 4038 | 1 | 295 | QNQFFIFIYFKTESGSVTRLEYSGVIS AHCNLCHPGSSQSPASAS*AAGTTG AHHHIQLLFVFLVETGFHHVQGAG LELLTSSDLPASASQSAWGLQV |
| 3764 | 9261 | A | 4039 | 6 | 151 | SQGLALLPRLISNPWVQAILLPWPP KVLGL*AEIAQNKMOK |
| 3765 | 9262 | A | 4040 | 101 | 318 | SNHTLGTS*HFFETVSCCIMLHRVE CSGAVIAHCNLELLGSSDSPASTS*V AGTTAVYHHTGLSWLLNLH |
| 3766 | 9263 | A | 4041 | 210 | 306 | SWPGTVAHICNPSALGGQGGWIA* GQAFRQA |
| 3767 | 9264 | A | 4042 | 2 | 147 | DFSVKTL*ARREWRDIFTVMKEKNF YPRKVYALKIPFKNEATKKVEV |
| 3768 | 9265 | A | 4043 | 160 | 525 | NTQTRSFGNRLMAPAQSSHKALTK KVMTCNPSETVHDSQECFFVLFFET VLVCLPGWSAVMLVRCSLCLLSSW DYRRVPPHLG*FLYF**R*CLTMLA RMVSNS*PQVIHLPRPKLLGLQA |
| 3769 | 9266 | A | 4044 | 3 | 72 | KTQVHFQGWQHSVHIITHPCWEKL ALSITPLR*DNRKLQAWNRPRLGPT CLFPRALALMCVLM**NIHEYNSFQ RVLWVLLVNC*ISKVGSTLCISSHIP AGRS |
| 3770 | 9267 | A | 4045 | 313 | 358 | |
| 3771 | 9268 | A | 4046 | 7 | 308 | AGGRRARAPHLGGRGAARGRL*RV RGHRERGLRAAPVPRPQQLRRGA AAGAVQPGQGVGRAGPPEGSEGSV AGVGLDLDSscyHHSSDFYICHPMP ISS |
| 3772 | 9269 | A | 4047 | 92 | 390 | ETGSHSVNLAGLQWCDHNSLQP*T |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGLKQSSYLSLLSS*DYRWVPPCPA NF*IFFVEIRSCHISQAGLDLPRSPD PVWGSQSAGTIGMSHHAQPREIC |
| 3773 | 9270 | A | 4048 | 65 | 375 | SQLTATSTSRVQ*HDLSSQPPPPGF KRFSLSLPSGCDYRHPPPHLANFL YFLVETGFCHVGQAGLELLTSSDLP ALASQSAGITGVRYCAWPTFLIMKT CIPSFPLPSTSPIPLP |
| 3774 | 9271 | A | 4049 | 12 | 292 | DIVSPVA*TRMQWHNLGSLQPPPPR FKQSLCFLPSWDYRCVPPCPAIF VFLAEMGFCHIGQAGLELLASSNPT TLASQSAEPPHLAATDF |
| 3775 | 9272 | A | 4050 | 40 | 343 | SSSSLILSSSVIYLLNLSDFLVLLY FLVFRFSVCSFCQFFVKNFNLIFYF FKHIKNICFKVCV*RLGFLDPLCAYF GCLLFL*VFSHVLSLHIPDDL |
| 3776 | 9273 | A | 4051 | 97 | 282 | |
| 3777 | 9274 | A | 4052 | 3 | 336 | FFETGSRFVTHAGVKWHNHDSLHP QPPRLK*FSYFSLLLSSWDHRHVPP RPANLVYLL*RGGPSMLPRASLEF PGLQVNSSLPSALPKVLGITG*GHRP RPKVTFHQRG |
| 3778 | 9275 | A | 4053 | 3 | 294 | CCFGDGVSLCRPGWSIECSGNHSSL QAVEPPRLR*SSRLSLLGSWDPSHV PLHLANF*TFCTHGVLA MLPLAGLK TPWAQTIPPHLSLPKVLGLQG |
| 3779 | 9276 | A | 4054 | 16 | 308 | MPQPN*SNPPVNCRLPRGPPSQVP PRIHLSPKYSPSEASAPDLQKKGNL QAPRRPGEVLETPRKPESSCMKFPF* REIKLPPPRLTSPVHSMVL |
| 3780 | 9277 | A | 4055 | 445 | 448 | IS*HCDASASIFRKKQRKQINKHPTL ASRVLGLAMEMQDETWCSGQSET VN*SQTAQNHPQPGS*PAGVCLWV ASSQHFTPQPLKKKPNPDSAKLNSA SDSLTEVILCKIFSAWQTDK |
| 3781 | 9278 | A | 4056 | 3 | 284 | CLSLLSSWDYKCLPPRLGYFLYF** RRGFTVLARMVVISRMVVISRMVIS *RRDPPASASQNAGITGVSHCARPK EQKLFYPEVSCLYLGLY |
| 3782 | 9279 | A | 4057 | 428 | 636 | DYHIVSLLHLF*FLETGSHSVTQAGI QWCDHSSL*PRTPLGKQSSCLSLPE* LGLQE*VTVPGSYSLFF |
| 3783 | 9280 | A | 4058 | 2 | 113 | FFGRDGVSLCCPDWS*TPGLKGSSC LGLPKCWDYRRE |
| 3784 | 9281 | A | 4060 | 36 | 359 | RSGVQNGFHQAEVLSVRLCFSTEAL GQNPMPPFAPPGATSSPGPRPSCHL HSQKL/TLLHAQTLVTPLPL*GLGLS AWRTL AGGAPGLHPFTTHALSTPET IPGAYRRT |
| 3785 | 9282 | A | 4061 | 17 | 168 | APGMVSGVLSACVVNGWSPGAPPA SVLQA/PQT*PF*SRPHVTSQPLLKA PH |
| 3786 | 9283 | A | 4062 | 2 | 375 | FFFFFFENHTNLLSYSSRGSGVQNGF HQPEVLSVRLCFSTEALGQNPMPPF APPGATSSPGPRPSCHLHSQKLPLLH AQT/VTPLPL*WPPWITQGPQST GHLPTTEILKLKHHRRVPPFCHAR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3787 | 9284 | A | 4063 | 309 | 620 | |
| 3788 | 9285 | A | 4064 | 3 | 218 | LRQSYSVTQAGVQWRNLGSLQPLP PGFKRFSCLSLRKS*DYRRPRLPNFC ILVKTGVHPCWSGWSQTLDLR |
| 3789 | 9286 | A | 4065 | 1 | 170 | NPKATPPQIVNGDQYCGDYELFVE AVEQNTLQEFLKLA*VKPVQSSPAG LHHHTPL |
| 3790 | 9287 | A | 4066 | 29 | 483 | RRLPAVQLPLTAALCPPARLSTPSM SGPARSTARRATGFREIKVPSKSEVT RILÆGKRIQYQLVDISQDNALRDEM RALAEQPQGHPTPDLSTGDQYCGD Y/DASFVEAVEQNTVAG\FPGSLGL KFKPCSRVSPCWSDSHHQHSPPAFQP GQ |
| 3791 | 9288 | C | 4067 | 33 | 236 | MRHHAWLIFVLLVETGFHHVQGAG LEHLISGGPPTSASQSAGITGVSHHA WPIYLFILLSGPSRLCF* |
| 3792 | 9289 | A | 4068 | 1 | 205 | AIGTDKGTRWPSEDDPGNLPEIFLFI LGPTADYV*RERQRSIELESFYRRV WGSPGGEGTGDLDEFDF |
| 3793 | 9290 | A | 4070 | 2 | 44 | LSSWDYRHHVPPRLANFCIFSRDGGF TMLARLVLS*PQVIHPPQPP*VL*L QACATTPG |
| 3794 | 9291 | A | 4071 | 173 | 369 | CSTLI*IRKVWLGAVAHAYNPNTLR GRGGRIA*GQVFKTSLGNNVKTCLF LPSPHNQQSLSGFLL |
| 3795 | 9292 | A | 4072 | 1 | 336 | |
| 3796 | 9293 | A | 4073 | 1 | 200 | |
| 3797 | 9294 | A | 4074 | 11 | 392 | |
| 3798 | 9295 | A | 4075 | 1 | 191 | |
| 3799 | 9296 | A | 4076 | 84 | 264 | |
| 3800 | 9297 | A | 4077 | 2 | 446 | DSARNSRVDGCE/IDRQKGTNDSLM MLMRELEDRFASEASGYQDNIALR EEEIRHLKDEMARHLREYQDLLNV KMALDVEIATYRKLEGEESRINLPI QTYSALNFRETSPEQRGSEVHTKK TVMIKTIETRDGEVVSEATQQQHEV L |
| 3801 | 9298 | A | 4080 | 3 | 196 | SRAKGPKNYNFGQGPPTKVKGPLA SPFFPLPPFPRPPWFPPPF*NPIFPW W*KGPKKPFLN |
| 3802 | 9299 | A | 4081 | 1 | 187 | SIRLFFFCFFF*AETGFRHIGQAGFGL LTSSVPPALASQSAGIIGVSHRARC SSLIVLHL |
| 3803 | 9300 | A | 4082 | 156 | 326 | KLEICRRARVSLKIGFIRPGTVAHAY NPSTLEGRGRQIT*DQEFETSLANM VKPCLY |
| 3804 | 9301 | A | 4083 | 3 | 448 | |
| 3805 | 9302 | A | 4084 | 1 | 4249 | AAATIRYLKTTMAWKTLPIYLLLLL SVFVIQVSSQDLSSCAGRCGEGYS RDATCNCDYNCQHMECCPDFKR VCTAELSCKGRCFESFERGRECD AQCKKYDKCCPDYESFCAEVHNPT SPPSSKKAPPPSGASQTIKSTTKRSP KPPNKKKTKKVIESEEITEHSVSEN QESSSSSSSSSSSTIWKIKSSKNSAA NRELQKKLVKDNKKNRTKKKPTP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KPPVVDEAGSGLDNGDFKVTTPDT STTQHNKVSTSPKITTAKPINRPSL PPNSDTSKETS LTVNKETT VETKET TTTNKQTSTDGKEKTTS AKETQSIE KTS AKDLAPTSKVLAKPTPKAETTT KGPAL TTPKEPTPTTPKEPASTTPKE PTPTTIKSAP TTPKEPAP TTTKSAPTT PKEPAP TTTKEPAP TTPKEPAP TTTK EPAP TTTKSAP TTPKEPAP TTPKKPA PTTPKEPAP TTPKEPTPTTPKEPAP T TKEPAP TTPKEPAP TAPKKPAP TTPK EPAP TTPKEPAP TTTKEPSPTTPKEP AP TTTKSAP TTTKEPAP TTTKSAPTT PKEPSPTTTKEPAP TTPKEPAP TTPK KPAP TTPKEPAP TTPKEPAP TTTKKP APTAPKEPAP TTPKETAP TTPKKLTP TTPEKLAP TTPKEPAP TTPPEELAPTT PEEPTPTTPEEPAP TTPKAAAPNTPK EPAP TTPKEPAP TTPKEPAP TTPKET APTTPKGTA PTTLKEPAP TTPKKPAP KELAP TTTKEPTSTTS DKPAP TTPKG TAP TTPKEPAP TTPKEPAP TTPKGTA PTTLKEPAP TTPKKPAP KELAP TTTK GPTSTTS DKPAP TTPKETAP TTPKEP APTTPKKPAP TTPETPPPTTSEVSTPT TTKEPTTIHKSPDESTPELSAETPK ALENSPKEPGVPTTKTPAATKPEMT TTAKDKTTERDLRTTPETTTAAPKM TKETATTTTEKTTESKITATTTQVTST TTQD TTPFKITTLKTTTLAPKVTTTK KTITTT EIMNKPEETAKPKDRATNS KATTPKPQKPTKAPKKPTSTKKPKT MPRV RKPTTPTPRKMTSTMPELNP TSRIAEAMLQTTTRPNQTPNSKLVE VNPKSEDAGGAEGETPHMLLRPHV FMPEVTPDMDYLPRVPNQGIINPM LSDET NICNGKPVDGLTTLRNGTLV AFRGHYFWMLSPFSPSPARRITEV WGIPSPIDTVFTRCNCEGKTFFFKDS QYWRFTNDIKDAGYPKPIFKGFGGL TGQIVAALSTAKYKNWPESVYFFK RGGS IQQYIYKQEPVQKCPGRRPAL NYPVYGEMTQVRRRRFERAIGPSQT HTIRIQYSPARLAYQDKGV LHNEVK VSILWKIGLPNVVTS AISLPNIRKPD GYDYYAFS\KDQYYNIDVPSRTARA ITTRSGQTL SKVWYNCP |
| 3806 | 9303 | C | 4085 | 258 | 362 | MFYRNL MKVRAELNCSAILIEIKA KVLTLFHSN* |
| 3807 | 9304 | A | 4086 | 2 | 236 | QSYNSDSLFFLR SFALVTQAGVQ WRDLGSLQLPSPGFK*FSCLSLPSS WVYRCPPDPANFLVLVETGFHHV GQGWS |
| 3808 | 9305 | A | 4087 | 224 | 464 | KIFLFFFFFKRQGLT LSCRLDCSVQ *HNHYPLQSRTPELKQSSCLSHPKY WD*RHEPLCLAPKKEDTLQEQL EIR LLIY |
| 3809 | 9306 | A | 4088 | 129 | 315 | ILKILWIFRIFLLSIKCF*TNMHVCV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SCLFIFLTVSFIEQTF*ISFFYASWIML LMSFFF |
| 3810 | 9307 | A | 4089 | 1 | 190 | FFF*IGPHSVAQAGVRWCDLGSCSL NLPGSSDPPASASQVAGTTGVHYYT QLIFKFFIEMRAP |
| 3811 | 9308 | A | 4090 | 1 | 5229 | |
| 3812 | 9309 | A | 4091 | 1 | 7044 | |
| 3813 | 9310 | A | 4092 | 170 | 422 | |
| 3814 | 9311 | A | 4093 | 1 | 3230 | |
| 3815 | 9312 | A | 4094 | 3 | 151 | DTATCCAKWNTEDKVSHVSTGGG AS*ELLEGKALPGVDATSTIYYFPF |
| 3816 | 9313 | A | 4095 | 2 | 1446 | SLRSARRQSAPSLTESPTSLPSCISK MSLSNKLTLDKLDVKGKRVVMRV DFNVPKNNQITNNQRIKAAVPSIK FCLDNGAKSVVLSHLLGRPDGVPM PDKYSLEPVAVELKSLLGKDVFLK DCVGPEVEKACANPAAGSVILLENL RFHVEEEGKGKDASGNKVKAEPK IEAFRASLSKLGDVYVNDVAFGTAHR AHSSMVGVNLPQKAGGFLMKKEL NYFAKALESPPFLAILGGAKVAD KIQLINNMLDKVNEMIIGGGMAFTF LKVLNNMEIGTSLFDEEGAKIVKDL MSKAENGVKITLPVDFVTADKFD ENAKTGQSTWASGITPG\WMGLDC CPSSRK\YAE\AVTRAKQMVWNGP V\GYFE\WEAFA\RGTKALMDEVVK A\TSRGLPSPS*GGWRPLPTCCAQM ETREDKSQPM*ATGGWCPVWQLE G*SPFLGVDALSQYLGTFPALLSPC AQPPKVNLGIFLHPLGH |
| 3817 | 9314 | A | 4096 | 1 | 747 | MDSSRARQQLRRRFLLLPDAAEAQL DREGDAGPETSTAVEKKEKPLPRLN IHSGFWILASIVVTYYVDFFKTLKEN FHTSRSPESPAPRRGGVRASVPQKL AEMLSQYGLIVFVAGLLLLLAWA VHAAGVSKSDLLCFLTALMLLQL/P VDAVVRGPQLRAPPLPPQGHARG CRLAARQRPPTVSTGRGEHVDSPPP AQRRLSYLPLRLGAEFASEPPSAPA HRA\TPPPVEVTPTEAGRFRQAKG ALS |
| 3818 | 9315 | A | 4097 | 1103 | 1295 | EQEGTGLERRRGSPMSKDWPPPHL TPPQGPCGIPVHSLSPPSFSPGPRNS K*ARRSTAPVDCK |
| 3819 | 9316 | A | 4098 | 1 | 1302 | MVAGSDNYHEVSLHDGVIGARGCP PPSPSARGARSPRPPGGCARQPTA GRDAEQPVWADRVRGGAAGL GRARRGLAESDLLCFLTALMLLQM LWYVGRSSAHRRLFRLKDTAGAG WLHRLWIPPAFGCRPEYDNGLEEI VFGFEPWIIVNLAMAFSIFYAMHA AASLFEVYSGISETSVLGDWSKPSTF DSKASGLRHLKTSKGKSSLVNASIP TPPSPFRPSQPSEPASQPAKPAKPAK PVSQPSQPSQT\PGKPAKPAKPPKPA KPPASQASQASQPGMPAKPAKPAK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | K/PKPGMPAKPARQPSQPAKTAKPA NQPSQSASQASQPASQPSRPACQPT KSARQPRQPSLPAKRANATYQRS HSASQDRHASEPTSQPSSQHSARP AATSQPDSRAANQSAVEQARQPSA KHSGKQQADSEAAAGS |
| 3820 | 9317 | A | 4099 | 684 | 902 | |
| 3821 | 9318 | A | 4100 | 143 | 551 | TNEFPFHRSRPPQIQTS*AHFPHLITD PDLLSPLSPSHHRSRPPEPTSPISPQIQ TC*AHFPHLITDPDLLSPLSPSHHRS RPPEPTFPISSPVISWAPAI SFPNCCC KQTATDSSGFHFCLIVLIAKSPKRISP G |
| 3822 | 9319 | A | 4101 | 14 | 209 | ASFKVWLIWE*RPWHGTYPSCKNW GKFASGSVTIWFKLPSGPLALSGIL MRLLLLSLSLHENSVS |
| 3823 | 9320 | A | 4102 | 126 | 265 | |
| 3824 | 9321 | A | 4103 | 74 | 196 | NLGMLAHAYNSRNLGGQVRTII*G QKFETSHENISRCLV |
| 3825 | 9322 | A | 4104 | 1 | 217 | NIYMFLICFVLIFNFLNELIT*KHIVIF ICWILSLLLLTLH*FWCHKFHVSW NLEFCIFYFGFKIKLDTFT |
| 3826 | 9323 | A | 4105 | 3 | 268 | DRVLLCCPGWSAVSQS*LTAPQTPG FK*SSHLSPSSWDYRHIPHLAKK QKYFK*RWSLPVLPRLV*NSWAQAI FPCQPPKGLGLQA |
| 3827 | 9324 | A | 4106 | 3 | 263 | DSLALSLRLECSGVISAHCNLCFLGS NNSPAAASRVAGTTGACH*DWLIFE FLVETGFHHIGQAGLELLTEVICLP WPPKVLGLQM |
| 3828 | 9325 | A | 4107 | 22 | 208 | SFSIQGPLLLKPNS*PGVVAHSYNPS TSGGQGRCT*GQEFESSLVHMAKP HLYQKIQKICR |
| 3829 | 9326 | A | 4108 | 122 | 339 | EKGFWFCAQGGKNLPGGNSLEPSA SGLKEIFGLNLLNWE*RGGPKTPG NFWIWKKGGV*PLWPGWG*NPGL |
| 3830 | 9327 | A | 4109 | 2 | 210 | KEKIFPSPGFKHPPPPF*KTPLK GK RIFFSPPRKNWPPQRIFKKAPPSSSSS SSSSSSSAQI*SFNSP |
| 3831 | 9328 | A | 4110 | 3 | 76 | ATSESLDVMAQQR*SRSGSPMARR |
| 3832 | 9329 | B | 4111 | 1 | 2142 | MGGAGSPQVILVSHTPQSASAACEE IAYQVAGVSGNLAPGNQPEKEGRA HQCLECDRAFSSAAVLMHHSKEVH GRERIHGCPVCRKAFKRATHLKEH MQTHQAGPSLSSQKPRVFKCDTCE KAFAPKPSQLERHSRIHTGERPFHCT LCEAFNQKSALQVHMKKHTGERP YKAYCVMGFTQKSNMKLHMKRA HSYAVAVAMGGTAQCPPGATACL GTAICPSGLRAQRPSNLSVPEAAKP KSGRNRKIEAPT WALSTSKDPQTEG LRNPQTCVQIRSNPFCAFAQGFS LIS ELRTLNCVGLCDSQSGKQQLGFYS GQPATEAWQKYS LAVCILRSEQEIS ATRLGLKNTNVNKL DGGCGAWNF LGMSEHNSPPSGRAILLPVVFTEV FPGPWTPEQGSICRMNLAPTQAF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LPKTGFPIDPQELLQGPIERTIWPGT VYTFRSAIVTARAVWVRPRMDRRA DLSSATQSASAEKFGGRVSAGHCA LPLPARPVTASVYGRRLARLRGLED SYPSALSAQVFLDSPAVGCGLETRL FIEAALGPPCRATVTSRGHLLDISIT KSPGRPCFLSVCLHGSDQQKRKGA AATAKRKSKGGGVNVEGRCTWPP EDPPKSWSLAFGPLQEKTELNLHP RCWARCLSHWELPPGPRGRAQAPD WTGSKSFREQLLTFTLWGVQEKISK HQANQGKEAPAYTGLEDSDPGGGLC AV* |
| 3833 | 9330 | A | 4112 | 1 | 551 | |
| 3834 | 9331 | A | 4113 | 3 | 288 | CIGLGVVAHACGPGTLGGRGGRIT* AREFGTSLGNIARSHLYKKRKNSES QMSLHLLTDLTPYISAAFPVDA DTQLSACTFQLKETPMPSF |
| 3835 | 9332 | A | 4114 | 3 | 344 | VQYYGPAT*VQDGS*GYRTHMYMI NQIWLQAVLKIITNKTGRALTILTQ QETQMRNAIYQNRLALDYLLAEG EVC RKFNLCCLHIDNQGQVFEDI VRDMTKLAHVPMQV |
| 3836 | 9333 | A | 4115 | 6 | 185 | LAGHDRVRL*SQLFRRLRREDCLSS GGRGCSEP*SHHHTPVWKTGLGPV SKEKKYNQIV |
| 3837 | 9334 | A | 4116 | 1 | 176 | QSIFQICIFFKFTVYMFKTFKFQTV FLCGRCWFL*KGLIIFFTLYFKTFHH IVRGIK |
| 3838 | 9335 | A | 4117 | 1 | 312 | GGEKNQDFTFKMESPSDSA VVLPST PQASCLSLPSN*DYRHPPPCPANFCI FSRDWVSTHVGPWSRTPDPQVIH RLGLPKTIRGSEEGIPDEYQLKGTLI YKL |
| 3839 | 9336 | A | 4118 | 1 | 112 | GKTFKQKQKQEQKKQK*ELK*KAM GKGPLAAGEIKKS |
| 3840 | 9337 | A | 4119 | 3 | 355 | SQSTKNLPSLARDMDIQIEAQRSP KRSPPRHIFELTKVKDKENPKVPV EKHQVIYKGIFIRITAETSQARKKW DDISKFLKEKKKYRSKILCTANQSIR N*VEIASHSGSCL*SMILTA*PATVA HAYNP |
| 3841 | 9338 | B | 4120 | 638 | 3862 | MKGTCVIAWLFSSLGLWRLAHPEA QGTTCQQRTEHPVISYKEIGPWLRE FRAKNAADFSQLTFDPGQKELVVG ARNYLFRLQLEDLSLIQAVEWECDE ATKKACYSKGKSKEECQNYIRVLL VGGDRLFTCGTNAFTPVCTNRSLN LAEIHDQISGMARCPYSPQHNSAL LTAGGELYAATAMDFPGRDPAIYR SLGILPLRTAQYNSKWLNEPNFVS SYDIGNFTYFFRENAVEHDCGKTV FSRAARVCKNDIGGRFLLEDTWTF MKARLNC SRPGEVPFYYNELQSTFF LPELDLIYGIFTTNVNSIAASAVCVF NLSAIAQAFSGPFKYQENSRSALP YPNPNPHFQCGTV DQGLYVNLTER |

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|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | NLQDAQKFILVHEVVQPVTTVPSFM EDNSRFSHVAVDVVQGREALVHIIY LATDYGTIKKVRVPLNQTSSSCLLE EELFPERRREPIRSLQLHSQSULFV GLREHVVKIPLKRCQFYRTRSTCIG AQDPYCGWDVVMKKCTSLEESLS MTQWEQSISACPTRNLTVDGHFGV WSPWTPCTHTDGS AVGSCLCRTRS CDSPAPQCGGWQCEGPGMEIANCS RNGGWTPWTSWSPCSTTCGIGFQV RQRSCSNPTPRHGGRVCVGNREE RYCNEHLLCPPHMFWTGWGPWER CTAQCGGGIQAARRRICENGPDCAGC NVEYQSCNTNPCPELKKTPWTPW TPVNI SDNGDHYEQRFYRTCKARL ADPNLLEVGRQRIEMRYCSSDGTSG CSTDGLSGDFLRAGRYSAHTVNGA WSAWTSWSQCSRDCSRGIRNRKRV CNNPEPKYGGMPCLGPSLEYQECN TLPCVDGVWSCWSPWTKCSATCG GGHYMRTRSCSNPAPAYGGDICLG LHTEEALCNTQPCPESWSEWSDWS ECEASGVQVRARQCILLFPMGSQCS GNTTESRPCVFDNFIPEVSVARSSS VEEKRCGEFNMFMIAVGLSSSILG CLLTLLVYTYCQRYQQQSHDATVI HPVSPAPLNTSITNHINKLDKYDSVE AIKAFNKNNLILEERNKYFNPHLTG KTYSNAYFTDLNNYDEY* |
| 3842 | 9339 | A | 4121 | 3 | 124 | NVNRPVSSNEIKIIKSLPVKKSP*LN GFNAEFTKHVKNL |
| 3843 | 9340 | A | 4122 | 1 | 197 | GFKQLS*LSLPNSWDHRHTTTTPRE MGFHHVGQAGPELPISGDPPAPASQ SAGITGVSHRTRPRI |
| 3844 | 9341 | A | 4123 | 1 | 268 | QLYHLSLQSSRDHRCEPPRPANFLII CRDEVYVAQAGLKLPSSTDPPASAS KSAGSTGVSHCTQAKFYFF*NLMG EMRGKNNKHLTSFK |
| 3845 | 9342 | A | 4124 | 3 | 301 | TEEIHGVL SWNLVPDNYPPYYHPPP PSYIYGAQHLLRLFVKLPEILGKMT FSDKNLKALLKHFDLFLKHLAEYH DDFFPE*AYVAACEAHYCTHNPRSI |
| 3846 | 9343 | A | 4126 | 2 | 214 | FFFFKEMGSHYVA*AAVKWLF TGA IITL*SLKLLDSNNTPALSECKLIITQ EASVLKIKKVEIKKTKNRN |
| 3847 | 9344 | A | 4127 | 2 | 382 | TMVLSPADKTNVCAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKL RVPVNFKLLSHCLLV T LAAHLPAEFTPAVHASLDKFLASVS TVLT SKYR |
| 3848 | 9345 | A | 4128 | 2 | 253 | |
| 3849 | 9346 | B | 4129 | 317 | 683 | AHKLRVDPVNFKLLSHCLLVTLAA HLPAEFTPAVHASLDKFLASVMHR ADLQIPLSWSLATGCQK LIEVDDER KLRTFY* |
| 3850 | 9347 | A | 4130 | 1 | 82 | VDGWVDGWVDG*MDR*VGRWID |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|--|---|----------------|-------------------------------------|---|--|---|
| | | | | | | GWVDG |
| 3851 | 9348 | A | 4131 | 1 | 240 | ASTFFFFSIDRVLLCCPGWTRTPGFI* SSCFGLPKCWDYRSEPPCLATFFFIK KKYKEEHFILLCQIVNMILLYQPT Q |
| 3852 | 9349 | A | 4132 | 3 | 180 | REPPLPAANFVFFVEMRSHHVRQA GPEPPSSDLPASASQSAGITGVHCH AWP*YTYL |
| 3853 | 9350 | A | 4133 | 2 | 238 | SPCAGILEDDRADYQGTRKTSEYSS VTP*EACHT*EGPIAFISWP*KVPIQL TFNERNRARGFQVPYGTYDRGLPG TH |
| 3854 | 9351 | A | 4134 | 7 | 259 | IVTAALFTLAPNQK*SKYPSSGKLIN KFWYIYKME*TSISNKQVSTTYSMQ AWVNLKSITLS*RHKGVYII*SHLYD ILEKTEL |
| 3855 | 9352 | A | 4135 | 141 | 309 | AFDEAIAKLYSVNE*SYKGSTVIMQ LVRVNLAVSATSTGFIVSFVFTYPIIP CYLQ |
| 3856 | 9353 | A | 4136 | 113 | 205 | HNLLMLFDLCLLYWL*LIFLIHELAE NLLN |
| 3857 | 9354 | A | 4137 | 3 | 215 | FETGSCSVTQAGVHWRDHSSLQP*S LGFKQPSNLSLPSSWDYRCTPPHLA NLCIFCKDRVTSYCPGWHPV |
| 3858 | 9355 | A | 4138 | 3 | 386 | |
| 3859 | 9356 | A | 4139 | 1 | 255 | IRLMKEGRMKGQAFIGLPNEKAAA KALKEANGYVLF GKPMVVQFARSA RPKQDPKEG*RKRTWLFNKVGK WELAPKPMGLDFSL |
| 3860 | 9357 | A | 4140 | 78 | 153 | |
| 3861 | 9358 | A | 4141 | 1 | 293 | LRLPGSSHSPASVS*VAGIAGACHH AWPNFCVFSRDQGFTHVGRAGLGA PDPLDPALPWSPKVMGFTRCEAHP CPSPRMRFLKYVSVPMVMVGRPE |
| 3862 | 9359 | A | 4142 | 3 | 48 | PLPRKSVEPGGGTKYKTEQKKRQE RRDRGSK*RKQKKAATSEEQQRK* AKTQEDGGTKRSPDGEEDPEKKIHR NREGTRKKGQDPRNGVNNKNREK EQN*RTHTS*SQKVRRTRRGNEV |
| 3863 | 9360 | A | 4143 | 1 | 276 | GTRDSV*GGLKLIPIFLMDFWKEPL GPALAHQLQYPGRD*SSDIWIRTA SLHTLPIVGPHLLGDLASFCTLLTPD PCQHVP RSRADTVEMG |
| 3864 | 9361 | A | 4144 | 1 | 154 | LVWS*EASKIPGGAEAAHPPTTF |
| 3865 | 9362 | A | 4145 | 2 | 231 | FFFESGSRSVTQAGVQ*HSLGSLQPL PPRFK*FSCLSLPSSWDYTHVPT NFCIFSGDGVSSCWPGWSRTPNLR |
| 3866 | 9363 | A | 4146 | 1 | 303 | GTRGSVKEGAKYTSHRDMGLSTFD RDADQWKENCANVYG*GCRYNNC QAANLNGIYYPGGSYDPRNNSAYE TDNGVWVVSFTGAHYSRAARMKI RPLVTQ |
| 3867 | 9364 | A | 4147 | 3 | 372 | HAGLGAHPLHHPVIOQEGFLPAPRG FGYRSEVD*IRIPAESTGQNSQCQLR K*KDDSYFHCYFCGCVCTCRGRL QSSTSHQCQAAL*LLPVCLTMLRC ISSLIYT*NLKTVHSVRLNFIYN |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| 3868 | 9365 | A | 4148 | 2 | 98 | RRPFFFFFFFASCI*NLISPNVQLSNFT CILRN |
| 3869 | 9366 | A | 4149 | 1 | 230 | SGRPFLFFFQKERVYFIPVVVLFYT VVVQ*LRKNVVRWQKTMEPPRSW LMQLGHTEEGPGYPLLGETETKLFR TA |
| 3870 | 9367 | A | 4150 | 1034 | 2354 | DRVLAPVAQTGVQWHDLSLQPPP PGFKRFFCLSLPSSWDYRPP*RPAN FC*FLVETGFRHVGQAGLGLTSGD PPASASQSSRITGVSHRARTMGLSR ALYRIPALKVWLLINVELKKQMMMA HVDVTCLINKSPSLTRPMGKRLSAE TGKGQKEKQKQTGAGCAVLPSRGF PPKAHHGRQPLTLAPSPPTFSPSP PHTHTHTHTCSPICPRQSRSFQGPR MPDPDPGDATCGAGPGGSAPARAA GPRSAPRRAKARVQARVQARAQAR WVRALTLLAAHPRLQVPARIARR AAQSSSSPPATPAKSPPEASGAAA PPALGLERFPGASPNHLTRSTCALR HVGAGGAALGGPGAPRLPHRLEV REEGRGRRGDGLGHGGCVEPAWEP GWRLPSTIKLFIKSKVSSEALEMPFL CICEHLLSYTYSRKHRNVI |
| 3871 | 9368 | A | 4151 | 387 | 478 | |
| 3872 | 9369 | A | 4152 | 757 | 1477 | HKENRNSLELRQNQSSPIWALPLHG LERKGLGRDHSSPHLPLLPSERL*K ASASQGPWECCPSRAAGPESGRCD QLWESPMASATWKPYRPQPSRSPQ RQRVVLPLVKGKTPPLFKLLQESV PGDLLPGELSL*PWEKPI*NNFAFNF SQQCKGMFKFPQFRSLARGSNPTSL TGVGPLPLPREFPGEEREGAPQIFKQ NTANGLGPSA*MRAGTAQGCWES* GGNTAPGPGAVNTAN |
| 3873 | 9370 | A | 4153 | 32 | 255 | SRRHDSLHRVTFCISDPHYRKWTNP DGTTSKIFGFVAKKPASPWENVCHL FAKLDPY*PAGAIVTFTNVPTAP |
| 3874 | 9371 | A | 4154 | 1 | 265 | CDTVLLCHPGWSAVAQSQLTTTSA SQIKRFSCNLNPSSQNTRRASHPAN FFYF**R*GFTMLVRLVSNSCPQVIH PPLPPKVLGLQA |
| 3875 | 9372 | A | 4155 | 92 | 333 | FLSFFFF*MGCHSVTQCGVKWHDLS SLQPPHLTFKWFSRLSLLSGWDYRC LAQHQAACCIFSRDGISPF*PCWYQT PDLR |
| 3876 | 9373 | A | 4156 | 16 | 181 | ICSLPSTVDVIEFLDYVVKVSLKL*SI IKICDSDKHTHIHTYGYVYIFSPGK PV |
| 3877 | 9374 | A | 4157 | 1 | 355 | TVSLSCSVAQAGVQWHNLGSLQPL PPGFK*FSCLSLPSSWDHRCPPCLA NFCIFL*RWGFARFCHVGEAGLELL TSSDLHTSDSQAIGTSHHAWPH LLVLTCVCAHTLFRHFYL |
| 3878 | 9375 | A | 4158 | 1 | 194 | FFFFFTISYIFYTLTTCWEFKQLAGN I/HL*GTVAFFYLKLLKLQDRLTNSF SSATTNVLAENS |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| 3879 | 9376 | A | 4159 | 112 | 270 | ILGNSLFKNYK*YLSPPAAVTHACNP NTLGGQGGPVT*AQEFETSLGNIVR PCL |
| 3880 | 9377 | A | 4160 | 1 | 211 | RFSCLSLLSS*DYRRVPPRPAIFVFL VETRFHYVGQDGLDFLTSCSARLYL PKCRDYRRELLCPAPASLL |
| 3881 | 9378 | A | 4161 | 2 | 253 | ETDSCSVAQTRVQWYDLGSLQQPP PRFKRFSCLSLPNSWDYKCVPTPI* FFLFLVEMEFHCAGQADLELLGSGD PPASAPK |
| 3882 | 9379 | A | 4162 | 198 | 276 | KPFMAQCSF*IYEAFSCTSSEIRY |
| 3883 | 9380 | A | 4163 | 3 | 193 | HFGRPRRADCLRSSV*DQPGQHGET PSTKNTKISQAWWWVPVPTT*EA EAGESLEPGGQRLQ |
| 3884 | 9381 | A | 4164 | 2 | 515 | DTEKMSPWDMELIPNNAVFPEELG TRVPLTDGECKTLIYKPLDGEWGTN PRDEECERIVAGINQVMTLDIASTFV APVDLQAYPMYCTGVAYPTDLSSI KQRLNRFYRRVSSLMWEVRYIEH NTRTFNEP*KPNGRPAKSGTDLLLH FIKDQTCYNIPLYNMCKKVL |
| 3885 | 9382 | A | 4165 | 3 | 418 | HEADKTNVVTGKTEVGAHAGEYG AQALERMFLSFPTTKTYFPHFDLSH GSAQVKGHGKKVADALTNVTRIK EMRNALCTLSDLAHKLLGDSCITL *LLSHCMLVTLAN*PSSEFTPAHTL VAKILAFVSTELTSKY |
| 3886 | 9383 | A | 4166 | 1 | 191 | CLETECRYVSQAGMQWHYPG*LQP *PPGYKLSSHLSLPSSWDYRHVPEH PTNFVYFFVERKSH |
| 3887 | 9384 | A | 4167 | 3160 | 3732 | |
| 3888 | 9385 | A | 4168 | 2 | 326 | PRSGSESFSCQLSPFFFFGDRVSLC GPG*SAVV*LQLM*PGPPKLKQSSC LCLPSSWDHRWAAPHLA*FFKFFFI ETGSYHLPQLVSNPWAQASLLPWP PKVLGLQV |
| 3889 | 9386 | A | 4169 | 2 | 163 | LIFVFVIVGTGFHHVGQAGLECLTSS DPSASASQSAGITGVNHHTRPPSAF GC*T*GTGFHHVGQAGLECLTSSDP SASASQSAGITGVNHHTRPPSAFGC |
| 3890 | 9387 | A | 4170 | 126 | 348 | HISIFETGSYSVTQAGAQLDGHSL QP*PPGLK*SSCLSLPSSWDYRHMPP CPANFYIFCRDGVSPRCSCGNF |
| 3891 | 9388 | A | 4171 | 1659 | 1970 | MLKGGAKIRSRRKTGVSHSLHSDL NFFFFWDKSIALSHRLEYNGAISAH CNLRLLGSSDSPASAS*VARITGMR HHTQLILVFFSRNGVLPCWPGWSRT PDLR |
| 3892 | 9389 | A | 4172 | 153 | 278 | MRPDTVAHTCNPSTLGGQGGRIT*T HEFETSLGDMMKPYLYK |
| 3893 | 9390 | A | 4173 | 3 | 254 | LQYLVISSKAWPS*KLEDGET*SA GENNNYNTIL*LDLFSHREGKWSKI PYV*AFFALQNNRKLCCQCIIDLALI AVISSQT |
| 3894 | 9391 | A | 4174 | 3 | 225 | SLTHLTATSILLK*FSCLGLPSSWDH RCPPLRLANFFAFLVETDFTMLARL V*NS*PEVIRSPRPSKVLGLRA |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 3895 | 9392 | A | 4175 | 1 | 344 | GGALSGGTPGFSPSPPGKTAAPGQS GNPPGGF*RVSPGGSQRGGFPGNT PAPGPLPSSSSSSKGGFGDCTPRDKS RKGGKPPFS*GGFFPQGSAPVKHLA APTNR YTSFHPQK |
| 3896 | 9393 | A | 4176 | 2 | 201 | QPGQY GKH PVL IKN SKIKPFWGDP VVPNAREG*A*KMVEPGKVRVQSA QIKALEFNLGPKKKVPF |
| 3897 | 9394 | A | 4177 | 39 | 225 | KSIQSYAI*YNVTCGFFKSALNGVG SVAFCSHHAEHFLGFVFINHEKS FQ FCQMLLLCMTR |
| 3898 | 9395 | A | 4178 | 322 | 451 | INSTDWAPWLT LVISALWEAEAA/G SRGQEIETILANTVKPRLY |
| 3899 | 9396 | A | 4179 | 234 | 383 | |
| 3900 | 9397 | A | 4180 | 86 | 216 | KQTLGQAWWLTPHIALWEAEVGR S*DQEIETILPNTVKPHRY |
| 3901 | 9398 | A | 4181 | 1 | 4123 | MEEVEEDRFKENLEGALAGQLLGD EATQALQVLAVELDVVVP GALHPQ RLHRLGAALVERQPVREVDHLVLP AVDDEHGRDLGHLLDVREGVEA VGLLGVAEGDAHARGERRVQHHR GTLVARGQVHGGHRADALPVQDD AVRADAVPGGAGAGSAAASNARA PFPPAGVPGPSSGCDPPVSPLSQVSA HWELCGPHILNASYLPARVRKPFLV HWPQGRTFLPAALAHPLGHEEFR QLCPQMSPNFGLESERPVRCQCN PGQHRGWLRRWHPLPPAPSLGSG QVLGHLSTTSSHPGAPSPPGHWCAA PDPADPAPVTRPPRAQSQARGTHLP PCPCRDPTLLPHALGSDPRQTPSC KAGAWAGRSPQLPPGCHHSNERDT SPVEALGTLWPPPHGSGPRFLQDKG AAGQMAEQTEL RAGHGRMAKLRS HRASWASPPDLAAASPHLAPSAA SADGLPATRAQTPRPPTPSRQALP PGSPSPAQGLPGGVDVGIEVPLGR PARAGTVAGGVGEDVAVEAGAQ ANVEAAHLAQVHGIAVREEDRVPG TRHAANIHAGDTVAAGALGGEDLD GVQLALAVLEVGT LRQGFWWTLR GTDVETYPFSAPRAASHGVGRHEEL PDPTGPCGGRLLSLTIHGV TIRYHAL LWARGPIMSKSQVLGEWEPVQGGK SSENDKWTMSDPGAEAPTCSRAAS GVDKEQQGRWQGLWNSHIKPLKIR MVKQNNIIPGETQILLRFTGWESKV NAKKQLPVGIKCEPMDQENEQTGG HETDGHRIVS VLIHFPLISILSYATW GLSLLCIPGSPVCTLLVRFSNVGTR WSLEVRGSPCGFGSNKVCVMTPEI KMVCVCEGKAGKAVGSGGVEGTK EVSTGNAEGPVRHEAVDGGVHLAF ALLQGLLWSLLLGPPLAGWGGGE LDAVPDSTSSATNVSMVVSAGPWS SEKAEMNILEINEKL RPQLAENKQQ FRNLKERCFLTQLAGFLANRQKKY KYEECKDLIKFMLRNERQFKEEKLA |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | EQLKQAEELRQYKVLVHSQERELT QLREKLREGRDASRSLNEHLQALLT PDEPKSQGQDLQEQLAEGLDWH STLSKSSAQKMTKMRMKMFK/CEE DEKVLESSAPREVQKAEESKVPEDS LEECAITCSNSHGPCDSIQPHKNIKIT FEEDKVNSSLVVDRESSHDGCQ/EC SKHSPSPWPHLFCHKRQHGG/DQPA LCPARRQR*TF*KSMRNCA/HQLAE KKQQFRSLKEKCFVTQVACFLAKQ QNKYKYEECKDLIKSMLRNERQFK EEKLAEQLKQAEELRQYKVLVHSQ ERELTQLREKLREGRDASRSLNEHL QALLTPDEPKSQGQDLQEQLAEG CRLAQHLVQKLSPENDEDEDVQ VEEDEKVLESSAPREVQKAEESKVP EDSLEECAITCSNSHGPCDSIQPHKN IKITFEEDKVNSSLVVDRESSHDGC QDALNILPVPGPTSSATNVSMVSA GPLSSEKAEMNILEINEKLCPQLAEK KQQFRSLKEKCFVTQVACFLAKQQ NKYKYEECKDLIKSMLRNERQFKE EKLAEQLKQAEELRQYKVLVHSQE RELTLREKLREGRDASRSLNEHLQ ALLTPDEPKSQGQDLQEQLAEGC RLAQHLVQKLSP |
| 3902 | 9399 | B | 4182 | 1 | 799 | MLQIPKQQQNEKYQVPQFDQSTIKN IESAKGLDVWDSWPLQADGTVAE YNGYHVVFALAGSPKDADDTSIYM FYQKVGDNIDSWSKNAGRVFKDSD KFDANDPILKDQTQEWSGSATFTSD GKIRLFYTDYSGKHYGKQSLTTAQI HFPLISILSYATWGLSLLCEIPGSPVC TLLVRFSGGPPMDPGSERKGFCRF RNHHQTGFSPAGANQRGPLAATLS GPGGEGQSAVARLTGEKKNHPGAQ YANRLSPRVGRFINAAGTTX* |
| 3903 | 9400 | A | 4183 | 260 | 387 | REVGRVRWLTPVIPARWEAEVGRS *GQEIKTILANTVKPRLY |
| 3904 | 9401 | A | 4184 | 1212 | 1442 | |
| 3905 | 9402 | A | 4185 | 3844 | 4180 | KYKKCVGCGGRSL*S*LLRRLRQEN RLSPGGGDCSEPRSSHCTPAWVTER /GDSVSKKKKKNLLTWLVNKLCP CRAWWLTVPVIALWEAEAGRSRGQ EITILANTVKPRLY |
| 3906 | 9403 | A | 4186 | 8 | 385 | |
| 3907 | 9404 | A | 4187 | 2 | 284 | |
| 3908 | 9405 | A | 4188 | 1477 | 1697 | |
| 3909 | 9406 | A | 4189 | 17 | 385 | |
| 3910 | 9407 | A | 4190 | 1 | 837 | GKVVLELERFLPQPFTGEIRGMCDF MNLSLADCLLVNLAYESSVFCTSI AQDSRGHIYHGRNLDYAFGNVLRK LTVDVQFLKNGQIAFTGTTFIGYVG LWTGQSPHKFTVSGDERDKGWWW ENAIAALFRRHIPVSWLIRATLSESE NFEAAVVKLAKSPLIADVNYIAGG TCPREGVVVTRNRDGPDIPLNPL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NGAWLRVETDYYHWKPAPKEDDR RTSANKALNATGQANLKLEALFQIL TVVPVYNNLTIYTTAMSAGSPYKY MTRIRNPS |
| 3911 | 9408 | A | 4191 | 653 | 727 | |
| 3912 | 9409 | A | 4192 | 26 | 161 | |
| 3913 | 9410 | A | 4193 | 3 | 186 | |
| 3914 | 9411 | A | 4194 | 28 | 186 | |
| 3915 | 9412 | A | 4195 | 356 | 428 | |
| 3916 | 9413 | C | 4196 | 35 | 430 | MKSCRXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXSETNSWEATRKNPFSSNSSEAFIS RSQGHKDAKKEFVPLXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXLQSHPLVR* |
| 3917 | 9414 | A | 4197 | 213 | 394 | |
| 3918 | 9415 | A | 4198 | 28 | 123 | |
| 3919 | 9416 | A | 4199 | 1578 | 1835 | SNKSLPHNCIPPQMRNYSRGNLLQY IDYVQLHRNLYAGEIYFHC*RKSA CNSSWREGAVGCLPMDFPRLHLSL SPSSLHCRNKP |
| 3920 | 9417 | A | 4200 | 213 | 305 | |
| 3921 | 9418 | A | 4201 | 1715 | 1850 | |
| 3922 | 9419 | A | 4202 | 4016 | 4315 | |
| 3923 | 9420 | A | 4203 | 28 | 239 | |
| 3924 | 9421 | A | 4204 | 7 | 216 | |
| 3925 | 9422 | A | 4205 | 1 | 576 | |
| 3926 | 9423 | A | 4206 | 1 | 500 | |
| 3927 | 9424 | A | 4207 | 1 | 1266 | |
| 3928 | 9425 | A | 4208 | 1 | 162 | |
| 3929 | 9426 | A | 4209 | 1 | 229 | |
| 3930 | 9427 | A | 4210 | 197 | 416 | |
| 3931 | 9428 | A | 4211 | 1 | 131 | |
| 3932 | 9429 | A | 4212 | 76 | 274 | |
| 3933 | 9430 | A | 4213 | 295 | 2530 | RPATMAARLPVSPARALLLALAG ALLAPCEARGVSLWNEGRADEVVS ASVRSGDLWIPVKSFDKNHPEVLN IRLQRESKELIINLERNEGLIASSFTE THYLQDGTDSLARNYTILGHY YHGHVIRGYSDSAVSLSTCSGLRGLI VFENESYVLEPMKSATNRYKLFP KKLKSVRGSCGSHHNTPNLAAKNV FPPPSQTWARRHKRETLKATKYVE LVIVADNREFQRQGDLEKVKQRLI EIANHVDKFYRPLNIRIVLVGVEVW NDMDKCSVSQDPFTSLHEFLDWRK MKLLPRKSHDNAQLVSGVYFQGT IGMAPIMSMCTADQSGGIVMDHSD NPLGAAVTLAHELGHNFNMHDTL DRGCSCQMAVEKGGCINASTGYP FPMVFSSCSRKDLETSLEKGMGVCL FNLPEVRESFGGQKCGNRFVEEGEE CDCGEPEECMNRCCNATTCTLKPD AVCAHGLCCEDCQLKPAGTACRDS SNSCDLPEFCTGASPHCPANVYLHD GHSCQDVGDCYNGICQTHEQQCV TLWGPGAKPAPGICFERVNSAGDPY |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|--------|-------------------------------------|---|--|---|
| | | | | | | GNCCKVSKSSFAKCEMRDAKCGKI QCQGGASRPVIGTNAVSIETNIPLQQ GGRILCRGTHVYLGDDMPDPGLVL AGTKCADGKICLNRCQCNISVFGV HECAMQCHGRGVCNNRKNCHCEA HWAPPFCDFGFGGSTDSPGPIRQAG KEARQEAESNRERGQGEPLGSQ EHASTASLTLI |
| 3934 | 9431 | A | 4217 | 2 | 119 | |
| 3935 | 9432 | A | 4218 | 2 | 147 | |
| 3936 | 9433 | A | 4219 | 10 | 216 | |
| 3937 | 9434 | A | 4220 | 245 | 455 | |
| 3938 | 9435 | A | 4221 | 1 | 2867 | MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQATGTSRWDG VSKKAPRHLSVPCTRPREARQEAE DSTSRLSAESGETDQDAGDVGPDI PDSYYGLLGTLPCEALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHIGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGQRMVEQSE KLVGVLEASRLWDMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLQPLPHFRVESFSE DEWNLLYAVTRAKKRLIMTKSLE NILTLAGEYFLQAE LTSNVLKTGV VRICCVG\QCNNALSPVDTVLTMK KL\PIY*ATGK\ENKGGYLCHSCAE QQHRDPWRFLTASPEQVRAMEPHF GGTSYCPRHEALLFLVF |
| 3939 | 9436 | A | 4222 | 57 | 302 | |
| 3940 | 9437 | A | 4223 | 1 | 550 | DAHIIGRIESYSCKMAGDDKHMFK QFCQEGQPHVLEALSPQTSGLSPS RLSKSQGEEEGPLSDKSRKTLFY LIATL NESFRPDYDFSTARSHFSRE PSLKLVLGNVNC SLFSAVREDFKD LKPQLWNAVGRGDLPLKCDIYS\Y |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NPDLDSDPSREDGSLWSFNFFYNKRLKRNRL |
| 3941 | 9438 | A | 4224 | 11 | 511 | GRTRSIAGEETTQRPGPNCCGGNCLCLHTLAINMRICYSQTTFFHPLRLKGQRWPFSSLELFPVGFPPRAHLLVQSTLPKPRPERAFTAPSLFPVTLGFCLGRILCQRLLLCPSCLATALSINGYSRTQECQSWKGRDTGLHKGKLLLEALGGTEGFGDRARAKIEDS |
| 3942 | 9439 | A | 4225 | 1 | 279 | |
| 3943 | 9440 | A | 4226 | 1011 | 1322 | |
| 3944 | 9441 | A | 4227 | 3 | 468 | TPLHVVYNEVMSVGGQKYGIRNAGYYALRSLRIEKFFAFWQDINNLTPLTCGRESRVKLEKGMDFIGRDALLQKQNGVYKRLTMFILDDHDSDDLWPWWGEPIYRNGQYVGKTTSSAYSYSLEHRHVCLGFVHNFS EDTGEEQVVTADFINRG |
| 3945 | 9442 | A | 4228 | 1 | 1236 | |
| 3946 | 9443 | B | 4229 | 1 | 1742 | MKRDNSGGCLPAPASAWPARPRQQAEWRALTRGPANHCGIISTLGEPPEPLIGLRTFQCCRLVTDGRVLAGTVSSEPTDGFRSPAPGPGRRTSAMVLLKLGKTPGEFFPFLGSSSQPPSHELNI GKRLDDTKILPGNMKDNFWEMGDTGPCGPCSEIHYDRIGGRDAAHLVNDQDPNVLEIWNLVFIQYNRFGNCVELQASAAFNWNNQRCKTRNRYICQFADLRRNLNIINDDITGRVHKDRKLLTGDSPFANALGKLAAQEMMAAYAVSLPKLTALLRVFSTVVRISIGERFSPIRVLRLRLRHTTPNYIYQRLIPYVCVLPPTTELSINLNMLTENDIPLFRALFLNNITDADARVLLQKRPREGWLTTDAFLYWAQQDFSGVKPLVAQHWEMTFADSADSVSSVHTLTDDLPLESLADQPGAGNVHLLIPPEGLLYRSLTLPNAKYKLTAQTLQWLAEETLPDNTQDWHWTVVVDKQNESVEDCLIPLFGKPGKGKCLEKSVWAAGRPF SYAGDKNRQLTRYSDTRWHEDSVNRNRFWSVMVGPSVRVNEWFSAYAMAGMAYS RVSTFSGDYLRVTDNKG S* |
| 3947 | 9444 | A | 4230 | 1 | 638 | |
| 3948 | 9445 | A | 4231 | 1377 | 1746 | |
| 3949 | 9446 | B | 4232 | 1 | 1716 | MSQYYQPQRPPHEIHLDSHAKFFPHHHLQVADSAAHLAASPLRRTHRALTWAQALPQEEGSGAPSPGAPSPPTKSFGRMTMSASAVFILDVKGKMESC YVVQDVLNSWSPAIPLLQPPKVSDDSGGHHIEECQCLPVYSFLYKTIEVGLRILQGAGGGEHPDNFVIVYELLDELMDFASRRPPTARSCRIHHSAEQQA GDGQVTGAPTVTNAVSWRSEGIKSMQRQRPSENRNRYHQAQVFLSGMPELRLGLNDRVSSSSLAAGQFKKSQWPTVWRYLCLYPAMRLPQIQDQCG |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|--------|-------------------------------------|---|--|--|
| | | | | | | QRQVCAGRNVVIWSIKSFPGGKEYL MRAHFGLPRWKRKRWRAGPPSGSS LDPLLHRLWDPGPMKIIKSGYQA LPWVRTSPRVAIPTSYQLEGRDGG LNTGFLTAPDADFRGRAGEEPAGR AGVSGWGAGTESSAAGCTAAAPRE GCSASARLLRADSAAGLGRAGGFA GRQCRHAAGGGCAGDRLSGAAAR GDVQECAAFTGWSWCIPSTLRQD GAAGFIVPPQSPFEGHDVWQHRHR PELLKQGASPNVQDTSQTVQSMTQ PALDSWTP* |
| 3950 | 9447 | A | 4233 | 1 | 372 | |
| 3951 | 9448 | B | 4234 | 48 | 1158 | MSASAVFILDVKGKPLISRNKGDV AMSKIEHFMPLLVQREEGALAPLL SHGQVHFLWIKHSNLYLVATTSKN ANASLVYSFLYKTIEVFCEYFKELE EESIRDNVVIVYELLDELMDFGFPQ TTDSKILQEYITQQSNKLETGKSRVP PTVTNAVSWRSEGIKYKKNEVFIDV IESVNLLVNANGSVLLSEIVGTIKLK VFLSGMPELRLGLNDRVLFELTGRS KNKSVELEDVKFHQCVRLSRFDND RTISFIPDGFELMSYRLSTHVKPLI WIESVIEKFSSHRSVEIMVKAKGQFK KQSVANGVEISVPVPSDADSPRFT SVGQRQVCAGEKRRYFGVLSLSGG AREYLMRAHFGLPKCEKERX* |
| 3952 | 9449 | B | 4235 | 153 | 458 | KKDLSLEEIQKKLEAAEERRKSHEA EVLKQLAEKREHEKEVLQKAIEEN NNFSKMAEEKLTHKMEANKENRE AQMAAKLERLREKDKHIEEVRKTK NPRPC* |
| 3953 | 9450 | A | 4236 | 3 | 182 | |
| 3954 | 9451 | A | 4237 | 49 | 607 | NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILS PRAKEFVPEFPLSPPKEEGFFPGGKF REN*EAAVEERRQSP*SCSS*RQLAE KLRAPRKKCFQKAIEENNFQ*NGQ KRKLTPHKMEANKETPERPQMAIA KLEPFAEEKDKAH*KKCGKNKESK DPADETEAGLI |
| 3955 | 9452 | A | 4238 | 1 | 356 | TELQQEQLQTVVGTYHGSPDQSHQ VTGNHQPPQONTGFPR/SNQPYYN SRGVSRRGSRGARGLMNGYRGPAN GFRGGYDGYRPSFSNTPNSGYTQSQ FSAPRDYSGYQRDGYQQNFIP |
| 3956 | 9453 | A | 4239 | 1 | 2206 | RLPPAFSSLSLRSEDALGHQPQRERS KSSGPPPPSGSSGSEAAAGAGAAAP ASQHPATGTGAVQTEAMKQILGVI DKKLRNLEKKKGKLDYQERMNK GERLNQDQLDAVSKYQEVNNEF AKELQRSFMALSQDIQKTIKKTARR EQLMREEAEQKRLKTVLELQYVLD KLGDDDEVRTDLKQGLNGVPILSEEE LSLLDEFYKLVDPERDMSLRLEQY EHASIHLDLLEGKEKPVCGTTYK VLKEIVERVFQSNYFDSTHNNHQNGL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CEEEEADSAPAVEDQVPEAEPEPAE EYTEQSEVESTHEYVNRQFMAETQFT SGEKEQVDEWTVETVEVVNSLQQQ PQAASPSVPEPHSLTPVAQADPLVR RQRVQDLMAQMGGPDNFIQDSML DFENQTLDPAlVSAQPMNPTQNMD MPQLVCPVHSESRLAQPNQVPVQP EATQVPLVSSTSEGYTASQPLYQPS HATEQRPQKEPIDQIQATISLNTDQT TASSSLPAASQPQVFQAGTSKPLHS SGINVNAAPFQSMQTVFNMNAPVP PVNEPE\TLKQ\QNQSQA\SYNQSFSS \QPSPS*QQTELQQ\EQLQTVVG\TY HGS\QDQSHQ\VTGNHQQ\PPQ\QNT GIST*AIRPYNSRGVSRGGSRGAR GLMNGYRGPIANGFR\GGYDGLPAP SFLCLKPNSGY\SHSPQFQCLPRDYL WPIQRDG\YIQQNFKRGSGQSGPRG APRGRG\GPPRPNRGMPQMNTQQV K |
| 3957 | 9454 | A | 4240 | 1 | 151 | |
| 3958 | 9455 | A | 4241 | 5 | 120 | |
| 3959 | 9456 | A | 4242 | 1 | 315 | EQMVSEDVPC/D/HRVHARIIGSR/G KAIRKIMDEFKVDIRFPQSGAPDPN CVTVTGLPENVEEAIDHILNLEEEYL ADVVDSEALQVYMKPPAHEEAWP CPLRTCSTV |
| 3960 | 9457 | A | 4243 | 107 | 4057 | PFCCGFPGLCVGVRSTMSSVAVLQTQ ESFAEHRSGLVPPQIKVATLNSEES DPPTYKDAFPPLPEKAACLES AQEP AGAWGNKIRPIKASVITQVFHVPLE ERKYKDMNQFGEQEQA KICLEIMQ RTGAHLELSLAKDQGLSIMVSGKL DAVMKARKDIVARLQTQASATVAI PKEHHRFVIGKNGEKLQDLELKTAT KIQIPRPDDPSNQIKITGTKEGIEKAR HEVLLISAEQDKRAVERLEVEKAFH PFIAGPYNRLVGEIMQETGTRINIPPP SVNRTIVFTGEKEQLAQAVARIKK IYEEKKKKTTTIAVEVKKSQH KYVI GPKGNSLQEILERTGVSVEIPSDSIS ETVILRGEPEKLGQALTEVYAKANS FTVSSVAAPSWLHRFIIKKKGQNL KITQQMPKVHIEFTGEDKITLEGPT EDVNVAQEQIEGMVKDLINRMDYV EINIDHKFHRHLIGKSGANINRIKDQ YKVSVRIPDSEKSNLIRIEGDPQGV QQAKRELLELASRMENERTKDLIIE QRFHRTIIGQKGERIREIRDKFPEVII NFPDPAQKSDIVQLRGPKNEVEKCT KYMQKMVADLVENSYSISVPIFKQF HKNIIGKGGANIKKIREESNTKIDLP AENSNSETIIITGKRANCEAARSRLS IQKDLANIAEVEVSIPAKLHNSLIGT KGRLIRSIMEECGGVHIHFPVEGSGS DTVVIRGPSSDVEKAKKQLHLAE KQTKSFTVDIRAKPEYHKFLIGKGG GKIRKVRDSTGARVIFPAEDKDQD |

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|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | LITIIGKEDAVREAQKELEALIQNLD NVVEDSMLVDPKHHRHFVIRGQV LREIAEEYGGVMVSFPRSGTQSDKV TLKGAKDCVEAAKKRIQEIIEDEA QVTLECAIPQKFHRSVMGPKGSRIQ QITRDFSQIKFPDREENAVHSTEPV VQENGDEAGEGREAKDCDPGSPRR CDIIISGRKEKCEAAKEALEALVPV TIEVEVPFDLHRYVIGQKSGGIRKM MDEFEVNIHVPAPELQSDIIAITGLA ANLDRAKAGLLERVKELQAEQEDR ALRSFKLSV\TVDPKLHSPGLSGRK GASNSQI\RGLKHDVNIQFPDKD\D ANQHQD\QITFTGYEKNHSSLPGDAI LRIVG\ELE\QMVSE\DVPLNHRVSR PASFGARGKSHPPKIMYEF\K\DIRF PNKSGAPKTPNCVNC*RGFPIENVE ESHSTQHPSILEEE\YLADVVDSEA LQ\VYMEPP/AHTEEAKGNFSRG\FD VRDAPL\TA\SSSEKAS\DMSSSEEFP SFWG*RWLPKTLP\WGPKTIMIKKE QNPLPAC |
| 3961 | 9458 | A | 4244 | 11 | 323 | |
| 3962 | 9459 | A | 4245 | 3 | 171 | |
| 3963 | 9460 | B | 4246 | 148 | 405 | XKLSVERKDPLAALAREYGGSKRN ALLKWCQKKTQGYAKRNLLAFE AAESVGIKPSLESEMLYTDRPDWQ SVMQYVAQIYKYFET* |
| 3964 | 9461 | A | 4247 | 2 | 438 | AVGGNGGCPRPSRVTSQSTCRFGPR TASHSASRAGLCTASR*VPGWV*CL HFQPLQMPTRDSSFSPDYSAPGRGC GQAGRCGAEHRRPGHRSSCC*NW* CQCSHNLVSSSGTISVEHCAWNHRI PGPRLPEGLFFPH*VCFVISM |
| 3965 | 9462 | A | 4248 | 3 | 256 | |
| 3966 | 9463 | A | 4249 | 3 | 444 | |
| 3967 | 9464 | A | 4250 | 3 | 828 | VKGVPGVKAERFIE*RMTAKHCALS LVGEPIMYPEINRFLKLLHQCKISSF LVTNAQFP AEIRNLEPVTQLYVRVD ASTKDSLKKIDRPLFKDFWQRFIDS VKALAVKQQRVYRLTLVKA\WNV \ESLQAYAQLGSLGNPDFIEVKGV YCRESSASSLTMAHVPWHEEVVQF VRELVDLIPEYEIACEHEHSNCLLIA HRKFKIGGEWWTWDYNRQELIQ EYEDSGGSKTFSKDY MARTPHWA LFGASERGFDPKDTRHQRKNKSKAI SGC |
| 3968 | 9465 | A | 4251 | 1 | 384 | |
| 3969 | 9466 | A | 4252 | 3 | 1225 | |
| 3970 | 9467 | A | 4253 | 1 | 864 | |
| 3971 | 9468 | A | 4254 | 1 | 1266 | GNSPPSELKWKAKSEDLRHRGLKA QAEIKGSTQQIGFTTDPMARSSPYP TDVARVVNAPIFHVNSDDPEAVMY VCKVAAEWRSTFHKDVVVDLCY RRNGHNEMDEPMFTQPLMYKQIRK QKPVLQKYAELLVSQGVVNQPEYE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CVSMHGVRNKPSYNSTKSSMDGLI LHPATGLVFVLSKQCEEIHQPVVWT CEQREAENATAEENRVLLAMVNPT VFFDIAVDGAEPLGRVSFEVGRAAA CGNGAQKVGRGRENFRCEPLERK GFGL*GVPCFHRLFPRVLCVQGGEL QQRHNGNWWASPIWGRKFERLK NFHP*KPYGSPGILSPWQNA GPQTQ MVPQFFICTAQDCSGWNGQAMWV FGTSERKAMNIVEAHWSRFGISR\N GKTQQRSPFADCGQLLISLTCVFIF NHPDHSL |
| 3972 | 9469 | A | 4255 | 3 | 275 | |
| 3973 | 9470 | A | 4256 | 125 | 315 | |
| 3974 | 9471 | A | 4257 | 3 | 292 | |
| 3975 | 9472 | A | 4259 | 1 | 3045 | MDKFLNTYTLPRLKQEEVESLNRPI TGSDIEAINSLPTKKKSRTRWHSRI LPEVQGGAEKEGILPNSFYEASIILIP KPASDTTKKENFRPISLMNINAKILN KILAKQIRQHIKKLIHHDQVGFIPGM HGLFNICKSVNIQHINRTNDKNHMI ISIDAEKPFDKIQHFMLKTLNKL QNLKLIGNFSKVSGYKINVQKSQA FLYTNNRQTESQIMNEFPFTIASKRI KYLGIQLTRDVKDLFKENYKALLN EIKEDTNKWKNIPCS\WEKTTLKFI W/NQKRAHIAKSIIISQKNKAGGITLP DFKLYCKATVTKTAWYWYQNRDI DQWNRTESEIMPHIYNHLIFDKPD KKKKWKGKDSLFNKWCWENWLAIC RKLKLDPFLTPDTKINSRRIKDLNVR PEMIKTLEENLGNTIQDIGMGKDFM SKTPKAMATKAKIDKWDLIKLSF CTAKETTIRVNRQPTWEKIFAIYSS DKGLISRIYNELKQIYKKKTNNPIEK WAKDMNRHFSKEDIYA AKKHKMKK CSSSLVIREIQIKTTMRYHLTPVRMA IHKSGNNRCWRGCGEIGTLLHCW WDCKLVQPLWKS VWRFLRDLELEI PFDPAIPLLAAPSLPSGLRSPSKSSPS PPSRCTLVILLHVFWDIVFFDGCEK KRWYILLIVLLTRLLVSACTFTEGY TVGFSTFEALRLGLSRYWLPCSSAC RRPIVGLQLVMINSNGNFQVIAMEGT VASECCHGNGKLTWHRPVLSVCSF SRCTVQAAGGSAILEDGDPLLAPL GSTPQAAVCRGPRGRELRAAPADS HLFQRDLWPFNKVIVHGEKGSNQT SQGLLNTGSEMTIVLENPKYHSGPP VRVSPDGGQVIEVLADPSYTGPTA LNNVFFAFQCNFYFDHIPENCGFSD PSDPQNLQKGEGCPSLVRASTAPPQ EKATEQPLLCKTTESPFGMTVGPCT DETLDHGAPSKHVPGTAHNELALL DLRVIKSAGSAAVHHKLKVLHWS SLSNNKGTGRLYEQVA |
| 3976 | 9473 | A | 4260 | 1 | 2526 | |
| 3977 | 9474 | A | 4261 | 1 | 3111 | |

MISSING AT THE TIME OF PUBLICATION

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VDTIAADESFSQVDFGGRLMKDYG ACMSLLSVRVFFKKCPISVQNFAVF PETMTGAESTSLVIARGTCIPNAEEV DVPIKLYCNGDGEWMVPIGRCTCK PGYEPENSVACKGPVNNTEKAKSG EMWFSPEEYGWEYAFLALRKCSQ CPEDAVAASGAVALENLMEHGHIR LDKASKDSESSTPHDPTLLFHSGPQP NFRHFQGWNTVTSEGLIHLPKSKT QSQCPLFGGSLDSRIDIGGAWYFC HTHTASSASTPSEEAGSLADPSNETE SLLFACTALCSPWECQLILDASLFQ GIMLMPRAVQFFKCWDKVTVRNQ WRMHSHGPSCLGVSFQKGLCQEM VYISTRGSSGLRPLVLSLHGWAVD TAIHTCIPFPTDIIWIQDLIAGLKDEW FDTHPGRRIGRPAQLCSSRSGVH |
| 3980 | 9477 | A | 4264 | 1 | 2653 | MGDFTNPLSTLDRSMRQKVNKDIQ ELNSALHQADLIDIYRNLPHESTYET FFSAPHHTYSKIDHILGSKAPLSKYR RSEIKINCLSDHSAIKLELRIKKLTQ NRSTTWKLNNLLNDYWVHNEMK AEIKMFFETNENKDTTYQNLWDTL KAVCRGKFIALNAHKRKQERSKIDT LTSQLKELEKQEQTTHSKASRRQEIS KIRGELKEIETQKTLOKINESRGWFF EKINKIDRLARLIKKKREKNQIHAI KNDKGDMSTNHTETIQTIREYYKHL YANKLENLKEIDKFLETYSPLRLNQ EEVESLNRPTGSEIAIINSLPNKRS PGPDGFTAKFYQRYKEELLISNFSK VSGYKINVQKSQAFLYTNNRQTES QIMSELPFTIASKRMKYLGIQPTRD MKDLFKENYKPLLNEIKEDTNKWK NIPCSWVGRINIVKMAILPKNWKKT TLKFIWNQKRARIAKSILSQKNKAG GIMLPDFKLYKATITKTAWYWYQ NRDIDQWNRTEPSEIMPHIYNHLIFD KPDKNKKWKGKDSL FNKWCWENW LAICRKLKLDPFLTPYTKINSRWIKD LNVRPKTIKTLEENPGNTIQDIGMG EDFMSKTPEAMATKAKIDKWDLIK LKSFCTAKETTIRLNRPPTEWEKIFA IYSSDKGLISRIYNELQQIYEKKTNN PIKKWAKDMNRHLSKEDIYAAKRH MKKCASSLAIREIQIKTTMRYHLTP VRMAIHKSGNNRCWRGCGEIGTLL HCWWDCCLVQPLWKS VWRFLRDL ELEIPFDPAIPLLG IYPKDYKSCCYE DTCTHMFIVALFTIAKTWNQPKCPT MIDWIKKMWHIYTMEYYADIKKDE FMSFVRTRMKLETIILSKISQEKKT KHRMFSLIGGN |
| 3981 | 9478 | A | 4265 | 1 | 2988 | |
| 3982 | 9479 | A | 4266 | 1 | 2515 | MGDFTNPLSTLDRSTRQKVNKDTQ ELNSAPHQADLIDIYRTLHPKSTEYT FFSAPHHTYSKTDHILGSKALLSEC KRTEIITNYLSDDSAIKLELRIKNLT |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | QNRSTTWKLNLLDDYVWHNEM KAEIKMFFETNENKDTTYQNLWDA FKAVCRGKFVALNAHKRKQGRSKI DTLTSQLEKEKQEQTHSKASRRQE ITKIRAELEKEIETQKTVQKINESRSW FFERINKIDRQLARLIKKKREKNLID AIKNDKGDITTDPTIEIQTIREYYKH LYANKLENLEEMDKFLDTYTLPR NQEEVESLNRPIGTSEIVAIINSLTTK KSPGPDGFTAIFYQRAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQKLISNFSKVSGYKINVQKSQAF LYTNNRQTESQIMSELPFTIASKRIK YLGQQLTRDVKDLFKENYKPLLKEI KEDTNKWKNI PCSWVGRINIVKMAI LPKVIYRFNAIPIKLPMTFFTELKKT TLNFIWNQKRAHIAKS/VLSQKNKA GGITLPDFKLYYKATVTKTAWY QNRD TDQWNRTEPSEIMPRIYNYLI FDKPEKNKQWGKDSL FNKWCWKN WLAICRKLKLDPFLTPYTKINSRWI KDLNIRPKTIKLEENLGITIQDIGM GKDFMSKTPKAMATKAKIDKWDLI KLKSFACTAKETTNRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSSSLAIREMQIKTTMRYH LTLVRMAIHKSGNNRCWRGRGEIG TLLHCWWDCCLVQSLWKS VWQFL RDLELEIPFDPAPILL |
| 3983 | 9480 | B | 4267 | 1 | 2634 | MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQGDLIDIYRTLHPKSTEYI FFSAPHHTYSKIDHILGSKALLSKCK RTEIITNDLSDHSAIKLELRIKNLTQ NCATTQKLNLLNDYVWHNEMK AEIKMFFETNENKDTTYQNLWDAF KAVCRGKFIALHAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQEIT KIRAELEKEIETQKTLQKINESRSWFF ERINKIDRLLARLIKKKREKNQIDAI KNDKGDITTDPTIEIRTTVREYYKHL YANKLENLEEMDTFLDTYTLPRLN QEEVESLNRPIGTAEIVAIINSLPTKK SPGPDGFTAIFYQFRKGLRQNSTT FMPKTLNKLIGDGYLKIRAIYDKP TANIILNGQKLEAFPLKTGTRQGW LSPLLFNIVLEVLAIRAIRQEKEIKGIQ LGKEEVKLSLFADDMIVYLENPIVS AQNLLKLISNFSKVSGYKINVQKSQ AFLYTNNRQTESQIMSELPFTIASKR IKYLGQQLTRDVKDLFKENYKPLLK KIKEDTNKWKNI PCSWVGRINIVKM AILPKVIYRFHA IPIKLPMTFFTELEK TTLKFIWNQKRACIAKSILNQKNKA GGITLPDFKLYYKAI VTKTAWY QNRDIDQWIRTEPSEITLHIYKYLIF DKPEKNKQWGKDSL FNK WY WEN WLAICRKLKLDPFLTPYTKINSRWI |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me- thod | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|-------------|-------------------------------------|---|--|---|
| | | | | | | KDLNIRPKTIKLEENLGFTIQDIGM GKNFMSKTPKAMATEAKIDKWDLI KLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPLKKWAKDMNRHFSKEDIYAA KKHMKKCSPLAIREMQIKTTMRY HLTPVRMTIISQETTGAAGEDVEK* |
| 3984 | 9481 | A | 4268 | 1 | 2429 | |
| 3985 | 9482 | A | 4269 | 1 | 2745 | |
| 3986 | 9483 | A | 4270 | 1 | 3210 | MVKGSIQQEELTILNIYAPNTGALRF IKQVLRDLQRDLDSHTIIMGDFHTP LSTLDRSTRQKVNKDIQELNSALHQ EDLIDIYRTLHPKSTEYTFFSAPHHT YSKIDHIVGSKALLSKCKRTEITNC LSDHSAIKLELRIKNTQNRSTTWK LNNLLNDYWVHNEMKAEIKMFFE TNENKDTTYQNLWDTFKA VCRGKF IALNAHKRKQERSKIDTLTSQKEL EKQEQTTHSKASRRQEITKIRAEKEI ETQKTLQNINESRSWFFERINKIDRP LARLIKKKREKNQIDA KNDKG DIT TDPTEIQTIREYKHL YANKLENL EEMDKFLNTYTLPTLNQEEVESLNR PITGAEIVAIINSLPTKKSPGPDGFTA EFYQRYKEELVPFLPKPQSIEKEGI LPNSFYEASIIIPKPGRDTTKKNFR PISLMNIDAKILNKILAKRIQQHIKN LIHHDQVGFIQGMQGWFNIRKSINVI QHINRAKDKNHMIIISDAEKAFDKI QQPFMLKTLNKLDDMIVYLENPIVS AQNLLKLISNFSKVSGYKINI QKSQA FLYTNNRQTESQIMSELPFTIASKRI KYLGIQLTRDVKDLFKENHKPLL N EIKEDTNKWKNI PCSWVGRINIVKM AILPKVIYR/FNAIPIKLPMTFFTELE KTTLKF IWNQKRARI AKSILSQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSERTPHIYNYL IFDKREKNKQWGKDSL FNKWCWE NWLAI CRKLKLD PFLTPYTKINSRW IKDLNVRPKTIKLEENLGFTIQDIG MGKDFISKTPKAMATKAKIDKWDL IKLKSFCTAKETTIRVNRQPTKWEKI FATYSSDKGLISRIYNELKQIYKKKT NNPIKKWAKDMNRHFSKEDIYAAK KHMKKCSPLAIREMQIKTTMRYH LTPVRMAIIKSGNNRCWRGCGEIG TLLHCWWDC KL VQPLWKAVWRFL RDLELEIPFDPAIPLLG IYPKDYKSC CYKDTCTRRKQLDCAEPVEPRKVG DGEWSLTKWTRPGSRALPWPPEQA KPYPPTLPTLAQDF |
| 3987 | 9484 | A | 4271 | 3 | 3655 | |
| 3988 | 9485 | A | 4272 | 1 | 3615 | |
| 3989 | 9486 | A | 4273 | 1 | 4038 | |
| 3990 | 9487 | A | 4274 | 1 | 3317 | MGDFNTPLSTLDRSTRQKVNKDTQ ELNSALHQADLIDIYRTLQPKSTEYT FFSAPHHTYSKIDHIVGSKALLSKCK |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | RTEITNYLSDHSAIKLELRIKNLTQS RSTTWKLNLLNDYWVHNEMKA EIKMFFETNENKDDTTYQNLWDAFK AVCRGKFIALNAHKRKQERSKIDTL TSQLEKEKQEQTHSKASRRQEITKI RAELKEIETQKTLQKINESRSWFFER INKIDRPLARLIKKKREKNQIDTIKN DKGDITTDPTIEIQTIREYYKHYA NKLENLDEMDFLHTYTLPRLNQE EVESLNGPITGAEIVAIIDSLPTKKSP GPDGFTAIFYQRYKEELVPFLKLKLF QSIEKEGILPNSFYEASIIPLKLRDGT TKKENFRPLSLMNIDAKILNKILAK RIQQHIKKLIHHDQVGFIPGMQGW NIRKSINVIQHINRGKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIIRAIYDKPTANIILNGQKLEAFP LKTGTRQGCPLSPLLFNIVLEVLR AIRQEKEIKAQNLLKLISNFRKVS KINVQKSQAFLYTNNRQTESQIMRE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLNEIKEDTNKWNIPCSWI GRNIVKMAILPKVIYRFNAIPIKLPT TFFTELEKTILKFIWNQKRAHIAKTI LSQKNKAGGIMLPDFKLYYKATVT KTAWYWYQKRDIDQWNRIELSEIIP HIYNHLIFDKPDKNKKWGKDSVFN KRCWENWLAICRKLKLDFTLTPYT KINSRWIKDLHVRPKAIKTEENLGI TIQDIGMGKDFTSKTPKAMATKAKI DKWDLIKLKSFTAKETTIRVNRQP TKWEKIFAIYSSDKGLISRIYKELKQ IYKKKTNNPIKKWAKDMNRHFSKE DIYAANRHMKKCSSSLAIREMQIKT TMRYHLTPVRKAIKKSGNNRCWR GCGEIGTLLHCWWDCKLVQPLWK TVWQFLRDLELEIPFYPAIPLGIYP KDYKSCCYKDTCTRMFIAALFTIAK TWNQPKCPTMIDWIKKMWHIYTM EYYAAIKNDEFMSFVGTWMKLEIII LSKLSQEQTCKHGIFSLIGGN |
| 3991 | 9488 | A | 4275 | 959 | 2955 | |
| 3992 | 9489 | A | 4276 | 1 | 2870 | MKAIEIKMFFDTSSENKDDTTYWNLW DAFKAVCRGKFIALNAHKRKQERS KIDTLTSQLEKEKQEQTHSKASRR QEITKIRAELEIETQKTLQKINESRS WFFERINKIDRPLARLIKKKREKNQI DAIKNDKGDITTDPTIEIQTIREYYK HLYANKLENLEEMDFLDTYTLPR LNQEEVESLNRPTGSEIVAIINSLPT KKSPGPDGFTAIFYQSWAETQPKK ENFRPISLMNIDAKILNKILAKRIQQ HIKKLIHHDQVGFIPGMQGWFNIRK SINVTQHINRAKDKNHMISIDA EKA FDKIQPFMLKTLNKLIGDGT YFKII RAIYDNPTANIILNGQKLEAFPLKTG TRQGCPLSPLLFNIVLEVLR AIRQE KEIKGIQLGKEEVKLSLFDNMIVY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LENPIVSAQNLLKLISNFSKVSQYKI NVQKSQAFLYTNNRQTESQIMSQLP FTIASKRIKYLGIQLTRDVKDLFKEN YKPLLKEIKEDTNKWKNI PCSGÆG RINIVKMAILPKNWKKTTLKFIWNQ KRARIAKSILSQKNKAGGITLPDFKL YYKATATKTAWYQNRDLQW NRTEPSEITPHIYNLIFDKPDKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSRWIKDLNIRPKTI KTEENLGITIQDIGMGKDFMSKTP KAMATKAKIDKWDLIKQESFCTAK ETTIRVNRQPTKWEKIFATYSSDKG LISRIYSELKQIYKKKTNNPIKKWAK DMNRHFSKEDIYAAKKHMKKCPSS LAIREMQIKTTMRYHLTPVRMAIHK KSGNNRCWRGCGEIGTLLHCWWD CKLVQPLWKS VWRFLRDLELEIPFD PAIPLLGHPKDYKSCCYNDCTRM FIAALFTIAKTWNQPKCPTIIDWIKK MWHIYTM EYAAIKNDEFVSFVGT WMKLEIILSKLSQEQTTHRIFSLIG GN |
| 3993 | 9490 | A | 4277 | 1 | 2982 | |
| 3994 | 9491 | A | 4278 | 1614 | 4577 | TEPKTKTT*LSQ*MQKKPLTKFSNPS C*KLSIN/IVLEVLARAIRQEKEIKGI QLGKEEVKLSLFADDMIVYLENPIV SAQNLLKLISNFSKVSQYKINVQKS QAFLYTNNRQTESQIMSELPFTTAS KRIKYLGIQLTRDVKDLFKENYKQL LKEIKEDTSKWKNI PCSWVGRINIV KMAILPKVIYRFNAIPIKLMPFFTE LEKTTLKFIWNQKRACIAKSILSQ NKAGGITLPDFKLYYKATVTKTAW YWYQNRDIDQWNRTEPSEITPHIYN YLIFDKPEKNKQWGKDSL FNKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTEENLGIIQDI GMGKDFMSKTPKAMATKAKIDKW DLIKLSFCTAKETTIRVNRQPRKW EKIFATYSSDKGLISRIYNELKQIYK KKTNNPIKKWAKDMNRHFSKEDIY AAKKHMKKCSPLAIREMQIKTTM RYHLTPVRMAIHKSGNNRCWRGC GEIGTLLHCWWDCKLVQPLWNSV WRFLRDLELEIPFDPAIPLLG IYPND YKSCCYKDTCTRM TITSVEEKSQSE KLSYIFLKEKICLMYVGLLNILVSL GKVPFWLYLGSRLATPPTSSQLFFIG GKERSPDEQGV DILIVLIFRYPSTDS AEQIKKKIEKALYQSLKTKQLSLTIN KPSFRLTRCGIRMTSSNMPLPASSST QRIVQGRETAMEGEWPWQASQLI GSGHQCGASLISNTWLLTAAHCFW KNKDPTQWIATFGATITPPAVKRN RKIILHENYHRETNENDIALVQLSTG VEFSNIVQRVCLPDSSIKLPKTSVF VTGFGSIVDDGPIQNTLRQARVETIS |

MISSING AT THE TIME OF PUBLICATION

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LPCLMIPSQMMLLENFSAAPGHRCW THMLDNGSAVSTNMTPKALLTISIP PGPNQGP HQCRRFRQPQWQLDPN ATATSWSEADTEPCVDGWVYDRSV FTSTIVAKWDLVCSSQGLKPLSQSIF MSGILVGSFIWGLLSYRFRGKPMLS WCCLQLAVAGTSTIFAPTFVIYCGL RFVAAFAGMAGIFLSSLTLMVEWTTT SRRAVTMTVVGCFAFSAGQAALGGL AFALRDWRTLQLAASVPPFAISLIS WWLPESARWLIKGKPDQALQELR KVARINGHKEAKNLTETPPPPPIPI PSPTAPPLSTPTITFTAITPSPAPPIS LTPQPPSLQNISTTFTTIVTIGNSTIIN STHTVTSITHHLHLHVARTHLMGVL DVSGETECVYLKVLMSVKEEVAS AKEPRSVLDLFCVPVLRWRSCAML VVKYAVLGRDLTSSLARSFLLISY YGLVFDLQSLGRDIFLLQALFGAVD FLGRATTALLSFLGRRTIQAGSQA MAGLAILANMLVPQDLQTLRVVFA VLGKGCFGISLTCLTIYKAELFPTPV RMTADGILHTVGRLGAMMGPLILM SRQALPLLPLYGVISIASSLVVLF LPETVQGLPLPDTIQDLESQKSTAAQ GNRQEAVTVESTSL |
| 4009 | 9506 | A | 4293 | 3672 | 3967 | LQPPPHGRRGLLHHLSPGHGPHHP VTPQTRSPAQP/PGQMGPAPLGGC LPPPPRPPTCRREK*TTETRFSPCWR TRPWGPGPPRPLSRGGPLPCAPA |
| 4010 | 9507 | A | 4294 | 1773 | 2213 | AHWLHLRLPHHRAQWAAALQPG PAGWGWSWQPQLCSAGRLCHGAI GRP/LSIFCWTWDLGASSCGHPAAR SMMASGVTWTSRGMGEKRVSSSTPF PIFFPAASPPPPSRLPNCPFCHRTLAE RAQHLASVRPGLHLSSPTCCMKCSC |
| 4011 | 9508 | A | 4295 | 1 | 616 | |
| 4012 | 9509 | A | 4296 | 93 | 502 | EERKRPHLGAWWENRKCFFSFQPD FKAAECRETVARPSLSIPQDCLSVSL ADTNQCLLEVRLARGVCRRAHLS PPVCIQSPLSQGH*LLCSK*SASIIGA GLANFQGTDSLVAEHPVSWIHNNSN FVFHPGYFRL |
| 4013 | 9510 | A | 4297 | 1537 | 2360 | TCCTNVVWGAPPHRDSRVSDRVHS QKSRRACYGQRNKRPGG*G*ILISA KKQLSPRR*LKVWPMRSASLQSM PLASPSVCPGGLLFLWP*QALLPS DCG/PLSLTRLSR*GGPPRPHWCSR FRWLCARVLL |
| 4014 | 9511 | A | 4298 | 1 | 493 | MEAPAELLAALPALATALALLLAW LLVRRGAAASPEPARAPPEPAPPAE ATGAPAPSRCAPEPAASPAGPEEP GEPAGLGELGEPAGPEPEPGDPA AAPAEAE/PGGGGEAGTHRGPRGP LPTPGAPAAAAPRRARERGRGLQ PRLPPGSAEPAARRKCR |
| 4015 | 9512 | A | 4299 | 2 | 418 | |
| 4016 | 9513 | A | 4300 | 8808 | 9100 | RKVLFFFFFEMKSRSAVRLGCSGTI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | SAHCNLCLPGSSDSPASASRVAGMT GAHNHIQLIFVFLVGMGFHHVGGQA GLELLT*VIHPPQSPKVLGLQV |
| 4017 | 9514 | A | 4301 | 3 | 101 | |
| 4018 | 9515 | C | 4302 | 5673 | 5894 | MWQLTPAILALGEIEAGGLFEPRRV KLAWPAQEELVSTKNTKISWVWW RAPVVPATQEA EVGGSLELERSRLQ * |
| 4019 | 9516 | A | 4303 | 1 | 241 | |
| 4020 | 9517 | A | 4304 | 58 | 180 | |
| 4021 | 9518 | A | 4305 | 2 | 325 | FFFFFFFFFETESLSVTQAGEPGHD LGSLEPPPPRFKQFSCSLPSSWIYR HVPPCPANFFFFLVETGFHHVGGQAG LKLLTSNDPPASASQSSGIRGVSHLT RLVS |
| 4022 | 9519 | A | 4306 | 206 | 386 | |
| 4023 | 9520 | A | 4307 | 2 | 260 | |
| 4024 | 9521 | A | 4308 | 5 | 227 | |
| 4025 | 9522 | A | 4309 | 676 | 1076 | FLLCFPPCLSPKFFLFLLGKIYSQSN WCVIVNWRIELGWMFNKICDSKIIF SLGSFLCKIKAHWGLWKSPTTSFQE RSPFFSSLFRAMRAKPSRSM/RLFF ELLVKSLPVASPV EPLSVIAEQSSQI CPCHGI |
| 4026 | 9523 | A | 4310 | 3 | 205 | |
| 4027 | 9524 | A | 4311 | 3 | 345 | |
| 4028 | 9525 | A | 4312 | 118 | 7473 | |
| 4029 | 9526 | A | 4313 | 1 | 297 | |
| 4030 | 9527 | A | 4314 | 366 | 504 | |
| 4031 | 9528 | A | 4315 | 1 | 2899 | MDAPKAGYAFEYLIETLNDSSHKKF FDVSKLGTKYDVL PYSIRVLEAAV RNC DGFLMKKEDVMNILDWKTQ SNVEVPFFPARVLLQDFTGIPAMVD FAAMREAVKTLGGDPEKVHPACPT DLTVDHSLQIDFSKCAIQNAPNPGG GDLQKAGKLSPLKVQPKKLPCRQ TTCRGSCDSGELGRNSGTFSSQIENT PILCPFHLQPVPEPETVLKNQEV EFG RNRERLQFFKWSSRV LKNVAVIPPG TGMAHQINLEYLSRVVFEEKDLLFP DSVVGTD SHITMVNGLGILGWGVG GIETEA VMLGLPVSLTLPEVVGCEL TGSSNPFVTSIDVVLGITKHLRQVG VAGKFVEFFGSGVSQLSIVDRITIA NMCPEYGAILSFFPVDNVT LKHEH TGFSKAKLESMETYLKAVKLFRND QNSSGEPEYSQVIQINLNSIVPSVSG PKRPQDRVAVTDMKSD FQACLNEK VGFKGFQIAAEKQKDIVSIHYEGSE YKLSHGSVVIAA VISCTNNCPYSVM LAAGLLAKKAVEAGLRVKPYIRTS SPGSGMVTHYLS SSGVLPYLSKLGF EIVGYGCSTCVGNTAPLSDAVLNA VKQGD LVTCGNFIWKKNFEGRLC DCVRANYLASPLV VAYAIAGTVNI DFQTEPLGTDPTGKN IYLDIHWPSR EEVHRVEEHVILSMFKALKDKIEM |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | GNKRWNSLEAPDSVLFPPWDLKSTY IRCPSFFDKLTKEPIALQAIENAHVL LYLGDSVTTDHISPAGSIARNSAAA KYLTNRGLTPREFNSYGARRGND VMTRGTFANIKLFNKFIGKPAPKTIH FPSGQTLDVFEAAELYQKEGIPLIIL AGKKYSGNSRDWAAKGPYLLGV KAVLAESYEKIHKDHILIGIGIAPLQF LPGENADSLGLSGRETFSLTFPEELS PG\ITLNIQTSTGKVFSVIASFEDDV\ EITL\YKHG\GLLNFV\ARKFS |
| 4032 | 9529 | A | 4316 | 1 | 178 | |
| 4033 | 9530 | A | 4317 | 165 | 403 | PSSRSRAPSPPTLCGASCCPTCPAC FPAPSRRAGAAGGAG*RPRGGPTST TCYGPTETWLYQLQTVGSRNTTTRT PKST |
| 4034 | 9531 | A | 4318 | 3 | 404 | |
| 4035 | 9532 | A | 4319 | 3 | 217 | |
| 4036 | 9533 | A | 4320 | 3 | 423 | SFFIHRTKGKGPLMSSSFKKLYFSLT TEALSFAKTPS/CQGQGC DKTRSRV TLQEWNDPLDHDLEAQLIYRHLLG VEAMLWERHRELSGGAEAGTMPTS PGKVPEDSLARLLRVLQDLREAHSS SPAGSPSEPNCLELQ |
| 4037 | 9534 | A | 4321 | 2 | 3040 | DPGVWLPPSRDPAMAKRSSLYIRIV EGKNLPAKDITGSSDPYCIVKVDNE PIIRTATVWKTLCPFWGEEYQVHLP PTFHAVAFYVMDEDALSRDDVIGK VCLTRDTIASHPKGFGSGWAHLTEVD PDEEVQGEIHLRLEVWPGARACRL RCSVLEARDLAPKDRNGTSDPFVR VRYKGRTRETSIVKKSCYPRWNETF EFELQEGAMEALCVEAWDWDLVS RNDFLGKVVIDVQRLRVVQEEGW FRLQPDQSKSRRHDEGNLGS LQLEV RLRDET VLPSSYYQPLVHLLCHEVK LGMQGPQQLIPLIEETTSTECRQDV ATNLLKLFLGQGLAKDFLDLLFQLE LSRTSETNTLFRSNSLASKSMESFLK VAGMQYLHGVLGPIINKVFEEKKY VELDPSKVEVKDVGC SGLHRPQTE AEVLEQSAQTLRAHLGALLSALSRS VRACPAVVRATFRQLFRRVRERFPG AQHENVPIAVTSFLCLRFFSPAIMS PKLFHLRERHADARTSRTLLLLAKA VQNVGNMDTPASRAKEAWMEPLQ PTVRQGVAQLKDFITKLVDIEEKDE LDLQRTL SL*APPVKEGPLFIHRTKG KGPLMSSSFKKLYFSLTTEALSFAK MPSSKKSALIKLANIRAAEKVEEKS FGSHVMQVIYTTDDAGRPQTAYLQ C/KGV PFCVRVQSHWEK**YQGHQI YLAGSGIPTSVAKGPAAAEIQPTPAS WAPTIPVPSVGTSGAAATKKTRQC VNELNQWLSALRKVSINNTGLLGS YHPGVFRGDKWSCCHQKEKTD TDF RSVPQTGVQWRDLGSLQSPPPRVK QFSCNLPSWDDRHSPPSLANFFV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | F*LEMGFHHVSQAALVLLLLLLLLL FDTESRSIIQAGVQWCNLGSLQSPFP RLG*FSCLSLPSTTGASHCTQLSQGC DKTRSRVTLQEWNDPLDHDLEAQL IYRHLLGVEAMLWERHRELSGGTE AGTVPTSPGKVPEDSLARLLRVLQD LREAHSSSPAGSPSEPNCLELQT |
| 4038 | 9535 | A | 4322 | 308 | 658 | |
| 4039 | 9536 | A | 4323 | 1 | 2662 | MAKRSSLYIRIVEGKNLPAKDITGSS DPYCIVKVDNEPIRYRPHQDRGA LSLSSARALPAKGTATVWKTLCPF WGEEYQVHLPPTFHAVAFYVMDE DALSRDDVIGKVCLTRDTIASHPKG FSGWAHLTEVDPDEEVQGEIHLRLE VWPGARACRLRCSVLEARDLAPKD RNGTSDPFVRVRYKGRTRTSIVKK SCYPRWNETFEFELQEGAMEALCV EAWDWDLVSRNDFLGKVVIVDQR LRVVQQUEGWFRLOPDQSKSRRHD EGNLGSLQLEVRLDETVPSSYYQ PLVHLLCHEVKLGMOGPGQLIPLIE ETTSTECRQDVATNLLKFLQGGLA KDFLDLLFQLELSRTSETNTLFRSNS LASKSMESFLKFALHVYLAPSWAD TAGKRCKGGCREKVGSWSGTGGD RINVTCCGPQVAGMQYLHGVLGPII NKVFEEKKYVELDPSKVEVKDVC SGLHRPQTEAEVLEQSAQTLRAHLG ALLSALSRSVRACPAVVRATFRQLF RRVRERFPGAQHENVPIAVTSFLC LRFFSPAIMSPKLFHLRERHADARTS RTLALLAKAVQNVGNMDTPASRAK EAWMEPLQPTVRQGVQKDFITK LVDIEEKDELDLQRTLSLQAPPVKE GPLFIHRTKGKGPLMSSSFKKLYFSL TTEALSFAKTPSSKKKSAIKLANIRA AEKVEEKSFGGSHVMQVIYTDAG RPQTAYLQCKCVNELNQWLSALRK VSINNTGLLSYHPGVFRGDKWSC CHQI*ITGQG\CDKTRVTG*PCREW NDLLDRDLESQLIYRHLLGVEAML WERHRELSGGAEAGTVPTKPLAKV PEDSLARLAPGCLQDLREAHSSSPA GSPSEPNLASLEAADVRPALRSPC |
| 4040 | 9537 | A | 4324 | 69 | 194 | |
| 4041 | 9538 | A | 4325 | 1350 | 2203 | TWRLDPQIISSPKPQPGGTYTLEV KSSKSKKVLSPHP*WPPLRLWQRIG GSPEGGTQAPDGLPPPPRPKSERV GSPKLSGGKR/EGSHPGGPPHITHP/ DGEKAKSSWFGLEAKDPTQKPS PHPVKPLSAAPVEGSPDRKQSRSSL SIALSSGLEKLKTVTSGSIQPVTPAP QAGQMVDTKRLKDSAVLDQSAKY YHLTHDELISLLLQRELERLSQRDEH VQELESYIDRLLVRIMETSPTLLQIPP GPPK |
| 4042 | 9539 | A | 4326 | 2 | 761 | |
| 4043 | 9540 | A | 4327 | 2 | 410 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4044 | 9541 | A | 4328 | 295 | 780 | |
| 4045 | 9542 | A | 4329 | 1 | 2203 | |
| 4046 | 9543 | A | 4330 | 1 | 190 | RFIMLVRLVFNS*PQ/CDPPASASQS AGITGMSHRARPELSVLTQGFNRW AFRLLLQCHSPDF |
| 4047 | 9544 | A | 4331 | 2 | 269 | |
| 4048 | 9545 | A | 4332 | 3 | 223 | DFEPSLQHCSSKLCRNILRASSCHSS WGRM*FPGSV*PTWKI*REESCEWS RTAINPKYKILLHGFVVRTVWR |
| 4049 | 9546 | A | 4333 | 2 | 366 | PCSEPPTRRSGATPSHPGGCGAKL CRNILRASSCHSSWGRM*FPGSV*P TWKI*REESCEWSCCTAINPSTRSCCT VCGTNCLEETPTTCPSTRGLQCGRG LTRATGNCPRNDGLTLLSLN |
| 4050 | 9547 | A | 4334 | 3 | 131 | |
| 4051 | 9548 | A | 4335 | 923 | 1442 | GGPCLCRPSWPAVLQVRSGLPSTIPS PWPLFCLPQSILLGPLEMPG*RPLLQ RPFYRMSLRTCQRRVRCWTWSVRC RTAWHTRVFLKLPDFTNDSSTTGF *AKPSALLSTGWS*WATA/CGGGA AALLATMLRAAYPAGQVLRLLPSP PAPGAKLCRNILRASSCHSSWGRM |
| 4052 | 9549 | A | 4336 | 1 | 137 | |
| 4053 | 9550 | A | 4337 | 876 | 1012 | |
| 4054 | 9551 | A | 4338 | 148 | 278 | |
| 4055 | 9552 | B | 4339 | 7 | 673 | MVEVTILMIMGLYRIYGFAVAVVS MILSYNVCSEGEVVSVMFSFVVTSS SCGMHRSTLLSSVYSHLIFDSAYVIN NVADALSRGFSMHCMHCDNLKTC HTSHGSVMAETA VINHKRKNSPRI VQSNDLTEAAYSLSRDQKRMLYLF VDQIRKSDGTLQEHDGICEIHVAKY AEIFGLTSAEASKDIRQALKSFAGKE VVFYRPEEDAGDEKGYESFPWFIKX * |
| 4056 | 9553 | A | 4340 | 786 | 1088 | |
| 4057 | 9554 | A | 4342 | 1 | 66 | |
| 4058 | 9555 | A | 4343 | 2 | 80 | |
| 4059 | 9556 | A | 4344 | 8 | 258 | |
| 4060 | 9557 | A | 4345 | 5 | 383 | |
| 4061 | 9558 | A | 4346 | 99 | 634 | TTMSSKRTKTKTKKRPQRATSN VFAMFDQSQIQEFKEAFNMIDQNR DGFIDKEDLHDMLASLGK/NPTDAY LDAMMNEAPGPINFMTFLTMFGEK LNGTDPEDVIRNAFACFDEEA/TGTI QEDYLRE/LLTTMGDRFTDEE/VDEL YREAPY*QKGGISNYIEFTRILTGRP PKHKDD |
| 4062 | 9559 | A | 4347 | 1 | 966 | |
| 4063 | 9560 | A | 4348 | 3 | 215 | |
| 4064 | 9561 | A | 4349 | 1 | 1416 | NSGGSGGGTSGSGSSSGQGKMGQS QSGGHGPGGGKKDDEDKKKKYEP VPTRVGKKKKKTKGPDAAASKLPLV TPHTQCRLLKLLKLERIKDYLLMEEE FIRNQEQMKPLEEKQEEERSKVDDL RGTPMSVGTLEEIINDNHAIVSTSVG SEHYVSILSFVDKDLLEPGCSVLLN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HKVHAVIGVLMDDTDPLVTVMKV EKAPQETYADIGGLDNQIQEIKESV ELPLTHPEYYEEMGIKPPKGVHPFG PTWPRVKTLAKAVANQTSVASFLR VVGVELIQKYLGDGPKLVRELFRV AEEHAPSIVFIDEIDAIGTKRY\DSN SGGE\REFHRTNVGN*LEPVGMGFD SRG\DVKVFPWATNRI\ETLADPALI RPGRI\DR\KNEFFLPDEKTKKRIFQI HTSRMTLADDVTL\DDLIHGLKIDLS GA\DI\KAIC\TEAGL\MGL*GERRMK VTNEDFKKSKENVLYKKQEGTPEG LYL |
| 4065 | 9562 | A | 4350 | 2 | 70 | |
| 4066 | 9563 | A | 4351 | 1 | 1605 | |
| 4067 | 9564 | A | 4352 | 3 | 193 | |
| 4068 | 9565 | A | 4353 | 3 | 127 | LFHPCQDSQQHH*CVCCRLTGHGA A*VHGPCQAVQTYRASH |
| 4069 | 9566 | A | 4354 | 2 | 323 | |
| 4070 | 9567 | A | 4355 | 3 | 85 | |
| 4071 | 9568 | A | 4356 | 49 | 413 | |
| 4072 | 9569 | A | 4357 | 3 | 338 | |
| 4073 | 9570 | A | 4358 | 1 | 3735 | |
| 4074 | 9571 | A | 4359 | 2 | 317 | |
| 4075 | 9572 | B | 4360 | 2576 | 2685 | MDGKNSSGSKRYNRKRELSYPKNE SFNNQSRSSSQKSKTFNKMPQRG GGSSKLFSSSFNGGRRDEVAEAQRA EFSPAQFSGPKKINLNHLLNFTFEPR GQTGHFEGSGHGSWGKRNKWGHK PFNKELFLQANCQFVVEDQDYTA HFADPDTLVNWDVFVEQVRICSEV PSCPICLYPPTAAKITRCGHIFCWAC ILHYLSLSEKTWSKPCICYSSVHKK DLKSVVATESHQYVVGDTITMQLM KREKGV LVALPKSKWMNVDPHPIHL GDEQHSQYSKLLLASKEQVLHRVV LEEKVALEQQLAEEKHTPESCFIEA AIQELKTREEALSGLAGSRREVTGV VAALEQLVLMAPLAKESVFQPRKG VLEYLSAFDEETTEVCSLDTPSRPLA LPLVEEEEA VSEPEPEGLPEACDDLE LADDNLKEGTICTESSQEPITKSGF TRLSSSPCYFYQAEDGQHMFLHP VNVRCLVREYGSLEERSPEKISATVV EIAGYSMSDEVQRHRYLSHLPLTC EFSICELALQPPVVSKEITLMEFSDDI EKRRQRQKKAREERRRERRIEIEE NKKQGGKCEVHIPLNLQQFPAPKF LYLLLFEKPRKETGKNVAMKAENR CRRRPPPALNAMS LGPRRARSAPTA VAAEAPVDAAELPQRRRHRLRHGQ EQRLQQLLR LFGQQQRATAAPLRL GGASRRV* |
| 4076 | 9573 | A | 4361 | 3 | 93 | |
| 4077 | 9574 | A | 4362 | 1 | 289 | VGNPQQEVQNIFKAKHPMDTEVTK AKIIGFGSALLEEVDPNPANFVGAGI IHTKTTQIGCLVRLEPNLQAQMYRL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | T/LRTSKEAVSQRLCELLSAQF |
| 4078 | 9575 | A | 4363 | 1 | 275 | |
| 4079 | 9576 | A | 4364 | 2 | 2803 | RGLAVFISDIRNCKSKEAEIKRINKE LANIRSKFKGDKALDGYSKKKYVC KLLFIFLLGHDIDFGHMEAVNLLSS NRYTEKQIGYLFISVLVNSNSELIRLI NNAIKNDLASRNPTFMGLALHCAS VGSREMAEAFAGEIPKVLVAGDTM DSVKQSAALCLRLYRTSPDLVPM GDWTSRVVHLLNDQHLGVVTAAT SLITTLAQKNPEEFKTSVSLAVSRLS RIVTSASTDLQDYTYFVPAPWLSV KLLRLLQCYPPPDPAVRGRLTECLE TILNKAQEPPKSKKVQHSNAKNAV LFEAISLIHHHDSEPNLLVRACNQLG QFLQHRETNLRYLALESMTLASSE FSHEAVKTHIETVINALKTERDVSV RQRAVDLLYAMCDRSNAPQIVAEM LSYLETADYSIREEIVLKVAILAEKY AVDYTWYVDLILNLIRIAGDYVSEE VWYRVIQIVINRDDVQGYAAKTVF EALQAPACHENLVKVGYYILGEFG NLIAGDPRSSPLIQFHLLHSKFHLC VPTRALLLSTYIKFVNLFPVKPTIQ DVLRSQSRLRNADVELQQRAVEYL RLSTVASTDILATVLEEMPPPERES SILAKLKKKKGPSTVTDLEDTKRDR SVDVNGGPEPAPASTSAVSTPSPSA DLLGLGAAPPAPAGPPSSGGSGLL VDVFSDSASVVAPLAPGSEDNFARF VCKNNGVLFENQLLQIGLKSEFRQN LGRMFIFYGNKTSTQFLNFTPTLICS DDLQPNLNLQTKPVDPTVEGGAQV QQVVNIECVSDFTEAPVLNIQVHGS GGTFQNVSLQLPITLNKFFQPTNEK FCQDFFQRWKQTSNPQQEVHNIFK AKHPMDTEFTKAKIIGVFGSELLAE VDPNPANFVGAGNIHTKTTQIGCP LRL*PNLQAQMYRLTLRTSKEAVS\ QRLCELLSAQF |
| 4080 | 9577 | A | 4365 | 2 | 231 | |
| 4081 | 9578 | A | 4366 | 1 | 224 | |
| 4082 | 9579 | A | 4373 | 131 | 381 | |
| 4083 | 9580 | A | 4374 | 93 | 449 | |
| 4084 | 9581 | A | 4375 | 11 | 594 | |
| 4085 | 9582 | A | 4376 | 1 | 1410 | |
| 4086 | 9583 | A | 4377 | 1 | 66 | |
| 4087 | 9584 | A | 4378 | 1 | 553 | RRGPLSQNGSFGPSPVSGGECSPPLT VEPPVRPLSATLNRDMPRSEFGSV DGPLPHPRWSAEASGKPSPPDPSG TATMMNS\SS*GSSPTRVLDEGMQT VLQEPEVPSVPSITSLAERPVAVNM APKGPPPPFPGVPLMSTPMGGPVPPPI RYGPPPPQLCGPFGPRALPPPPFGPM RPPLCLRE |
| 4088 | 9585 | A | 4379 | 1 | 3589 | AFLSKVEEDDYPSEELLEDENAINA KRSKEKNPGNQGRQFDVNLQVPDR |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | AVLGTIHPDPEIEESKQETSMILDSE KTSETAAKGVNTGGREPNTMVEKE RPLADKKAQRPFERSDFSISIKIQT ELGEVFQNKDSYDLKNDNPEEHLK TSGLAGEPGELSKEHDHGNTKYM GTESQGSAAAEPEDDSFHWTPHTSV EPGHSDKREDLLIISFFKEQQLQR FQKYFNVHELEALLQEMSSKLKSA QQESLPYNMEKVLDKVFRASESQIL SIAEKMLDTRVAENRDLGMNENNI FEEAAVLDDIQDLIYFVRYKHSTAE ETATLVMAPPLEEGLGGAMEEMQP LHEDNFSREKTAELNVQVPEEPHLL DQRVIGDTHASEVSQKPNTKDLDP GPVTTEPTPMDAIDANKQPETAEE PASVTPLENAILLIYSFMFYLTSLV ATLPDDVQPGPDFYGLPWKPVFITA FLGASFAIFLWRTVLVVKDRVYQV TEQQISEKLKTIMKENTELVQKLSN YEQKIKESKKHVQETRKQNMILSDE AIKYKDKIKTLEKNQEILDDTAKNL RVMLESEREQNVKNQDLISENKKSI EKLKDVISMNASEFSEVQIALNEAK LSEEKVKSECHRVQEENARLKKKK EQLQOEIEDWSKLHAESEIKSFE KSQKDLEVALTHKDDNINALTNCIT QLNLLECESESEGQNKGGNDSDEL ANGEVGGDRNEKMKNQIKQMMDV SRTQTAISVVEEDLKLQLKLRSV STKCNLEDQVKKLEDDRNSLQAAK AGLEDECKTLRQKVEILNELYQQKE MALQKKLSQEYERQEREHRLSAA DEKAVSAAEEVKTYKRRIEMEDE LQKTERSFKNQIATHEKKAHENWL KARAAERAIAEEKREAANLRHKLL ELTQKMAMLQEEPVIVKPMGKPN TQNPPRRGPLSQNGSFGPSVSGGE CSPPLTVEPPVRPLSATLNRRDMPR SEFGSDGPLPHPRWSAEASGKPS SDPGSGTATMMNSSSRGSSPTRVL DEGK\VNMGPK\GAPSPKEFPLMS TPMGGPV\PPPIRYGPPQLCGPFGP RHLPPFGPGMRPPLGLREFAPGVP PGRDLPLHPRGFLPGHAPFRPLGS LGPREYFIPGTRLPPPTHGPEYPPP PAVRDLLPSGSRDEPPASQSTSQD CSQALKQSP |
| 4089 | 9586 | A | 4380 | 3 | 148 | |
| 4090 | 9587 | A | 4381 | 1885 | 2826 | CLQEAIMDGTETIAVSPRSLHSELMC PICLDMLKNTIGSA*ASVPLTDHSG L PFSYPRNKECPTCRKKLVSKRSLRP DPNFDALISKIYPSREEYEAHQDRV LIRLSRLDRGGTLGGGTGPPSPPGA PSPPEPGDPYLQSSSEALWL*ACPP SHSRVYVKTGNATVDHLSKYLALRI ALERRQQQEAGEPGGPGGGASDTG GPDGCGGEGGGAGGGDGPEEPALP SLFHLLQLSSLFSPLSLLPPPQTLNGS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LTLELVNSPRRPLPRQGLTLRALSLP GSPQHHPGKLLTGGCALGFSTPATLH TGKQPYVCAT |
| 4091 | 9588 | A | 4382 | 2 | 456 | DRGGTLGGGTGPPSPPGAPSPPEP GGDPYLQSSSEALWL*ACPPSHSR VKTTGNATVDHLSKYLALRIALERR QQQEAGEPGGGGGASDTGGPDGC GGEGGGAGGGDGPEEPALPSLFHLL QLSSLFSPLSLLPPPQTLNGSLTLEL V |
| 4092 | 9589 | A | 4383 | 58 | 1262 | CLQEAIMDGTETIAVSPRSLHSELMC PICLDMKNTMTTKECLHRFCSDCI VTALRSGNKECPTCRKKLVSKRSLR PDPNFDALISKIYPSREEYEAHQDRV LIRLSRLHNQALSSSIEEGLRMQA MHRAQVRVRPIPGSDQTTMSGGE GEPGEGEGDGEDVSSDSAPDSAPGP APKRPRGGGAGGSSVGTGGGGTGG VGGGAGSEDSGDRGGTLGGGTGPG PSPPGAPSPPEPGGEIELVFRPHLLV EKGEYCQTRYVKTTGNATVDHLSK YLALRIALERRQQQEAGEPGGGGG GASINTEELNVC GGEGGGAGGGDG\ PKEPALPSLEGVSEKQYTIYIAPGG GAFTTLNGSLTLELVNEKFWKVS RPLELCYAPHRIQSDPHPGDKPEE RGPLG |
| 4093 | 9590 | A | 4384 | 3 | 221 | |
| 4094 | 9591 | A | 4386 | 2 | 271 | |
| 4095 | 9592 | A | 4387 | 54 | 990 | HSIMMKIPWGSIPVLMLLLLGLIDI SQAQLSCTGPPAIPGIPGTPGPDG QPGTPGIKGEKGLPGLAGDHGEFGE KGDPWIPGNPGKVGPKGPMGPKGG PGAPGAPGPKG\DSGDYKATQKIAF SATRTINVP/LLRRSQTNFRPRCITN MNTN\YE\PRSGKFTLQGCPLY*FN LSTPSSRG\NLCVNLMRGRERAQE/ VWVTFC\DYCLTN\TFPGSPQGGNGP QLKKAPKGGGGGEKKTVLPAGPPN KNFTYWGMGGCPTAIFSGFLAFFQI WEGLTCGLASHPTAPPAQQRSLYP QQQPYDQAKCTQ |
| 4096 | 9593 | A | 4388 | 3 | 493 | |
| 4097 | 9594 | B | 4389 | 272 | 2158 | MGPLMVLFCLLFLYPGLADSAPSCP QNVNISGGTFTLSHGWAQSLTYS CPQGLYPSPASRLCKSSGQWQTPGA TRLSKAVCKPVRCPAPVSFENGIIY TPRLGSYPVGGNVSFECEDGFILRG SPVRQCRPNGMWDGETAVCDNGA GHCPNPGISLGAVRTGFRFGHGDKV RYRCSSNLVLTGSSERECQNGNVW SGTEPICRQPYSYDFPEDVAPALGTS FSHMLGATNPTQKTESLGRKIQIQ RSGHLNLYLLDCSQSVSENDLIF KESASLMVDRIFSFEINVSAIITFAS EPKVLMSVLNDNSRDMTEVISSLEN ANYKDHENGTTNTYAALNSVYL MMNNQMRLLGMETMAWQEIRHAI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ILLTDGKSNMGGSPKTAVDHIREIL NINQKRNDYLDIYAIGVGKLDVDW RELNELGSKKDGERHAFILQDTKAL HQVFEHMLDVSKLTDITICGVGNMS ANASDQERTPWVHTIKPKSQETCR GALISDQWVLTAAHCFRDGNDHSL WRVNVGDPKSQWGKEFLIEKAAIS PGFDVFAKKNQGILEFYGDDIALLK LAQVKMSTHARPICLPCTMEANL ALRRPQGSTCRDHENELLNKQSVL CTFWSPLNKSKPKI* |
| 4098 | 9595 | A | 4390 | 2 | 201 | |
| 4099 | 9596 | A | 4391 | 1 | 130 | |
| 4100 | 9597 | A | 4392 | 2 | 215 | |
| 4101 | 9598 | A | 4393 | 3 | 300 | |
| 4102 | 9599 | A | 4394 | 3 | 310 | |
| 4103 | 9600 | A | 4395 | 2 | 228 | |
| 4104 | 9601 | A | 4396 | 2 | 448 | PRVRKDAVRDGLRAVKNAIDGCV V/PGAGAVEVAMAEALNKYKLSVK GKAQLGVQAFADALLVIPKVLAQN SGFDLQETLVKI*AEHSESGQLVGV DLNTGEPVVAEEAGIWDNDCVKK QLLHSCVTIATNILLVDEIMRAGMS SLKG |
| 4105 | 9602 | A | 4397 | 2 | 100 | |
| 4106 | 9603 | A | 4398 | 3 | 174 | |
| 4107 | 9604 | A | 4399 | 1 | 147 | |
| 4108 | 9605 | A | 4400 | 1 | 104 | |
| 4109 | 9606 | A | 4401 | 153 | 480 | TTLKQQFSFMSYKAVKLKVFLIMSC YPRNPSHFP*CGA/WVMCPLRVGSE RRLCPFMATS\QSLSNKFHNRKIFMS REIKFRNLLKKNETQLMYLQIFRW YTKQRLFLF |
| 4110 | 9607 | A | 4402 | 1 | 186 | |
| 4111 | 9608 | A | 4403 | 3 | 478 | |
| 4112 | 9609 | B | 4404 | 56 | 390 | XAAVYVQPFLDKSGLEKYLYPASAA APFLLYPGIPAAAAFFCLSSVLSP PPEKAGAAAATLLPHEVAPLGAPHP QHPHGRTHLPFAGPREPGNPRESSAQ EDPSQPGKEAP* |
| 4113 | 9610 | A | 4405 | 2 | 485 | |
| 4114 | 9611 | A | 4406 | 105 | 183 | |
| 4115 | 9612 | A | 4407 | 1 | 1560 | MLRKKEKANYRLLAERTRKRPRKA SAELQRKHYPMLRGHLRFLPGRL RPLPSNPRLAFPAAERGGGHCGRMR HFPVSTQERGADPVHPASPLPPNQ APNAGHSPPTPRSPNTSSPRRRRRR PESGWGRPGGGFTSILRPDSPLPTRV QYGTERKRRGQSSRDAPSARRQSV GGANWEGGGAKRARRGTGPAG WRAEGGGAACRGSARASPAFRGRG PLPPFASGRVPGRCGLRQWLQEK LLGPSDHLSCFQMPGTSVCDCAACL RACTEKPCDSNMWDSQAPWTGLK TRLTYRIFTINDLRQDWWRDYFEK YGKIETIEVMEDRQSGKKRGFAFVT FDDHDTVDKIVGRGGSGNFMGRG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GNFGGGGGNFGRGGNFGRGGYGGGGGSRGSYGGDGGYNGFGGDGGNYGGGPGYSSRGGYGGGGPGYGNQGGGYGG/G/GGGYDGYNEGNGFGGGNYGGGGNYNDG\GNYSG\QQQS\NYGPMKGGSLGG\RSSGSPYGGGYGSG\G\GSGGYGSRRF |
| 4116 | 9613 | A | 4408 | 2 | 370 | |
| 4117 | 9614 | A | 4409 | 1 | 159 | |
| 4118 | 9615 | A | 4410 | 3 | 261 | |
| 4119 | 9616 | A | 4411 | 1 | 8748 | |
| 4120 | 9617 | A | 4412 | 1 | 2176 | |
| 4121 | 9618 | A | 4413 | 37 | 441 | |
| 4122 | 9619 | A | 4414 | 1 | 1940 | PVLRHAVWLKSEKSSFGLCAPLRKGSFLQKSWIFFRPVMAKDLTRIAIVNHDCKCKPKKCRQECKKSCPVRMGKLCIEVTPQSKIAWISLTCIGCGICIKKCPFGALSIVNLPSNLEKETTHRYCANAFKLHRLPIPRPGEVLGLVGTNGIGKSAALKILAGKQKPNLGKYDDPPDWQEILTYFRGSELQNYFTKILEDLKAIIKPQYVDQIPKAAKGTVGSILDRKDETKTQAIVCQQLDLTHLKERNVEDLSGGELQRFACAVVCIQKADIFMFDEPSSYLDVKQRLKAAITIRSLINPDRIIIVVEHDLSDVLDYLSDFICCLYGVPSAYGVVTMPFSVREGINIFLDGYVPTENLRFRDASLVFKVAETANEEEVKKMCMYKYPGMKKKMGEFELAIVAGEFTDSEIMVMMLGENGMGKTTFIRMLAGRLEPDEEGEVPVLNVSYKLQKISPKSTGSRVQLLREKIRDAYTHPQFVTNVMKPLQIENIIDQEVQTLSSGGELQRVTLAL*LGQNLDPVYL\DEPPA\YLDSEQRMAARVVKRFIPHAKKTA\FVVGWTWTFIMATYLADRIVIVFD\GVPSTKNTVANSPQTLLAGMNKFLSQLEITFRDPNNYRPRINKLNSIKDVEQKSGN\YFFLDD |
| 4123 | 9620 | A | 4415 | 1 | 122 | |
| 4124 | 9621 | A | 4416 | 2 | 1382 | |
| 4125 | 9622 | A | 4417 | 135 | 282 | |
| 4126 | 9623 | A | 4418 | 2 | 1652 | |
| 4127 | 9624 | A | 4419 | 3 | 279 | |
| 4128 | 9625 | A | 4420 | 8 | 353 | |
| 4129 | 9626 | A | 4421 | 1 | 1542 | |
| 4130 | 9627 | A | 4422 | 1 | 496 | |
| 4131 | 9628 | A | 4423 | 70 | 365 | |
| 4132 | 9629 | A | 4424 | 1 | 3771 | |
| 4133 | 9630 | A | 4425 | 2 | 285 | |
| 4134 | 9631 | A | 4426 | 1 | 724 | |
| 4135 | 9632 | A | 4427 | 58 | 197 | |
| 4136 | 9633 | A | 4428 | 640 | 813 | |
| 4137 | 9634 | A | 4429 | 3 | 268 | |
| 4138 | 9635 | A | 4430 | 1 | 1512 | |
| 4139 | 9636 | A | 4431 | 3 | 1625 | |
| 4140 | 9637 | A | 4432 | 1 | 330 | GKTITLEVEPSDTIENVKAKIQDKEG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IPPDQQRLLIFAGKQLEDGRTLSDYNI QKESTLHLVLRRLRGGIKYNCCKMI CRKCYARLHPRAVNCRRKKKCGHT NNLRPKKKVK |
| 4141 | 9638 | A | 4433 | 2 | 544 | DPRLQFFFFLSSLLQRGDRAGWW RRFFGTQTCRVFVKTLTGKNLHPL RYETQ*HPLKNVQKPKISRTKEGIP PDQAAS**FAGK\QLE\DGRTLSDY NIQKESTRAPWLLRL\GGIIEPFSP GLPKKYN\CDKMI\CRKCYAR/LFHP RCLSTCRK\KKCGSHQTTLRPQRRR SNKGGFFP |
| 4142 | 9639 | A | 4434 | 385 | 499 | |
| 4143 | 9640 | A | 4435 | 2 | 127 | |
| 4144 | 9641 | A | 4436 | 3 | 424 | |
| 4145 | 9642 | A | 4437 | 1 | 110 | |
| 4146 | 9643 | A | 4438 | 1 | 110 | |
| 4147 | 9644 | A | 4439 | 1 | 110 | |
| 4148 | 9645 | A | 4440 | 1 | 110 | |
| 4149 | 9646 | A | 4441 | 1 | 108 | |
| 4150 | 9647 | A | 4442 | 3429 | 7466 | |
| 4151 | 9648 | A | 4443 | 4048 | 4181 | |
| 4152 | 9649 | A | 4444 | 682 | 829 | |
| 4153 | 9650 | A | 4445 | 163 | 320 | EFEGFNPLKLGEAGWARWLTVPVIPA L*ETEAGGSRGQEIETILANTVKPHL Y |
| 4154 | 9651 | A | 4446 | 1122 | 1446 | |
| 4155 | 9652 | B | 4447 | 124 | 27844 | XRSTVPPRISAYERPVWPGEWNDP RGPGRRASAVVSPREGNWGVLRDP RLQARKPRMVRSRQMCNTNMSVP TDGAVTTSQIPASEQETLVRPKPLLL KLLKSVGAQKDTYTMKEVLFYLGQ YIMTKRLYDEKQQHIVYCSNDLLG DLFGVPSFSVKEHRKIYTMIRNLV VVNQQESSDSGTSVSENCHLEGGS DQKDLVQELQEEKPSSSHLVSRPST SSRRRAISETEENSDELSGERQKRKH KSDSISLSFDESALCVIREICCERSS SSESTGTSPNPDLDAGVSEHSGDWL DQDSVSDQFSVEFEVESLDSSEYSL SEEGQELSDDEDEVYQVTVYQAGE SDTDSFEEDPEISLADYWKCTSCNE MNPPLPSHCNRCWALRENWLPEDK GKDKGEISEKAKLENSTQAEFGDV PDCKKTIVNDSRESCVEENDDKITQ ASQSQESSEDYSQPSTSSSIYSSQEDV KEFEREETQDKESVSSLPLNAIEP CVICQGRPKNGCIVHGKTGHLMAC FTCAKKLKKRNKPCPVLTGHIRTEQ PIIILPKKHKKKKERKSLPEEDVAVS SNVDFDTLTKKKVYLNKCLKERSV FKGFQGMGQHWTFINLDKPSNPS SHEVVAWIRRLRVEKTGHSGTLDP KVTGCLIVCIERATRLVKSQSAGK EYVGIVRLHNAIEGGTQLSRALET TGALFQRPPLIAAVKRQLRVRTIYES KMIEYDPERRLGIFWVSCEADTYSR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TLCVHLGLLLGVGGMQELRRVRS GVMSEKDHMTMHDVLDQWLY DNHKDESYLRRVVYPLEKLLTSHK RLVMKDSAVNAICYGAKIMLPGLVI RYEDGIEVNQEIVVITTKGEAICMV EHDKEFFHPRYHHREFRFDLSKIPE GEAVTAAEFRIYKDYIRERFDNETF RISVYQGIGSLPARQPYLWASEEGW LVFDITATSNHWVVPNRHNLGLQL SVETLDGQTINPKLAGLGRHGPQN KQPFMVAFFKATEVHFRSIRSTGSK QRSQNRSKTPKNQEALGWPTMCTD ELSFGLDVLTLQSLFEKRTAAGTRG RPCKKHELIVSFRDLGWQDWIAPAE GYARYYCEGECAFLNSYMNATNH AIVQTLVHFINPETVPPKPCAPTQLN AISVLVYFDDSSNVILKKYRNMVVRA CGCH* |
| 4156 | 9653 | A | 4448 | 2 | 129 | |
| 4157 | 9654 | B | 4449 | 1 | 462 | MSQOYYVRLCQIQSPSPRSVGRENL VLVGDFPDPTLKRVRKGRGCAHCG LTDLPEPTAQVLVEQGDALWFH NVISEEFGVGVNIFWKHLPSECYDK TDTYGNKDPTAASRAAQILDALK TLAELPEEYRDFYARRMVLHIQDK AYSKNSE* |
| 4158 | 9655 | A | 4450 | 3 | 366 | |
| 4159 | 9656 | A | 4451 | 1 | 167 | |
| 4160 | 9657 | A | 4452 | 2 | 382 | TMVLSPADKTNVKA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLVRDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDFLASVS TVLTSKYR |
| 4161 | 9658 | A | 4453 | 2 | 252 | |
| 4162 | 9659 | B | 4454 | 31 | 449 | MVLSPADKTNVKA/WGKTYFPHF DLSPGSAQVKGHGKKVADALTNA VAHVDDNAQRAVRPKRPTRTSFG WTRSNFKLLSHCLLVTLAAHLPAEF NPCGARLPQGVPFGCYAPC* |
| 4163 | 9660 | A | 4455 | 2 | 81 | |
| 4164 | 9661 | A | 4456 | 2 | 81 | |
| 4165 | 9662 | A | 4457 | 3 | 452 | |
| 4166 | 9663 | A | 4458 | 1 | 493 | RPRIRHEHRLRENPPWFLFPAAKTN VKAGLG*G*GSHPPSNVAKTLERIM FLSFPTTKTYFPQLRTLSHGFISQV* GPRSRRLPDALTKRPWRHVDDHAQ TRCPALSDLVAHKLVRDPVNFKLL SHCLLVTLAAHLPAEFTPAVHAYL DKFLASVSTVLTSKYR |
| 4167 | 9664 | B | 4459 | 208 | 420 | MGNPKVKAHGKKVLTSLGDAIKHL DDLKGTFAQLSELHCDKLHVDPEN FKLLGNVLVTSIAIHFGIEFTPE* |
| 4168 | 9665 | A | 4460 | 40 | 534 | SRRHGSVSHREAKATIASLWGKVN VEDAGGETMIRLALVYPWPQRSF ASFSSLFSASAIMGNPKVKAHGKK VLTSLGDAIKHLDDLKGTFAQLSEL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HCDKLHVDPENFKLLGNVLVTVLA IHF\GKEFTPEVQASWQKM\VTGV ANA\LSSTYHLNSLPMMQNf |
| 4169 | 9666 | A | 4461 | 2 | 171 | |
| 4170 | 9667 | B | 4462 | 10 | 351 | MAPRTLVL LLSGALALTQTWAGSH SMRYFYTSVSRPGRGEPRFIAVGYY DDTQFVRFDSDAASQRMEPRAPWI EQEGPEYWDNRNTRNVKAHSQTDR VDLGTLRGYYRCVSHSL* |
| 4171 | 9668 | A | 4463 | 1 | 986 | |
| 4172 | 9669 | A | 4464 | 3 | 1282 | |
| 4173 | 9670 | A | 4465 | 1 | 1004 | MAVMAPRTLLLLL LGALALTQTWA GSHSMRYFTTSVSRPGRGEPRFIAV GYVDDTQFVRFDSDAASQRMEPRA PWIEQGPEYWDNRNTRNVKAHSQI DRVLDGTLRGYYNQSEAGSHTIQM MYGCDVGSDGRFLRGYQQDAYDG KDYIALNEDLRSWTAADMAAQITQ RKWEAAARVAEQLRAYLEGTCVEW LRRHLENGKETLQRTDPPRTHMTH HAVSDHEATLRCWALSFP AEITLT WQRDGEDQTHTCHVQHEGLPKPL TLR WEPSSOPTIPVGIAGLVLF GAV ITGAVVAAMWRRKSSDRKGGSYS QAASSDSAQGS DVSLTACKV |
| 4174 | 9671 | A | 4466 | 1090 | 2175 | |
| 4175 | 9672 | A | 4467 | 1 | 780 | |
| 4176 | 9673 | A | 4468 | 59 | 169 | |
| 4177 | 9674 | A | 4469 | 89 | 134 | |
| 4178 | 9675 | A | 4470 | 864 | 1885 | |
| 4179 | 9676 | A | 4471 | 89 | 176 | |
| 4180 | 9677 | A | 4472 | 1 | 1127 | |
| 4181 | 9678 | A | 4473 | 1 | 405 | |
| 4182 | 9679 | A | 4474 | 3 | 199 | |
| 4183 | 9680 | A | 4475 | 3 | 607 | |
| 4184 | 9681 | A | 4476 | 1017 | 2029 | |
| 4185 | 9682 | A | 4477 | 844 | 1572 | |
| 4186 | 9683 | A | 4478 | 1 | 846 | |
| 4187 | 9684 | A | 4479 | 452 | 1220 | |
| 4188 | 9685 | A | 4480 | 1 | 1254 | |
| 4189 | 9686 | A | 4481 | 1 | 1383 | |
| 4190 | 9687 | A | 4482 | 1 | 1290 | |
| 4191 | 9688 | A | 4483 | 666 | 1606 | |
| 4192 | 9689 | A | 4484 | 1 | 1236 | |
| 4193 | 9690 | A | 4485 | 1 | 1269 | |
| 4194 | 9691 | A | 4486 | 719 | 1175 | |
| 4195 | 9692 | A | 4487 | 1 | 1182 | |
| 4196 | 9693 | A | 4488 | 1 | 1377 | |
| 4197 | 9694 | A | 4489 | 1 | 1335 | |
| 4198 | 9695 | A | 4490 | 1 | 2456 | |
| 4199 | 9696 | A | 4491 | 1 | 1827 | |
| 4200 | 9697 | A | 4492 | 1 | 1011 | |
| 4201 | 9698 | A | 4493 | 452 | 950 | |
| 4202 | 9699 | A | 4494 | 1 | 1433 | |
| 4203 | 9700 | A | 4495 | 1 | 1933 | |
| 4204 | 9701 | A | 4496 | 641 | 2107 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4205 | 9702 | A | 4497 | 1 | 2582 | |
| 4206 | 9703 | A | 4498 | 1 | 1095 | |
| 4207 | 9704 | A | 4499 | 1544 | 525 | |
| 4208 | 9705 | A | 4500 | 2 | 161 | |
| 4209 | 9706 | A | 4501 | 3 | 452 | |
| 4210 | 9707 | A | 4502 | 25 | 622 | EFHRLRENPPWFLFPAAKTNVRAIA WG*RSGAHAGÆYGAELERIMVLF PPPTPKPYFPELRT*AHGFCPKVKGP TAKKVAERA*PNAVAHVVDGHAPN GAVPP*ADLQRRTSFRVDPVNFQAP *ATCLLVTLAAHLPAEFTPAV\HA SLGQVPGLSVSTVLTSTKIPVKLEPSV GHAFLPLWAFPPAPPPLSCTRTPVG L |
| 4211 | 9708 | A | 4505 | 2 | 213 | |
| 4212 | 9709 | A | 4506 | 2 | 382 | TMVLSPADKTNVKAA/WGMFLSFP TTKTYFPHFDLSHGSAQVKGHGKK VADALTNAVAHVDDMPNALSALS DLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASVS TVLTSKYR |
| 4213 | 9710 | A | 4507 | 2 | 252 | |
| 4214 | 9711 | A | 4508 | 1 | 466 | WSPQTQREPTMVLSPADKTNVKAA WGKVGAHAGEYGAELGRIFLSFP PTKTYFPHFDLSPGSAQVKGHGKK VADALTNAGAHVDDMPNALSSPE ATLHAHKLRVDPVNFKLLSHCLLV LAAHLPAEFTPAVHASLDKFLASV STVLTISKYR |
| 4215 | 9712 | A | 4509 | 256 | 391 | NELHAENLKNEDDVTGLLGFWT LIISLTAGFSCCSFSWTVTYFDSFEP GMFPPTPLSPARFKK*R*CRHWTIRI LDSTYNIPNCWILLQLFLDSDL |
| 4216 | 9713 | A | 4510 | 2 | 490 | |
| 4217 | 9714 | A | 4511 | 1 | 160 | |
| 4218 | 9715 | A | 4512 | 1 | 150 | |
| 4219 | 9716 | A | 4513 | 1 | 73 | |
| 4220 | 9717 | A | 4514 | 2 | 213 | ISPFYHLCQMLKTADVLRMMALWR CRDALLS*GGSSIEIPLFLLYGSREL LGFCFTGMNHCAQSIYNRF |
| 4221 | 9718 | C | 4515 | 186 | 365 | MFQLLYDSLXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXIYNRF* |
| 4222 | 9719 | A | 4516 | 251 | 454 | GGSSIEIPLFLLYGSRARTWILF*EM AAGRVQWLTSVIPALWEAEAGSR GQEFKTSIAKRVKPHLY |
| 4223 | 9720 | A | 4517 | 3 | 192 | |
| 4224 | 9721 | A | 4518 | 1 | 129 | |
| 4225 | 9722 | A | 4519 | 23 | 115 | |
| 4226 | 9723 | A | 4520 | 1 | 1582 | GRGWRAVLGWSRRRSGLEPATVGS SMALLFLLPLVMHGVSRAMGTAD LGPSSVPTPTNVTIESYNMNPVYW EYQIMPQVPVFTVEVKNYGVKNSE WIDACINISHHYCNISDHVGDPSNSL WVRVKARVGQKESAYAKSEFAV CRDGKIGPPKLDIRKEEKQIMIDIFH PSVFNVDGEQVDYDPETTCYIRVY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NVYVRMNGSEIQYKILTQKEDDCD EIQCQLAIPVSSLNSQYCVSAEGL HVWGVVTEKSKEVCITIFNSSIKGSL WIPVVAALLFLVLSLVFICFYIKKI NPLKEKSIILPKSLISVVRSALETGP ESKYVSLITSYQPFSLKEVVCCEPL SPATVPGMHTEPNPGKVEHTEELSS ITEVVTTEENIPDVVPGSHLTPIERE SSSPLSSNQSEPGSIALNSYHSRNC ESDHSRNGFDTSSCLESSESLSDSE FPPNNKGEIKTEGQELITVIKSPPPSF CYDKPAHVLVDLLVDDSGKESLIG YRPTNEDSQRFHEISLSCTQL |
| 4227 | 9724 | A | 4521 | 1 | 408 | |
| 4228 | 9725 | A | 4522 | 2 | 377 | |
| 4229 | 9726 | A | 4523 | 50 | 326 | |
| 4230 | 9727 | A | 4524 | 3 | 1948 | AAAAAAVPASFGLCSRDPAPPQP ASMSGIKKQKTENQKSTNVVYQA HHVSRNKRQVVGTRGGFRGCTV WLTGLSGAGKTTISFALEEYLVSHA IPCYSLDGDNVRHGLNRNLGFSPGD REENIRRIA EVAKL FADAGLCITSF ISPFADRENARKIHESAGLPFEIFV DAPLNICESRDVKGLYKRARAGEIK GFTGIDSDYEKPEPTEPVLTNLST VSDCVHQVVELLQEQNIVPYTIKDI HELFVPENKLDHVRAEAETLPSLSIT KLDLQWVQVLESEGWATPLKGFM EKEYLQVMHFDTL DGMALPDGVI NMSIPIVLPVSAEDKTRLEGCSKFVL AHGGRRVAYLTETA EF/HTEHRKE ERCS/RVFWGTTCTKHPHIKVMVME SGDWLVGGDLQVLEKIRWNDGLD QYRLTPELEKQCKEMNADAVFAF QLRNPVHNGHALLMQDTRRRLLER GYKHPVLLHPLGGWTKDDDVPLD WRMKQHAAVLEEGVLDPKSTIVAI FPSPMLYAGPTEVQWHCSRMIAG ANFYIVGRDPAGMPHPETKKDLYE PTHGGKVL SMAPGLTSVEIIPFRVA AYNKAKKAMDFYDLARHNEFD FIS GTRMRKLAREGENPPDGFMAPKA WKVLT DYRSLEKN |
| 4231 | 9728 | A | 4525 | 1 | 626 | |
| 4232 | 9729 | A | 4526 | 66 | 409 | LGLLQVTTNPPSPNTYLLKMLFK LRTPPFISHHSFILKNYDIQYFSMRDI DRLGIQKVMERTFDLLIGKRQRIH LSFDIDAFDPTLAPATGTPVVGGLT YREGMYIAEEIH |
| 4233 | 9730 | A | 4527 | 1 | 1257 | |
| 4234 | 9731 | A | 4528 | 3 | 1086 | FSVLRIMSLRGSLSRLLQTRVHSILK KSVHSAVIGAPFSQGGQKRKGVEH GPAAIREAGLMKRLSSLGCHLKDFG DLSFTPVPKDDLNNLIVNPRSVGL ANQELAEVVSRAVSDGYSCVTLGG DHSLAIGTISGHARHCPDLCVWV DAHADINTPLTTSSGNLHGQPV SFL LRELQDKVPQLPGFSWIKPCISSASI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VYIGLRDVPPEHFILKNYDIQ\YFP MKDIDRLGIQKVMERTFDLLIGKRQ RPIHLSFDIDAFDPTLAPATGTPVVG GLTYREGMYIAEEIH\NTGLLSALDL VEVNTQLATSNEEAKTTADLAVDV IASSFGQTREGGHIVYDQLPTPSSPD ESENQARVRI |
| 4235 | 9732 | A | 4529 | 1 | 128 | |
| 4236 | 9733 | A | 4530 | 3 | 126 | |
| 4237 | 9734 | A | 4531 | 1 | 79 | |
| 4238 | 9735 | B | 4532 | 214 | 268 | XELEKLQVVRQLEAEPGLPPVQPV FITVDPERDDVEAMARYVQDFHPR LLGLTGSTKQDEDQDIYVDHSIAIY LLNSDGLFTDYYGRSRSAEQISDSV RRHMAAFRSVLS* |
| 4239 | 9736 | A | 4533 | 23 | 257 | AYLIDDTEAQSRRGSQAKATPLEGLR TQPSSRPLGGIKLV*YEVLCLLMTA LKAI/TQIQLPATSHSAARLRGVLP AIR |
| 4240 | 9737 | A | 4534 | 3 | 229 | |
| 4241 | 9738 | A | 4535 | 1 | 297 | |
| 4242 | 9739 | A | 4536 | 67 | 552 | GPWRFCFSEAVSEPTTVAFDVRPGG VVHSFSHNVGPGDKYTCMFTYASQ GGTNEQWQMSLGTS\EDHQHFTCT IWRPPRGKSYL\YFTQFKAEVAGRL RFEYRHGLTFKARILKGESDVPLEN LRNFEVTKTAVGSQGPAPKLTC PKLVIVAKASRTEL |
| 4243 | 9740 | A | 4537 | 2 | 232 | RDGTVHARAANKNRVISVLLPSDLV H*LWEP*PDED*DA*SETGDIDHRV TEESHE*PAFHNFMQESMAQYWK NNK |
| 4244 | 9741 | A | 4538 | 2 | 1094 | RHPVCLLVLMAGSGKTTFFVQRLT GHLHAQGTTPPYVINLDPVHEVPFP ANIDIRDTVKYKEVMKQYGLGPNG GIVTSLNLFATRFDQVMKFIEKAQN MSKYVLIDTPGQIEVFTWSASGTIT EALASSFPTVVIYVMDTSRSTNPVT FMSNMLYACSIKYTKLPFIVVMNK TDIHDHSFAVEWMQDFEAFQDALN QETTYVSNLTRSMSLVLEFYSSLR VVGVS\AVLGTGLDELFFVQVTSAAE EYEREYRPEYERLKKSLANAES\QQ EREQLERLRKDMGSVALDAGTAKG VFTVDSLSPVLHPSDLILTRGTLDEE DEEADSDTDDIDHRVTEESHEEP AFQNFMQESMAQYWKRNK |
| 4245 | 9742 | A | 4539 | 710 | 1053 | |
| 4246 | 9743 | A | 4540 | 3 | 281 | |
| 4247 | 9744 | A | 4541 | 30 | 320 | |
| 4248 | 9745 | A | 4542 | 3 | 115 | |
| 4249 | 9746 | A | 4543 | 1 | 137 | |
| 4250 | 9747 | A | 4544 | 3 | 32 | |
| 4251 | 9748 | A | 4545 | 1 | 135 | |
| 4252 | 9749 | A | 4546 | 1 | 2694 | |
| 4253 | 9750 | A | 4547 | 3 | 544 | |
| 4254 | 9751 | A | 4548 | 2 | 323 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4255 | 9752 | A | 4549 | 1 | 384 | |
| 4256 | 9753 | A | 4550 | 1 | 1299 | MASPVAAQAGKLLRALALRPRFLA AGSQAVQLTSRRWLNLOEYQSKKL MSDNGVRVQRFFVADTANEALEAA KRLNAKEIVLKAQILAGGRGKGVF NSGLKGGVHLTKDPNVVGQLAKQ MIGYNLATKQTPKEGVKVNKVMV AEALDISRETYLAILMDRSCNGPVL VGQPQGGVDIEEVAASNPELIFKEQI DIFEGIKDSQAQRMAENLGFVGPLK SQAADQITKLYNLFLKIDATQVEVN PFGETPEGQVVCFDAKINFDDNAEF RQKDFAMDDKSENEPIENEAAKYD LKYIGLDGNIACFVNGAGLAMATC DIIFLNGGKPANFLDLGGGVKEAQV YQAFKLLTADPKVEAILVNIFGGIV NCAIIANGITKACRELELKVPLVVR EGANVQEAQKILNNSGLPITSAIDL EDAAKKAVASVAMK |
| 4257 | 9754 | A | 4551 | 1 | 590 | RVRTKDPNVVGQLAKQMIGYNLAT KQTPKEGVKVNKVMVAEALDISRE TYLAILMDRSCNGPVLVGSPQGGV DIEEVAASNPELIFKEQIDIFEGIKDS QAQRMAENLGFVGPLKSQVEAILV NIFGGIVNCAIIANGIPKACRELELK VPLVVRLEGTNVQEAQKILNNSGLP ITSAIDLEDA\AKKAVA\SVAKK |
| 4258 | 9755 | A | 4552 | 3 | 168 | |
| 4259 | 9756 | A | 4553 | 3 | 95 | |
| 4260 | 9757 | A | 4554 | 3 | 354 | |
| 4261 | 9758 | A | 4556 | 1 | 95 | |
| 4262 | 9759 | A | 4557 | 156 | 364 | GPVE*KPVEEESRGLLD*GLPGMD WGWWFGKGGDPPLAQLNCPSTV SEIIGRDLSGFPAPPGEPPA |
| 4263 | 9760 | A | 4558 | 1 | 2523 | |
| 4264 | 9761 | A | 4559 | 3 | 469 | |
| 4265 | 9762 | A | 4560 | 3 | 132 | |
| 4266 | 9763 | A | 4561 | 1 | 2961 | MGAASCEDEEFLKLVFGEEKEAPP LGAGGLGEELDSEDAPPCCRLALGE PPPYGAAPIGIPRPPPRPGMHSPPPR PAPSPGTWESQPARSVRLGGPGGG AGGAGGGRVLECPISIRITSISPTPEPP AALEDNPDWGDGSPRDYPPPEGF GGYREAGAQQGGAFFSPSPGSSSL SWSFFSDASDEAALYAACDEVESEL NEAASRFLGSLPLSPRASRPWTPE DPWSLYGPSPGGRGPEDSWLLLSAP GTPASPRPASPCGKRRYSSSGTPSS ASPALSRRGSLGEEGSEPPPPPLPL ARDPGSPGPFDYVGAPPAESIPQKT RTTSSEQAVALPRSEEPASCNGKLP LGAEESVAPPGSRKEVAGMDYLA VPSPLAWSKARIGGHSPIFRTSALPP LDWPLPSQYEQLRIEVQPRAHHR AHYETEGSRGAVKAAPGGHPVVKL LGYSEKPLTLQMFICTADERNLRPH AFYQVHRITGKMVATASYEAVVSG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TKVLEMTLLPENNMAANIDCAGIL KLRNSDIELRKGETDIGRKNTRVRL VFRVHVPQGGGKVSVQAASVPIE CSQRSAQELPQVEAYSPSACSVRGG EELVLTGSNFLPDSKVVFIERGPDG KLQWEEEA TVNRLQSNEVTLT TV PEYSNKRVS RPVQVYFYVSNGRRK RSPTQSFRLPVICKEEPLDSSLRGF PSASATPFGTDMDFSPRPYPSPYH EDPACETPYLSEGFGYGMPLYPQT GPPPSYRPLRMFPETRGTTGCAQP PAVSFLPRFPSPDPYGGRGSSFLGL PFSPAPFRPPPLPASPPLEGFPQS DVHPLPAEG\YNKVGPGYGPGE GAP EQEKS RGGYSSGFRDSVPIQGITLEE VSEIIGRDL\SGFPETSLEKKPPALKP RETVITLATPAPASALPPFPFLELV ATEAWGQPLAPLSPSFCLSHCLPLPS PSLGCGPQAWLA ALEGLGGKECVE EGGG |
| 4267 | 9764 | A | 4562 | 19 | 387 | |
| 4268 | 9765 | A | 4563 | 1 | 373 | |
| 4269 | 9766 | A | 4564 | 2 | 343 | |
| 4270 | 9767 | B | 4565 | 19 | 507 | MEANGLGPQGFPPELKNDTFLRAAW GEETDYTPVWCMRQAGRYLPEFRE TRAAQDFFSTCRSPEACCELTLQPL RRFPLDAAIIFSDILVVPQALGMEVT MVPSKGPSFPEPLREEQDLEALRDP EVEASKLGYGFQAITPYPTTTGWDV CRLIGFCWC PHGP* |
| 4271 | 9768 | A | 4566 | 3 | 339 | |
| 4272 | 9769 | A | 4567 | 3 | 679 | |
| 4273 | 9770 | A | 4568 | 1 | 139 | |
| 4274 | 9771 | A | 4569 | 1 | 526 | HERFETTYFKKFPAGYYVTGDGCQR DQDGYWITGRIDDMNLNVSGHLLS TAEVESALVEH*RLLOEA\AVVGHP HPCEGVNASYCFVTLCDGHTFSPKL TEELKKA\VMRKRLAPFATPDYIQN APGLPKTRSGKIMRRVLRKICS/VT DHDLDGDMSTVADPS\VISHLFSHRC LTIQ |
| 4275 | 9772 | A | 4570 | 537 | 2357 | GVCHQRRLAPQAWPGAGTDSLLLA TRWATGAPGHCCWHLPARHTCGSP GLSPVPQPASAGPPGGLWERHSRE YIKTWRPR/YFLKSDGSFIGYKERP/ EAPDQTLPLNNFSVAGCLGMS\EC QLMKTERPRPNT/FVIRCLQWTTVIE RTFH/VDSPDE/REEWMRAIQMVAN SLKQ/RAPGEDPMDYKCGSPSD/SST TEEMEVAVSKARA/KVGTFGKVILV REKAT/GRYYAMKILRKEVIIA/KVR APGIALASLCGGCVCLQDEVAHTV/ TESRVLQNTRHPFLTALKYAFQTHD RL/CFVMEYANGAVFHLSRERVFTE ERAR/FYGAEIVSALEYLHSRD/VVY RDIKLCAQEKGDTHSP*KVSPSLSSR ITLAPTGTQVSTVRGTSDP/AVECS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HSGTPHSSWNEQLHTTVWTRLIG YVEGKPHRGAVPRYMGVGQRVLE DN/DYGRAVDWWGLGVVME/MM CGRLPFYNQDHERLF/ELILMEEIRF PRTLSP/EAKSLLAGLLKKDPKQ/RL LP/PFKPQVTSEVDTRYFDD/EFTAQ SITITPPDRCECWGPRAESRCLPHAE PSSAAVPDGFAPAGPLSPQDAWRGR RGWRRRERAGAAGRTRVRRGHLPE VMPAFLAS |
| 4276 | 9773 | A | 4571 | 64 | 1537 | VTAYHAATMNEVSVIKEGWLHKR GEYIKTWRPRYFLLKSDGSFIGYKE RPEAPDQTLPLNNFSVAECQLMKT ERPRPNTFVIRCLQWTTVIERTFHV DSPDEREEWMRAIQMVANSCLKQRA PGEDPMDYKCGSPSDSSTTEEMEV AVSKARAKVTMNDFDYLKLLGKG TFGKVILVREKATGRYYAMKILRKE VIIAKDEVAHTVTESRVLQNTRHPF LTALKYAFQTHDRLCFVMEYANGG ELFFHLSRERVFTEERARFYGAEIVS ALEYLHSRDVVYRDIKLENMLDK DGHKITDFGLCKEGISDGATMKT CGTPEYLAPEVLEDNDYGRAVDW WGLGVVMEYMMCGRLPFYNQDHE RLFELILMEEIRFPRTLSPKASLLA GLL\KKDPKQRLG\GGPSDAKEVME HRFFLSINWQDVVQKLLPPFKPQV TSEVDTRYFDDEFTAQSITITPPDRY DSLGLLE\LDQRT\HFP\QFSYSASIRE |
| 4277 | 9774 | A | 4572 | 2 | 423 | |
| 4278 | 9775 | A | 4573 | 1 | 106 | |
| 4279 | 9776 | A | 4574 | 3 | 58 | |
| 4280 | 9777 | A | 4575 | 1 | 191 | |
| 4281 | 9778 | A | 4576 | 3 | 325 | |
| 4282 | 9779 | A | 4577 | 3 | 277 | |
| 4283 | 9780 | C | 4578 | 77 | 292 | MVDFCPCPSICFXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXHSWIS IS* |
| 4284 | 9781 | A | 4579 | 645 | 849 | |
| 4285 | 9782 | A | 4580 | 3 | 140 | EANKENREAQMAAKLERLPEKD*A /HLEEVKKN\ESKDPADETead |
| 4286 | 9783 | A | 4581 | 49 | 605 | NSARGLSLSQLIVQNTLPVACLLFT MASSDIQVKELEKRASGQAFELILSP RSKESVPEFPLSPPKEEGFFPGKFR EN*EAAEERRQSP*SCSS*RQLAEKR EVHGKEVLQKAIEENNNFQ*NGQK RKLTPHKMEA**RDPREATNGLPKL EPFAEEKDKAH*KKCRKNKESQRP CPRDLKPD |
| 4287 | 9784 | A | 4582 | 1 | 567 | VVREPAFSLA/EAQFTARYFSTSSIP NV\NKA\PV\IRRSKHM*QGVTLPI E\HYHEGTD\SL*TALV*ARVGNQLA KLKR\NYAKAVELLVQLASLQTSFV TLDEAIKITNRRVNAIEHVIIPIERT LAYIITELDEREREFEYRLKKIQEKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KILKEKSEKDLEQORRAAGEVLEPANLLAEKDEDLLFE |
| 4288 | 9785 | A | 4583 | 1 | 748 | MSGKDRIEIPSRMAQTIMKARLKG AQTGRNLLKKKSDALTFRQILKK IETKMLMGEVMREAAFSLAFAKFT AGDFSTTVIQNVNKAQVKIRAKKD NVAGVTLVPFEHYHEGTDSEYELTG LARGGE\QLAKLKRNYAKAVELLV ELASLQTSFVTLDEAIKITNRRVNAI EHVPIPRIERTLAYIITELDERVREEF YRLKKIQEKKKILKEKSEKDLEQRR AAGEVLEP\ANLLAEKDEDLLFE |
| 4289 | 9786 | A | 4584 | 166 | 238 | |
| 4290 | 9787 | A | 4585 | 53 | 203 | |
| 4291 | 9788 | A | 4586 | 357 | 498 | |
| 4292 | 9789 | A | 4587 | 262 | 397 | |
| 4293 | 9790 | A | 4588 | 68 | 422 | |
| 4294 | 9791 | A | 4589 | 70 | 361 | |
| 4295 | 9792 | A | 4590 | 259 | 2603 | |
| 4296 | 9793 | A | 4591 | 246 | 667 | |
| 4297 | 9794 | A | 4592 | 25 | 471 | |
| 4298 | 9795 | A | 4593 | 2 | 3788 | |
| 4299 | 9796 | A | 4594 | 1 | 700 | |
| 4300 | 9797 | A | 4595 | 604 | 1047 | SNNRTDNPTSVAYLSKETDVVAKG WPHCLWVVAVAILVLEAIKIIQGGK DFTVWTS HDVNGILGAKGNSWLS KRLRYQALLLEGPVLQIHTCVALN PAIFLPEDGEPIKHDYQQIVAQTYVT *EDLLEVPLANPDNLNLYTNGSSFFV |
| 4301 | 9798 | A | 4596 | 1 | 1410 | |
| 4302 | 9799 | A | 4597 | 510 | 755 | |
| 4303 | 9800 | A | 4598 | 59 | 411 | SWPSDKQTLVVQRGQKMEQANHP DPTDHMSQLMWT/VLPQGFRDSPH LFGQALAQDLGHFSSPGTLVLQYV DDLLATSSEASCQATLALLNFLA NQGYK/LSRSKAQLCLQQVKYLCL |
| 4304 | 9801 | A | 4599 | 1 | 565 | |
| 4305 | 9802 | A | 4600 | 126 | 492 | CNNSMTSLQVRLKVCPRPCRTSM/L PIRII*KLPQVCLDLL*IREGEWDMY PCWAKFPCPYSLKGT*PIAWGILWS FGDFFAY/IPLMQQQKH*FSSQNTRR NEEGQI*WPLLMHSQKPAPLPVV |
| 4306 | 9803 | A | 4601 | 1 | 342 | |
| 4307 | 9804 | A | 4602 | 55 | 219 | LGNKHLLGSIDPRGSWVTGEYIFLR PIIAA*GRQ*DFLPFELWWTSLNNS WAFS |
| 4308 | 9805 | A | 4603 | 339 | 1371 | ASHPLRGLLCGPSLPNEPCPLLHGT QSHRPLKG*GVRAHSTGLAGSSTCR PLRDPLGEASWAPESAQGL*IHQSA LCI*LKLKPAGQRAKLGDRLDIPDR RKSSSTILGRAGDLQPAMPEPTLSV GSCAAQASPMNPAPCSTAPSPIDHS RAEECGRIARDWQAAPPAGPCGIH WVKPAGLLSLLRDCKYTNRHSVSS SRFANTNQHPASSSGFVNAPIDTLY LANLVGTWRTFVASSGIVNAPISTL SKQTTWLYQSAGCGKESTQASGAQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TGGTSFKSLETTGSISEASSAKHCTE LFSRFTTFNPDSVPSDGVVGDTAGT VWPGVLKGEPCHLGTCYRCVLDPH PTPSESDTIQGIHVQVCYMSTLHDA DVCDTNDPVTHTNKKYIYSTEFTS NNPELRSEDETVFRALEKWKTSQET IGEMDFYICNDPHPDALYQNGLSK MQDTVSLSVFSPSVAA |
| 4309 | 9806 | A | 4604 | 749 | 1002 | QLKKGTSNLLVSKPSPVWIPTGTLT QIMGTGVANIC*PVF*KD*GELGKM NYAMMSTITQGKEENPAFLKWLWE ALRKYTPLSP |
| 4310 | 9807 | A | 4605 | 1 | 1632 | |
| 4311 | 9808 | A | 4606 | 307 | 543 | |
| 4312 | 9809 | A | 4607 | 1 | 1149 | |
| 4313 | 9810 | A | 4608 | 119 | 409 | GDICHLGLTPVGSHSLSCSR*QV A*VGAVTAATIGTGILLQQLAFLVC NWLLLSGSSNFPRSALICFKSEREK GTCIQVGPNSPPPTACKGHN |
| 4314 | 9811 | A | 4609 | 1 | 2433 | |
| 4315 | 9812 | B | 4610 | 97 | 1065 | MHAVHTSLLVERTILTTTKERGSTL QYPLRPGAHKGLQDIVKRFKAQALI RKCSSPCNTPILGVQKPNGQWRLV QDLRLINEAVIPLYPVVPNPYNLLSQ IPEEAWEFTVLDLKDAPFCIPLHSDS QFLAFEDPTDHTSQTWTVPVPPGF RDSPPFLGQALAQDLGHFSSPGTLV LQYVDDLLLATSSEASCQQAATDLL NFLANQGYKTHSRSDAPVGFTRDR HLVATEKIPRGREPLSSLA VYTRGR PTRTGARRTIVSRIRDRFRFFRYLA QREPLYQQSLLIHLQLDSQPALSV VIGKVPNVVELTPNFGTAAQV* |
| 4316 | 9813 | A | 4611 | 1 | 2403 | |
| 4317 | 9814 | A | 4612 | 1 | 2838 | |
| 4318 | 9815 | A | 4613 | 1908 | 4698 | SNDRTEDDCGKHPFMSSPP/TEPWV CLIEGQEIDFLLDTGTTFSVLIPCLG RLSSRSVTIQILGQPVTTRYFSHLLS CNWETLLFSHAFLVMPESTPLLGR DILAKAGAIISMKTGNKLPICCPLE GINPEVWALEGQFGRAKNAHPLQIR LKDPISFPYQRQYPLRPEAHKGLQDI VKHLKAQDSVRKCSSPCNTPILGVQ KLNSQWRLVQDLRLINEAVIPLYPV VRNPYTLLSQVPPEAEWFTVLDLK DAFFCIPLHSDSQFLAFEDPTDHTS QLMWMVLPQRFRDSPHLFGQAQA QDLGHFSSPGTLVLQYSEIAKTLTY LIKEMERANTHLVEWEPEAETAFAFET LKQALVQAPALSLPTGQNFALYVIE RAGIALGVLTQTHRTTPQPVAYLSK EIDVVAKGWPHCLRTVVA VAVLVS EAIKIIQGKDFTVWTTTHDVNGILGA KGGLWPSDNCLLRYQALLLEEPVL QIHMCIAINPATFLPEDGEPIKHDCQ QIIVQTYATQDDLLEVPLANPDFNL YNSGSSFVENGIQRAGYAI VSDVTV |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | LGSKPLSPGTSTQLAELVALTRALE LGKGKRINVYTD SKYAYLILHAHA AIWKEREFLTSGGTPIKYHKEIMELL HTVQKPKEVAVLHCQSHQKGSARR IFCLTRIPGTRVCKNPHVSLSGISEW PLRDHTPLCFRPKALLA WVHEEICS MGCKDPGWNSLKVSEEDRKMQUES LETSRDLLNGFDQNVNDMDMSKVQ AEGASDGDEELIGKWRKGLSMLW KILSIENMMNVWKDGTIKDAIIVIEK AVKAIKPETINSCQRNLCPDVVHDF TRFTTEPIKDIKEIGDLAIKLGIFESS NSTQFLNQFVPDDRSLPHNKLKLFY KPEFYSSYPLVSCLDHYVDQVGARI SMSFCVTTVTASGSGSWTCGVSQ LKLSYAD |
| 4319 | 9816 | A | 4614 | 1529 | 2945 | |
| 4320 | 9817 | A | 4615 | 3 | 374 | |
| 4321 | 9818 | A | 4617 | 3 | 112 | |
| 4322 | 9819 | A | 4618 | 359 | 465 | |
| 4323 | 9820 | A | 4619 | 3 | 381 | MRILMVGLDAAGKTTILYKLLGEI VTTIPTIGFIFVVDSDNRERIQEVAD ELQKMLLVDELDAVLLLFANKQD LPNAMAISEMTDKLGLQSLRNRTW YVQATCATQGTGLYEGLDWLSNEL SKR |
| 4324 | 9821 | A | 4620 | 395 | 552 | |
| 4325 | 9822 | B | 4621 | 1289 | 1603 | MVVTISPNSFLYRMVVLPAASNPTI KMRICFLPNSREKREEIVRPMVVA LVMGRSRRGLGRPRAFSFQAPROT KREGREAAEEERGRQKRLSGPCAD EDPAQE* |
| 4326 | 9823 | A | 4622 | 2 | 116 | |
| 4327 | 9824 | A | 4623 | 156 | 403 | |
| 4328 | 9825 | A | 4624 | 8 | 2648 | WIQYSSTTL PNDWNKRKKKEKKA MLSARAKTPRKPTV/KKGSQTNLKD PVG\YCRVRLGFPDQECCIEVINNTT VQLHTPEGYRLNRNGDYKETQYSF KQVFGTHTTQKELFDVVANPLVND LIHGKNGLLFTYGVGTSGKTHMT GSPGEGGLLPRCLDMIFNSIGSFQAK RYVFKSNDNRNSMDIQCEVDALLER QKREAMPNPKTSSSKRQVDPEFAD MITVQEFCKAAEEVDEDSVYGVFVS YIEIYNNYIYDLLEVPFDP/IKPKPP QSKLLRED\KNHNMYVAGCTEVEV KSTEEAFEVFWRGQKKRRIANTHL NRESSRSHSVFNIKL VQAPLDADGD NVLQEKEQITISQLSLVDLAGSERTN RTRAEGNRLREAGNINQSLMTLRTC MDVLRENQMYGTNKMVPYRDSKL THLFKNYFDGEGKVRMIVCVNPKA EDYEENLQVMRFAEVTQEVEVARP VDKAICGLTPGRRYRNQPRGPVGN EPLVTDVVLQSFPLPSCEILDINDE QTLPRLIEALEKRHNLRQMMIDEFN QKSNFAFKALLQEFDNAVLSKENHM |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | QGKLNEKEKMISGQKLEIERLEKKN KTLEYKIEILEKTTTIYEEDKRNLLQ ELETQNQKLQRQFSEKRRLEARLQ GMVTETTMKWEKECERRVAAKQL EMQNKLWVKDEKLKQLKAIVTEPK TEKPERPSRERDREKVTQRSVSPSP VPLLFPDQONAPPRLRHRRSRASG DRWVDHKPASNMQTETVMQPHVP HAITVSVANEKALAKCEKYMLTHQ ELASDGEIETKLIKGDYKTRGGGQS VQFTDIETLKQESPNGSRKRRSSTV APAQPDGAESIEWTDVETRCVSGC GR*GAGSQLGPGYQHHAQPKRKK P |
| 4329 | 9826 | A | 4625 | 1 | 331 | |
| 4330 | 9827 | A | 4626 | 142 | 461 | |
| 4331 | 9828 | B | 4627 | 136 | 906 | XPELKPVDKESVVMKFPDGFEEKFS PPILQLDEVDFYYDLKHVIFSRLSVS ADLESRICVVGENGAGKSTMLKLL LGD LAPVRGIRHAHRNLKIGYFSQH HVEQLDLNVSACGTAGHASFLGRP EEEYXGWCDSGVPRMKRFKAGVP GSCGYAKEGGVTRVERKDFDQYRA LLQGTVSAAKAFL* |
| 4332 | 9829 | A | 4628 | 1 | 233 | |
| 4333 | 9830 | A | 4629 | 1 | 312 | |
| 4334 | 9831 | A | 4630 | 2 | 119 | |
| 4335 | 9832 | A | 4631 | 1 | 145 | |
| 4336 | 9833 | B | 4632 | 78 | 236 | MSYIPGQPVTAVVQRVEIHKLRQGE NLILGFSIGGGIDQDPSQNPFSEDKT DK* |
| 4337 | 9834 | A | 4633 | 102 | 583 | IRVEMSYIPGQPGTAVVQRGEIHKL RQGENLILGFSIGGGIDQDPSQNPFS EDKTDKGIYVTRVSEGGPAEIALQ IGDKIMQVNGWDMTMVTHDQAR KRLHQALRRRLVRL\VTRQS\LQK\ AVQQSMPVLAATTILRLLPAASLYS NATSTLWSPSGFC |
| 4338 | 9835 | A | 4634 | 1 | 373 | |
| 4339 | 9836 | A | 4635 | 3 | 86 | |
| 4340 | 9837 | A | 4636 | 1 | 204 | |
| 4341 | 9838 | A | 4637 | 1 | 767 | |
| 4342 | 9839 | A | 4638 | 20 | 515 | |
| 4343 | 9840 | A | 4639 | 3 | 391 | HEESRSVSQAGVQWRYLGSLQRPP PRFKRFSCLSPSSWDHRCCTTS*LAN F*YL VETGFHHVELLTSSDLPTSAS QSAGITGVSHHAWPWFALNVFKDG CESPWP HN KLEFYTAYYNFFNTGTT LRPPL |
| 4344 | 9841 | C | 4640 | 201 | 368 | MGKSKXAFRXXSXGIVFIQGTFPXE YNXXPRGIKVSQEXNXXXXXCXKI GGEDVX* |
| 4345 | 9842 | A | 4641 | 1 | 307 | RLFFFFETVSHSVTQARVHLSHLGS LQPLLPTFKQFSLSLPGS*DYRRL LHPANF*FSVETGFHHVGOAGLEL LTSGDPPTSASQSAGITGVSHRAWP ST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4346 | 9843 | A | 4642 | 1 | 310 | |
| 4347 | 9844 | A | 4643 | 49 | 360 | DRVSVTQAGVQWCNLSLQPLPPR FR*FSCLSLSSWDYRRPPRPANF* FLVETGFHHVGQAGLKLLTSSDPPT SASQSAEITGVSHRAWPVLSSPQPF FF |
| 4348 | 9845 | A | 4644 | 2 | 119 | |
| 4349 | 9846 | A | 4645 | 1 | 276 | FFFFFFFFLTQSLTHSVTRLECSGVI SAHCNLCLLGSSS*LASAS*VAGTT GANHYAQLIFVFLVEMGFHHVGRA GLKL/HDLK*SKVLGLQA |
| 4350 | 9847 | A | 4646 | 2 | 273 | LRQFSLLLPRVECSGAISHCNLCLL GSSDSPASASRVSGITGTHHQTWLT FFVFLVEMGFHHVGQAGLQLLT*V IRPPRPPKVLGLQA |
| 4351 | 9848 | A | 4647 | 1 | 106 | |
| 4352 | 9849 | A | 4648 | 1 | 485 | SSIDTLGRRVGQPAPGSPGASNHLC CESYPWQLLQPCPVQAGARAELVP VPAHHPGDPVKTEP*RGQGASSGSC TCWGCPTAQAQAQ\PSSPAAPMRK EGPPSL*SERTGRPSRGVTSAGSDG AQPGSA*HSPWPGIVLLSVRYLQETI NHRPGGRPTGFSS |
| 4353 | 9850 | A | 4649 | 1 | 623 | CDLNSQPRSTDGTFDLTVLSNDGVH STVTSNIRVFFAGFSNATVDNSILLR LGVPTVKDFLTNHYLHFLRIASSQL TGLGTAVQLYSAYE/GEQ*NVSFGQ L*SENHNQYVNPSSGRSHLLERHSK RSF/FROSGVKVESVDHDS CVHGPC QNGGSCLRRLAVSSVLKSRESLPVII VANEPLQPFLCKCLPGYAGSWCEID IDECLPSP |
| 4354 | 9851 | A | 4650 | 1 | 446 | LMLRPRKLQEPVPHHHLGFQCPSS PLLPP\GPPPHKV*PLGFQEGGQHS SSLNFVAHSTPAKP/PPGCVCPSLPA SHAHCLSRVIGGVGLRNCTVVPTRG GGSQLPALLPSLIVPLIVHQSPVSS LQPIRHDLPAPGDGTHSSAYC |
| 4355 | 9852 | A | 4651 | 2 | 388 | SHGSYVMYHDQVEFISGMKHW/FN TKIQTIIY*KNEEKNMIISTNAENG HDKILLPFMIKTHITLGI*GNVLILIT GIHKQFFWQQGGWGGACGGGRVL LFPQAGVQWWDHSSLQPQPSLNSF SNSSL |
| 4356 | 9853 | A | 4652 | 115 | 413 | LHIYSQPKFRKGTKKIH*W*KDSVFH SSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSPMQLIQENTG/IMLQDI GFGKDYLSKTSKAQATKQK*TRKH WEMLQDIGFGKDYLSKTSKAQATK QK |
| 4357 | 9854 | A | 4653 | 3 | 129 | NTLLKKTVSFHQCCWKNWISICRKI KLDSYLSPTYTKIKSKLIKLNKVRPET MQLIQENTG/IMLQDIGFGKDYLSK TSKAQATKPK*TRLLSLTIYKNQVK VD |
| 4358 | 9855 | A | 4654 | 1 | 405 | LTLKPNSGFRFPFQVATR*IKYPGIH PAKEVKDLYRKT*KTLKGITDGN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | Q*KTIRGSWIGRINITEMAILPKAIYR FNTTPIKLPMAFITQLEKTIQKFIWN QKGAQIAKRILSKKTNSQTSHTVL QTIRI |
| 4359 | 9856 | A | 4655 | 3 | 448 | FFFFFAFLLLGLLHQIPDVSPTGKYT TLLPLMIILMISGIKEVIYIINDMADK IVKEHKTVMTRLWDTFKWKEVKC GLNTVKALEMGELPSLQDTPDVF *QHSNPG*RDCKTRQGFDREQLLY QCRDILPPROQAFKLQSLRAQP |
| 4360 | 9857 | A | 4656 | 2 | 502 | KKKKERKRKRTPIKKWAKDDRHF TGDKIKMVNKNIKCSISLVIS*MQI KAITIHPTRLAKVKCLPRMGR/KGIL FYCW WARKLEQ/SFRKIFIP*NPGVR LLSTNPRKICAPFAKNTRASETWTK LLLAALCVVTPN*KQTNC PSTAGMS NLLASMDHTGRTVSGHA |
| 4361 | 9858 | A | 4657 | 61 | 364 | KTVWF CARVEGQGNLG*WKPRLP GLKHFPGLSSQ/WNRKLPDGPTNPG *FWNFKKKGGFPLWPKRI*IFGPGD PPSRASKRAGITGITHGAGPRFNFKK WR |
| 4362 | 9859 | A | 4658 | 2 | 436 | KLIIFLYTSNEQREFEIKNTIPFTLAPP KIK*LGTNLT/KWIQELYEKIYKSVM KNIKELNKWRSSYGK GKSSSSSSSS SSSLDIACSWLRLKIVKISGLHNL YRFNIVPIEIPETYLV DVNKLIPQFIW RGKRHRIVNKIVE |
| 4363 | 9860 | A | 4659 | 3 | 480 | GSHDFFDKLILKFIWNSRPRIAKTIL KKKNKVGGTLTCLDFKTYRATV*I KTVWYWD/QIRHI/DQWSRITSPEIN PYIYCQLIFNRYTKTIQ/YGNNRLFN K*C*DMRRVKSDPFLTY/PYIIN*K MIIDVKAMIMKL/LEGNTGMSLSDF GLRKALDVTTKV |
| 4364 | 9861 | A | 4660 | 362 | 408 | CQVISVLW FYSSVLGWL VWIFCFSL KF*/WKSRSRQANPILKNKTRVLIL PDIKTPK\AGVIKPVW*QCS*KVW GEKVWY WQKMTQIVQWDRTESPQ IDN*SLTKEIQWRKDSL FNKW*GNN WTAPFSS/RSLNLNKDLTAVTKIKSK WVTDLNVKHKTINLL |
| 4365 | 9862 | A | 4661 | 93 | 367 | KVWGEKVWY WQKMTQIVQWDRTE SPQIDN*SLTKEIQWRKDSL FNKR* GNNWTAPFSS/RSLNLNKDLTAVTK IKSKWVTDLNVKHKTIKLL |
| 4366 | 9863 | A | 4662 | 123 | 397 | KVWGEKVWY WQKMTQIVQDRDRA ESPQIGH*SLAKEIQWRKNSL FNKW *GDHWAAAFSSSSSI*TKTLQ/CTKI KSKWVTDLNVKRKTIQLL |
| 4367 | 9864 | A | 4663 | 2 | 433 | ETADFGPLVLD/DDSVD RDIAEAI REYLKAKSGAAQTGAGRGQPGAA QPSRAAGSGSRCKPELSHGSAPTSV CPPKLVPGSGGGPGSQRSSSED*GS AFPVRASSNDSFEQSIKAEIEQLLNE KR*HATPKCDG\SIDKKPDP |
| 4368 | 9865 | A | 4664 | 94 | 445 | HHQLTLESLGKSKNSPRLSPSLGAC |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | LSCIIWQPAKGQG\SGDGGNWQRG KTAETE/SAAIGGETEWTAKCP*YSC L/GVGPTALTSQPPT/PEAEHPQA/GG TYRDLHPDPTWKTGWCHFVFC |
| 4369 | 9866 | A | 4665 | 52 | 119 | |
| 4370 | 9867 | A | 4666 | 987 | 1324 | VSNTPSARNQGRASSPGNSSPE/SSS ESAPAAATANGCDEAHLIPGGKFREP LKQGRGPELGPRPRALGGPRGSI/RP GSGGSFRG*LGGQMLLEPAASPGTQ PSGHLPALCGLSN |
| 4371 | 9868 | B | 4667 | 3888 | 8771 | MRLWSWVLHLGLLSAALGCGLAE RPRRARRDPGRAPPRPAAGPATCA TRGPRPPRLAAAAAAGRAWAEVR VPRRRQREARGATEEPSPPSRALY FSGRGEQLRVLRADLELPRDAFTLQ VWLRAEGGQRSPAVITGLYDKCSI SRDRGWVVGIIHTISDQDNKDPRYFF SLKTDRARQVTTINAHRSYLPQW VYLAATYDQGFMKLYVNGAQVAT SGEQVGGIFSPLTQCKVLMLGGA LNHNRYRGYIEHFLWKVARTQREIL SDMETHGAHTALPQLLLQENWDN VKHAWSPMKDGSSPKVEFSNAHGF LLDTSLEPPLCGQTLCNDTEVIASY NQLSSFRQPKVVRYRVVNLYEDDH KNPTVTREQVDFQHHQLAEAFKQY NISWELDVLEVSNSLRRRLILANC DISKIGDENCDEPNHTLTGHDGGD CRHLRHPAFVKKQHNGVCDMDCN YERFNFDGGECCDPEITNVQTCTFD PDSPHRA YLDVNELKNILKLDGSTH LNIFFAKSSEEELAGVATWPDKE ALMHLGGIVLNPSFYGMPGHTHTM IHEIGHSLGLYHVFRGISEIQSCSDPC METEPSFETGDLCDNTNPAPKHKSC GDPGPGNDTCGFHSFFNTPYNNFMS YADDDCTDSFTPNQVARMHCYLDL VYQGWQPSRKPAVALAPQVLGHT TDSVTLEWFPIDGHFFERELGSAC HLCLEGRILVQYASNASSPMPCSPS GHWSPREAEGHPDVEQPCKSSVRT WSPNSAVNPHTVPPACPEPQGCYLE LEFLYPLVPESLTIWVTFVSTDWDS SGAVNDIKLLAVSGKNISLGPQNVF CDVPLTIRLWDVGEEVYGIQIYTL EHLEIDAAMLTSTADTPLCLQCKPL KYKVVRDPPLQMDVASILHLNRKF VDMDLNLGSVYQYVWITISGTEESE PSPAVTYIHGRGYCGDGIIQKDQGE QCDDMNKINGDGCSLFCRQEVSN CIDEPSRCYFHDGDGVCEEFEQKTSI KDCGVYTPQGFLDQWASNASVSHQ DQQCPGWVIGQPAASQVCRTKVID LSEGISQHA WYPCTISYPYSQLAQT TFWLRAYFSQPMVAAVIVHLVTD GTYYGDKQKETISVQLLDTKDQSH DLGLHVLSCRNNPLIIPVVHDLSPF YHSQAVRVSFSSPLVAISGVALRSF |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | DNFDPVTLSSCQRGETYSPAEQSCV HFACEKTDCELA VENASLNCSSSD RYHGAQCTVSCRTGYVLQIRRDDE LIKSGTGPSVTVTCTEGKWNKQVA CEPVDCSI PDHHQVYAASFSCPEGT TFGSQCSFQCRHPAQLKGNNSL LTC MEDGLWSFPEALCELMCLAPPPVP NADLQTARCRENKHKVG SFCKYKC KPGYHVP GSSRKS KKR AFKTQCTQ DGSWQEGACVPVTC DPPP KFHL YQCTNGFQFNSECRKCEDSDASQG LGSNVIHCRKDG TWNGSFHVCQEM QGQCSVPNELNSNLK LQCPDGYAIG SECATSLDHNSESI LPMNVTVRDI PHWLNPT RVERVVCTAGLK WYPHP ALIHCVKGCEPFMGDNYCDA INNR AFCNYDGGDCCTSTVKT KKVTPFP MSCDLQGDCA CRDPQAQEH SRKDL RGYSHG* |
| 4372 | 9869 | A | 4668 | 1 | 183 | GRDGVLPCCPGWP*SP ELKQSA/CL GLPKCWDY/RARATAPGLLFFSYAK ICPCLTSCQYSKC |
| 4373 | 9870 | A | 4669 | 3 | 462 | TYQSFSPSHMLPLRGYDVW*TTLFQN P*HG*PGLQRFPLANMLCGPSGSHL VLLKL*RSVTLNHREALICLPPE*YV EPSGTK\CIAGWGETKGTGNDTVLN VSLNDISNQE*NNQHRGHVR*S*M STDGLQASVGAL***YGGPHSWFIH HRG |
| 4374 | 9871 | A | 4670 | 1 | 360 | ARGPQRSERSSRRPAPPSRSSGS*RC SCIPWPTLLLRGPR*RPL*NARYMKI LASPFQLSHPRKGPRRWH/AGVLS PPAAPPSSSSSVPEAGGPPIKKQKAD VTL SALNDSDAHS DVVDM |
| 4375 | 9872 | A | 4671 | 70 | 631 | RQRPQRSERYYWRAAPS*GDKVG PQMASQOPSASLYPYPSTSHITAGS RLGEFHEL GWLEVRWFVVDPLAC RENCETGVWAMGLSVFLSVIHS LT QRSFINTDSVLCHAQRETNVCPCAR EGPCL*PSPSARSQRPRSPGSRTPQ EKS RPRDAAASSAPRAS*RRRRPPII PLRPLWTLTSWPRAPPHGDAAAAA TREPEFHL |
| 4376 | 9873 | A | 4672 | 93 | 338 | |
| 4377 | 9874 | A | 4673 | 1 | 660 | FRRFRWRRRLH*AGPASSAGGSPGE ASGTMSGELPPNINIKEPRWDQSTFI GRANHFFTVDPRNILLTNEQLESA RKIVHDYRQGIVPPG\LTENELWRA KYIYDSAFHPDTGE\KMILIGKNGQ AQGF PWNMTITGCM DGRFTGTP AVLFWQWINQSFNAV VNYTNRSGD APLTVNELGTAYVSATTGAVATAL GLNALTKHVSPLIGPF GPFA CVA |
| 4378 | 9875 | A | 4674 | 1 | 387 | FFF*RWVSHSVAQAAVRWRNHGSL *PKTLGPK*SSH/CQSP*RAWDS*AH AHYHPA*FLNFFL*RQGPLSMF PK MVLNSRPQAVPPT*ASQSDGITGVS HHTLALKV/CLFKMKYFE**TEKGI |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | HFKRTK |
| 4379 | 9876 | A | 4675 | 3 | 383 | GQLQARPPAPAAADCPPWTLRGSA LVPWLVPWRKASPQLSPGSPEC* A PSARPQDPPRPAGQIQDRASEHAAR GGPCGVLRADGALPALPPDRARPQ VCGRGEVAARARW*RSSGRRGTRK RNGE |
| 4380 | 9877 | A | 4676 | 490 | 1013 | WASCSSSREYQCCFQTVPPGFSRVM KFFTFPGSCKHFPAPL/PAPQACTSF GLAGLPPNALPLILVPAPPA/SSLAN PQLVQPPVPGLVPRPSRSCSA/RP SA/RLARPPETPAR/PRAPSSAPRTRT PS*GRARSGGSAGNAPSARRTPQGP TRAACSLARILDLAGSWRVLRP |
| 4381 | 9878 | A | 4677 | 1 | 447 | KKFVIPDFEFTGHVDRIEDVKELT GGKVAAYIPQLAKSNPDLWGVSCL TVDGQRHSEGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAIVVS SLIKMDCNKA*KFDFVLQYLNKMA |
| 4382 | 9879 | A | 4678 | 3 | 284 | QLGQYGETPSLLK/IKIRIQKVAGHG GRHL*SQLLRSLRQKNLLNP\GGRS CSEPLRHCTPAWVTERDSVSKKK KKKKEKERKKKKAGCGGSRL |
| 4383 | 9880 | A | 4679 | 122 | 196 | CWFENVNSKSGFWVLF*FKAKLVN |
| 4384 | 9881 | A | 4680 | 2575 | 2786 | ADTESITL*FYHFFFFLRL/DSVAQA GVQWCDLGLLQV/LPPGFTPFSCLS LPSSWDYR/RPVITPS*FFVFLVEM/G FTALARMVLIS*PCDPPVSASQSAGI TGVSHCAOPTFIPK |
| 4385 | 9882 | A | 4681 | 3 | 512 | YNQKVDLFSLGIIFFEMSYPHMTA SERIFVLNQLRDPTSPKFPEDFDDGE HAKQKSFIWLLNHDPAKRPTATEL IKSEL/LPPPQMESE/LHEVL/HHTL/ ANVDGEGPYRTIDGPRSFQRISPAI DYTYDQRHS*KGTSSIRAAKLLHL VRETMIRICTRHGACQT |
| 4386 | 9883 | A | 4682 | 1 | 382 | EESILGEVGEALTSAGEELKIDRFF*I VEGLRHNSSQLNVTSMQLINALDTS PDDLDFRLHIINEFMRCGLKEILPHL *GIKNDGLDMQLKDFDEHNEEDLL ECNHRLEDIRAELDESVDVHMLW S |
| 4387 | 9884 | A | 4683 | 1 | 472 | GIMLPDLKLYDIAMVAKSAWYWH KNGHKVLWNKMAQN/HIYGQLVF VKVPKYTQWGKGSFNEWNQE/N/ WISACRRMKLDPYVSTKINSKWIK AYTIR/PETVKLLEENIGKKLIDI/GP G**FLALAPQTQATKA*IDKWDFIK VKTFCTARETVNTEKRH |
| 4388 | 9885 | A | 4684 | 182 | 345 | RFPLCSFPPTLPCEGICFPFA/FCHDC KFPEAFPTRL/PVEPAEL*VNSTSSLH KL |
| 4389 | 9886 | A | 4685 | 205 | 395 | VNLGIFGKNGAPPG/PEGRGGILGHR NPPPRGLNK*PPLTFQGTGTPGSSSS S*VNLGIFGKNGAPPGGQGGPKTPG PKEWAGLAPQKGGTTGLDPLGPPK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KGFNNHPGGIREFPGN |
| 4390 | 9887 | A | 4686 | 35 | 389 | NLFYKVLQSAGFFSMDHEDDVDFL ARFSQLVTGKRQSLIVSWTT*IQNG DIKNAQEALAAETRMALTLR*LAP DDGTSSKI/LGFCCDYVQILKHL\DQ QKAGAAAIMSVATKELMMKT |
| 4391 | 9888 | A | 4687 | 3 | 547 | GGAGRRAWAGVGGAPGAGGGPAE AGAAAEEGAHRGDGAVRAGAGG GRRYRPRRVQDPGGPAE/G*TWPPS PSSRCSSPCVPGRG*/PSEPQDPAAV SLPTSSVPETRGAPAGPIRGAPAGL RCQP*EARPGCVYWLISGGWCSPLF PWKLPGPRRPKQL*APRAGPCRPSL PCRLATGHDF |
| 4392 | 9889 | A | 4688 | 65 | 414 | WKCADTNVAQGPRVQQVLQLRGT PIPNHCALCLLREKQRQLCPRGSGN PAERSKPRRIQPEDATPAQALPRLP KGGGPGKSPTRGKHLGWGRDLFAS LSPAKATCLPPSIDNKP |
| 4393 | 9890 | A | 4689 | 75 | 787 | HVAFASGQRCNKSLPTPKVVPVVG LFPRPRPPWAALVALGLAWHPLAGI PRGCCVPHRHNAPEGKRLPFVSPS GHRARSTWAETRPQGPRGSLASLCP AHMDLSIWKTARGATFSFQQGPPG SWRGQT/RGPVSPLRPAPPPP*RPDK DGGGGS/PDQRAGRTRKAEVGGCL ASMRPPAPLT*TRRGR*RRPAPAP ARTAPSPRCSAPSSAAAPASAGPPP APGAPPTP/PRPRPYALRR |
| 4394 | 9891 | A | 4690 | 8 | 382 | QEYWE*LYAYTF*NRDELDEFFDRH ILPNFTQEEYTT*NNPVSVEIEFVI/ NNISTPKKNPK*TSDDFTSKFC*T FKEELIPVLYKHFQKIVEEEVLPHLF CELSITFLKLDRRCEVRRLHR |
| 4395 | 9892 | A | 4691 | 2 | 389 | NRKRIELTRKVLFEKHMARDVQNE HLTRFVGACTDPPNICILTEYCPGRS LQDILENESITLDWMFRNSLSSDIC* GMLFIHNAA/IC*HGNLNSFNVLIR DLSRFN*FSFSSESPVNCIQIIVHISP |
| 4396 | 9893 | A | 4692 | 2 | 544 | TKAPKYIKQTLIDPKGEVDYNNMIIV G/DANTPLSKTDRSSIQ*INKETVEL NHILDILGLTAIYRTFHPTATE/YFFS SAHGTLRSRINYTLGPKPGCEKIVKH RNYIKYPFLNTIELENNKRNSENT NTWKLNNMFLKD*WINEEIKKEI*K LLETNENGNTM*QNLWDMTKAVL RMKFIT |
| 4397 | 9894 | A | 4693 | 1 | 373 | MPHSVPGVLMSPGIIPPTGLTAAAAA AAAATNAAIAEAMKVKNIKLQAMS NYHASNNQHGANSHQGMISRVAL DLPLSILPNLYTMPLVLQHSHTYN HLTYS*LHNLQTIP*INLDQRAPSLP |
| 4398 | 9895 | A | 4694 | 185 | 417 | NSELNGKEAALQ/IMILEREIGVEKA LNVQKGRVSESLKLLANRPGMVAH ACNPSTLGGQGGWVIVIRSGVRDQP *PHG |
| 4399 | 9896 | A | 4695 | 88 | 432 | TDLFLFVCLRLS/LLSVAQAGVQWF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DLSSQPPPPRFRFSCLSLLSSWNH RCTPPRLV/N/FFVFLVEMGFTMLAR MVSIS*PCDLPTSASQSAGITGINCR TQLTY*F*KFSVDSL |
| 4400 | 9897 | A | 4696 | 3 | 390 | YRIPYYVSTDCENLLKRFELELNPVK RLTLKQIMNDRWINARHEEDELKPF AEP*LADILDQKGIYIIGMGYSQEEI WESLTKMKYDEITATYLLGRKSS HLDASDSTSSTNLSLAKGRPSTDFN NSTG |
| 4401 | 9898 | A | 4697 | 289 | 365 | SPRLGLPKCWDYRHEPPHPAAFH*G CVLFIFYFIFLKQEL/NSLTQAGVQW RDLSSLQPPPPG\FK*FSRLSQSS*D YSCVPPRLAFCIFFW*KRGLTMLTR LVSNS*PQ/CDPPALASQSAGITGMS HHTQPHSIVL |
| 4402 | 9899 | A | 4698 | 33 | 397 | NAYNQLKVCASSPWLFCCANFSSY YFYDSHNVIQG*NMTYCT/VM*YLL ITGSLSAHLKNMSLKRIMKSYRSGA ESATEEPFTILYESQFSVGGNELDFQ VKTLSPVIVVHGSQDNNATA |
| 4403 | 9900 | A | 4699 | 2 | 371 | LNTVIANGVAMASRPYQPTHVNVH IHQESTLTHLLKAGGTLKKTLEHFG DTVSSTATIGYEQLALWVTQILLGR *E/CVILECVLILGPWTALSASRCF WAESVEIVPRAGAIVHDKQPVKLA |
| 4404 | 9901 | A | 4700 | 3 | 441 | GFEDKVFYVWFDATIGYLSITANYT DQWERWWKNPEQ/ALGAEDNYTL VSHLIATEYLNIEDGKFSKSRGVGV FGDMAQDTGIPADIWRFYLLYIRPE GQDSAFSWTDLLLKNNSELLNNG NFINRAGMFVSKFFGGYVPEMVLTP |
| 4405 | 9902 | A | 4701 | 2 | 375 | CITRDLKWGTPVPLEGFEDKVFYV WFDATIGYLSITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLAKLLDLKKQLA VAEGNPLKPLKARRKSKRPWLIESH FNR |
| 4406 | 9903 | A | 4702 | 1 | 3093 | |
| 4407 | 9904 | A | 4703 | 2 | 2717 | GEMRLFVSDGVPGLPVLAAGRA RGRAEVLSTVGPEDCVVPFLTRPK VPVLQVDSGNLYFSTSAICRYFFLLS GWEQDDL TNQWLEWEATELQPAL SAPLYYL VVQGKGEDVLGSVRRRA LTHIDHSLSRQNCPLAGETESLADI VLWGAQYPLLQDPAYLPEELSALH SWFQTLSTQEPQRAAETVLKQQG VLALRPYLQKQPQSPAEGRAVTNE PEEEELATLSEEEIAMAVTAWKGL ESLPLRPQONPVLPVAGERNVLITS ALPYVNNVPHLGNIIGCVLSADVFA RYSRLRQWNTLYLCGTDEYGTATE TKALEEGLTPQEICKYHIIHADIYR WFNISFDIFGRTTTTTQQTKITQDIFQ QLLKRGFVLQDTVEQLRCEHCARF LADRFVEGVCPFCGYEEARGDQCD KCGKLINAVELKKPQCKVCRSCP VQSSQHLFLDLPKLEKRLLEEWLGR |

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|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | LPGSDWTPNAQFITSWLRLDGLKPR CITRDLKWGTPVPLEGFEDK\VFYV WFDATIGCLS\ITANYTDQWERWW KNPEQVDLYQFMAKDNVPFHSLVF PCSALGAEDNYTLVSHLIATEYLN YEDGK\FSKSRRVGVFGDMAHDTG IPPDISRFYL\YIRPEGQDSAFSWTD LLLKNNSELLN\NLGNFINRAGMFVS KFFGGYVPEMVLT\PDQRLLGHVT LELQHYHQLEKVRIRDALRSILTIS RHGNQYIQVNEPWKRIKGSEADRQ RAGTVTGLAVNIAALLSVMLQPYM PTVSATIQAQLQLPPACSILLTNFL CTLPAGHQIGTVSPLFQKLENDQIES LRQRFGGGQAKTSPKPAVVETVTT AKPQQIQALMDEVTKQGNIVRELK AQKADKNEVAEVAKLLDLKKQL AVAEGKPPEAPKGKKKK |
| 4408 | 9905 | A | 4704 | 180 | 490 | VENGNNSLTIMNRRARQKINKEVA DL*NTMNQMDLTDIDGTFYPKAEY TFFSSKCGTF*RTDHMLGHKTS\LD KFKKIKVIQNYLFNHNGVKLEINNS KKMRKF |
| 4409 | 9906 | A | 4705 | 2 | 405 | KNLNNRLFIFP*IKEEIKRQIRK*FEW NEKEKTIYQNLWDAPKAKLKEKCI VLYVKEETSQITDLSFHLKTPEKEE HVKPKVNRRMEIIRIRAEIHAVKYRK PTETNETKSWSFENFSKIDTPLIKMI RKKKVD |
| 4410 | 9907 | C | 4706 | 217 | 486 | MDDPRGHASPVTRTQKPQASRLLV GLRAGGLSWGHWGRGKPPRGRV PAAALGAAVVAAMASPDWPAGP KQGRWADLAALLCGLRPA* |
| 4411 | 9908 | C | 4707 | 13 | 216 | MLYWDCKRYKVKDKTQAWDFAG NISVKGAELSQTRAASGPRRQAQVT FSVWRGGLQVMAEEGRVDVC* |
| 4412 | 9909 | A | 4708 | 132 | 1424 | VKHGPQGGPRRQAQGDQVFGVGV LPGEWPEEGTQKGGPPLKTLGTGD GDKIGEPPTRAPRFRTGQPGPRDGL VGPGGELAKPWGPPRGLGPASCPP GNTPLPARPEY*HLGWVGC*RMG QGNLGVPSK/PVFGSSGPNVGSTNC DNFGSFGLSVPMFPNGPIQALFEG DLWDLGRTGHGTT\PGGQCKPLSPG PKKLQGL*TC*SSLALQG/RLSLGAQ SGGRGKQSESESPCPNP*APPVVG YGITRPVGFGRGPSQPG/LMGRPGSS ALWA*NPELPNCPGLPQPCPQEV QSFGPPGVRRGLKGGQDCHRRG EGSSKCAQGGHPAPA*WNPLVYTP ASPFPRPASGKPRS/RPSCGLRAP* HLRRPCLTPPFRPQGLLGSSPCPQK APDSGLLHSP\TSPRGLSGQCNP LHPQLNQSNRDR |
| 4413 | 9910 | A | 4709 | 1 | 340 | RHEERTTGILTSVGLASDTSLICVIE DFFDTALIISRSSSEGIQMLDSFLLS L*LLVTEETVNHL\QQEDRPCMDTL DCG/LQVAISEALRRLTTSKSRDDL |

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|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | HIWYDDESIV |
| 4414 | 9911 | A | 4710 | 12 | 398 | TYLDLPLPGFCIYDF/VPPFSSSECFIF VFMVCFFLAFILSFSSSSSPNSFFDLF FLALPQLPTLRGLFV*ALFQILSWVV FPVKFSLGCVFYLFQFIFKQLAFFH HV*ETFSVPVFLICKYWDD*TYFS |
| 4415 | 9912 | A | 4711 | 111 | 453 | YPFIIITFNTLGVAGNCL/KLTYTI** MPTANIILKKLKAFLSR*RTR/H/GCP QSI*ARRII*DIQIAKEDVKLYLFTDD MILYVENPEESTQKDLL\NKVNVKS GYNINMIIRCISM |
| 4416 | 9913 | A | 4712 | 1 | 184 | SSRDILLCTDIASRGLDSTGVELVVN YDFPPTLQDELAARRRRSLPGLASS VKEPLPQAT |
| 4417 | 9914 | A | 4713 | 1 | 1630 | MALTRPVRLFSLVTRLLAPRRGLT VRSPDEPLPVVRIPVALQRQLEQRQ SRRRNLP RPVLVRPGLLVSARRPE LNQPARLTLGRWERAPLASQGWKS RRARRDHFSIERAQQEAPAVRKLSS KGSFADLGLEPRVLHALQEAPEV VQPTTVQSSTIPSLLRGRHVCAAE TGSGKTL SYLLPLLQRLLGQPSLDS LPIAPRGLVLVPSRELAQQVRAVA QPLGRSLGLLVRDLEGGHGMRRIRL QLSRQPSADVLVATPGALWKALKS RLISLEQLSFLVLDEADTLLDESFLE LVDYILEKSHIAEGPADLEDPFNPK AQLVLVGATFPE\GVGQLLNKVASP DAVTTITSSKLHCIMPHVKQTFRLR KGADKVAELVHILKHRDRAERTGP SGTVLVFCNSSSTVNWLG YILDDHK IQHLRLQGQMPALMRVGIF\QSFQK SSRDILLCTDIAS\RL\DSTGVIELV VNY\DFPPTL\QDYIHRAG\RVG\RVG SEVPGTVISFVTHPVDVSLVQKIEP AARRRRSLPGLASSVKEPLPQAT |
| 4418 | 9915 | A | 4714 | 79 | 410 | IVYWVEVENRDHYAAYLGWEEAP YSDRAYAPQEKDLGPMDIRIGLL*K NWIPLQDDLYPVDMLHTSVG*EMEI LNNCRNQGV*RMSKDRRETLETYQ QL/L*LLQTSPLYLA |
| 4419 | 9916 | A | 4715 | 185 | 449 | TTILAWGDYLSLENSRSGPN*L*LLS GCTVQSFGLDWNGLLK*DSLTRLP ALCSLQLGRK\VETITHYDCEGLGL KHLWKPAVEAYG |
| 4420 | 9917 | A | 4716 | 154 | 364 | MWRWFSLPPFSLAGVELAPPVSRR SPRGP/TPYGLPRVPLWPLHSTALYC P\PSRPTSAPFTPHPLPKLRG |
| 4421 | 9918 | A | 4717 | 9 | 1805 | SPATSP*ETAGPVKRSRNGSSPAADP EALSPPTARLQRTVPPI*LNQQLSS PLHFAAGGGHAEIVQILLNHPETDR HITDQQGRSPLNICEENKQNNWEEA AKLLKEAINKPIEDPLAILILFDEAR YNLLKGFYTAPDAKLITLASLLLQI VYGNYESKKHKQGFLNEENLKSIVP VTKLKSAPHWTNRILHEYKNLSTS EGVSKEMHHLQRMFLQNCWEIPTY GAFFTGQIFTKASPSNHKVIPVYV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|--|--|
| | | | | | | GVNIKGLHLLNMETKDFQYFYV D |
| 4422 | 9919 | A | 4718 | 200 | 529 | EDVSKPVPWTLNGSCTSPLISHSDN QKCPYPFVIPAMGNPENIEDAYVA VIRPKNTASLNSREYRAKSYEILLHE VPIEGQKKRERKFYWKRNFKATV K*HKAYWIT |
| 4423 | 9920 | A | 4719 | 177 | 321 | QTCSMDTKWQLYISPHQS**QPEMP SIFSSDPSLQCVCLIIICKRLLS |
| 4424 | 9921 | A | 4720 | 166 | 627 | MWRWFSLPFSLAGVELAPPVS/S KDTERSHPYGLPRVPLWPLHSTKW VGQSPGEGGQGPSLSHSSFPFPRHS SPAQLPVAEKPSVAKRKPS*GFPR PTRAPKAQVSGVGDPPAHLFTVLP SPRTSAPFTPHPLPKLRGPRSSKALA FHSA |
| 4425 | 9922 | A | 4721 | 3 | 610 | STFNNEP*PEKQEQNKHKIRRKQI IRA*INKIE/TKNQCKRTMKQKVAFF QKLNKTDKPLARLRKKRQDKIRNE KDITTDTAEIQRIRGYEQLYANKL ENLEEIDNS*THTTY*DLQEEIQNL NRLITSNKVEAIKSLPVKKS LGPDG FTAIFYQTFKEELIPILLKF*KVEEE RVLPN*FYEASITLMPKPKDKDT |
| 4426 | 9923 | A | 4722 | 1 | 454 | LAHCNICLLGSSNSASVSQVAGITG GCHYTQLIFLFLVEMGFHHVGQVG LELPTSGDLPALASQSVGITAVSPLC PTRIIFFEAESCLCWPGWSPNPGLKQ SPCLGFPKCWDYQPDLTMP*FYL LELEIKFGVHVLWKSFLIKIENYYC |
| 4427 | 9924 | A | 4723 | 1 | 318 | KEECNKEEKESREKK/NEKEKIE*KE EEVRKEEKSLNKDKDKKRRRKREK GEGRKKEGILKVKKDGPNPSNGHA RMPKER*LYDVVRGTPHSSDHGDT AIFQTCIL |
| 4428 | 9925 | A | 4724 | 42 | 200 | LICT*MLIVALLVIARNWKQIRC/SST /DEWLNKLW*IPMEYY*AIEKEPTIG TC |
| 4429 | 9926 | A | 4725 | 50 | 403 | VVYHVMVLLKVICHHFLTLFFS FRSLILYLFILFMISLYLSCFLYNFL FIPSSSIFSHICFLMIIVLI*FFFYALFIH FNPIILYLNLYLLSLFLIESLFDYYLCL ISFVIFY |
| 4430 | 9927 | A | 4726 | 3 | 282 | VQGQEPLTASMLVAA/PPQEQQQM LGERLFPLIQTMHSNLAGKITGMLL EIDNSELLHMLESPELSRСКVDEAV AVLQAHHAKKEAAQKDSKAK |
| 4431 | 9928 | A | 4727 | 780 | 1249 | LVVFMSIPLCSSTHPSILQGLKLVPL EQGQPPPLLFHIVRCS DIEQALNHH QVLSFPQC*PTAFPGSQAPQPAVHV QGQEPLTAS\ML\AGAPPQEQQQML GERLFPLIQTMHSNLAGKITGMLEI DNSELLHMLESPELSRСКVSWGSDP AASVLM |
| 4432 | 9929 | A | 4728 | 510 | 2771 | NLEPSHQDRGEVQSRGEGRIVRRAF CLRCCGRGSRPPPVSVSPSPPTPA RPRRAGATCEPARARAPAPKAPLCP |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AAGPIRSPLAGLGVVGGGEMNAAA SSYPMASLYVGDHSDVTEAMLYE KFSPAGPVLSIRVCRDMITRRSLGY AYVNFQQPADAERALDTMNFVVIK GKPIRIMWSQRDPSLRKSGVGNVFI KNLDKSIDNKALYDTFSAFGNLS KVVCDENGSKGYAFVHFETQEAAD KAIEKMNGMMLNDRKVFGFRKSR KEREAEKGAKAKEFTNVYIKNFGEE VDDSLKELFSQFGKTLVSVKVMRD PNGKSKGFGFVSYEKHEDANKAVE EMNGKEISGKIIFVGRAQKKVERQA ELKRKFEQLKQERISRYQGVNLYIK NLDDTIDDEKLKKEFSPFGSITS AKV MLEDGRSKGFGFVCFSSPEEATKAV TEMNGRIVGSKPLYVALAQRKEER KAHLTNQYMQRVAGMRALPANAI LNQFQPAAGGYFVPAVPQAQGRPP YYTPNQLAQMRPNPRWQQGGRPQ GFQGMPSAIRQSGPRPTLRHLAPT GSECPDRLAMDFGGAGAAQQGLTDS CQSGGVPTAVQNLAPRAAVAAAAP RAVAPYKYASSVAAALILPYS LCRHPSP/PAVHVQG/QEPLTASMLAACNPP /QKQKQILGERLFPLIPTMH PNLAG KVTGMLLEID\NSELLH MLESPELSR SK\VDEAVA VLQA\HHAQERSCEPGR CCCCCYLLDPRKTD SKAK |
| 4433 | 9930 | A | 4729 | 7 | 365 | LYTRHPPSPSCIMTACFGSHIRY RSD *VPTPVL RPAVIRSVGGGDC SERLGLRPRPI/PELGPHTPTR PPPPWQNVQRADPVAVTPCRS REGSQAEP LPRGRGAVSSSTTR PGLPAPNRP |
| 4434 | 9931 | A | 4730 | 1 | 1520 | AEGACGPRQPNKGAGAPPQGP ATH LPGPRSGLSSTATMTANGT AEAVQIQFGLINCGNKYLTA EAFGKVNASSLKKKQIWTL EQPPDEAGSAAVCLRSHLGRY LAADKDGNTCEREVPGPDCR FLIVAHDDGRWSLQSEAH RRYFGGTEDRLSCFAQTVSP AEKWS VHIAHPQVNIYSVTR KRYAHL SARPADEIAVDRD VPWGVDSLITLAFQDQRYSV QTADHRFLRHDGRLVARP EPATGYTLEFRSGKVAFRD CEGRYLAPSGPSGTLKAGKAT KV GKDELFALEQSCAQVVLQ AANERNVSTRQGM DLSANQ DE\RPTRRPSSWRSTATPKS VPSVPTRASTGR*RPPGACSP PPPARMPAATLTSSGVTGASH *GRPMASL*PPRRMGSWPPR WRQQGTQSSSS*SSSTAPSS CSAGSMASAAARSRAPWTP TAPAMTSSSWSTMAPTTSKTP QANTGRWAVTPRSPAAATLL WTSSSSS ATITRWPSRWAGAT |
| 4435 | 9932 | A | 4731 | 131 | 677 | PSSLS/CDIFLRSPISTPSP SPLPRTPTSTPVHV KQGTAGS VINNPYVIMDKQPGQVIGAT TPSTGSP TNKISTASQISQ GTGSPVPKIHGSSFVTSTV KVIKQE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PGEAPHVPATGAASQSPLPQYVTVK GGHMAVSPQKQVITPGEAIAQSAK VQPSKVL/GQIG*CLPTLARADLLYS VC |
| 4436 | 9933 | A | 4732 | 131 | 362 | PSSLS/CDIFLRSPISTPSPSPLPRTPTS TPVHVKQGTAGSVINNPYVIMDKQ PGQVIGATTPSTGVY*IHICTI*RV |
| 4437 | 9934 | A | 4733 | 1 | 4461 | |
| 4438 | 9935 | A | 4734 | 2 | 614 | STTTERENYRPIFLMNTDGRILSIILP SQI***MKKIIYHDQVGFIPGMQRWL NVHK\TMHVIHHINKMKGKNYLIIS ADAEKSLGKTYHCFMMKTLNKLGI EGTLNIRKGIYD*STANILLTGKN*K AFPLRTGIRQGCPLSPLLNTVWDIQ AKVIRQDKQIKGIENGQEEVKLSHF ADDIILYL*TEKPKDSTKLLKWVN |
| 4439 | 9936 | A | 4735 | 164 | 613 | NLNMEATGTDEVDKLLTKFISAWN NMRYSWVLKTKTYFSRNSPVLLLG KCYHFKYEDEDKTLPAESGCTIEDAT *LREM*KNFRKDSISRIWLTREEFP QIEGSALTTCGWGCTLRGTGQMLL AQGLILHFLGRAWTWPDALNIEKLE L |
| 4440 | 9937 | A | 4736 | 40 | 359 | |
| 4441 | 9938 | A | 4737 | 4274 | 5256 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVT*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNIILPKFNHLC\TH\TH\THLTLFST YLKNDRDKTIMCKLSLIG*LAESLEF GGSGENV\DYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWLDLGT LSV |
| 4442 | 9939 | A | 4738 | 133 | 359 | LLNFMLLFHRYYALKVSYFKSSLDR KLELLWNKYWVNTLSSSSLLTVS/ DYTCKECI*ILSKLHSRLISETLFHRK |
| 4443 | 9940 | A | 4739 | 1 | 353 | NWTL*TLKKIFSLKDAIKRIKIQSVR WKKIFAKHTSDKGVES\NIYKELS*I NKASSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSYHYTSIRVA KMKKTDYVTSW |
| 4444 | 9941 | A | 4740 | 1 | 375 | LVPKRA*YWHKNTSSSSSSSSS/PSS HLHIYSQPKFRKGTKKIHW*KDSVF HSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSPMLIQENTG/IMLQD IGFGKDYLSTSKAQATKQK*TRKH WEMLQDIGFGKDYLSTSKAQATK QK |
| 4445 | 9942 | A | 4741 | 1 | 296 | FRRSL/DSVAQAGVQRRHLGSLQAP PRGFTPFSCVSLASWDHRSPLRPA NFFVFLVETGFHVLARMVSIS*PCD RPT\SGFQSTGNTGVSHRTWPLLL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4446 | 9943 | A | 4742 | 3 | 380 | FLEEYNPPKVSQEEITSSSSSSSSSSSSSSSSSLSSDIES/VIKNTSSNNNKKNPDPDGFTAKFYQM*KDELISTLLKIISK/IFHSNSFCE*QTTR*FAISITWRAKPDKDTPOKEPYRLISLINIHSC |
| 4447 | 9944 | A | 4743 | 3 | 369 | SFTLIKKT KDIIIRKANYKTMSLRKIA AVILNKILAN*IEH/RIKRIIHNNQIRF I/SGTQVWLN I*K*INVTHHINRLKK KNYMIILIYEEKTFDKIKHPFM/IK/VLSKLG TENFFKLIKHIWRKI |
| 4448 | 9945 | A | 4744 | 70 | 345 | KVWGEKVWY WQKMTPIVQWDRT ESPQIGN*SLTKEIQWRKDSL FNKW *GNHWTAPFSS/RSLNLNKDLTAVT KIKSKWVTDLNVKHKTIKLL |
| 4449 | 9946 | A | 4745 | 3 | 345 | KFNNLDEMDKFADRQKLPYLAQEE RQNLN/*PYLLKNLNVQNLPISKTSA PDELICKFYETFKNEIILLCSLFQK MELSQHIHDSNLT LTQKI*K*YRTE ENYRDISLINTYAK |
| 4450 | 9947 | A | 4746 | 35 | 355 | PHPPWWSLSSSPPSQHSFLPSPAYM PSPSGNSM/CYLSPSRGM*APSRQGP SSFHQLCPKCLKGCWARHMP SK*G WNGNPPFVSLNYPWARNRPSLLTH FVMWEAPRP |
| 4451 | 9948 | C | 4747 | 27 | 416 | MMKRLGMFNIQHCKKLSSWVLLM KYLGNAPPSSSCLMRGNYSTWKMN SPTISSPSSWENEDRRSASLHLPKLSI TGTYDLKSVLGSTGASLKVFQQWG AGPLPGFTEGGHPXKVFQGPCIKAV LEPFDE* |
| 4452 | 9949 | B | 4748 | 5 | 763 | MPSSVSWGILLLAGLCCLVPVSLAE DPQGDAAQKTD TSHHDQDHPTFNK ITPNLAEFASFSLYRQLAHQSNSTNIF FSPVSIATAFAMLSLGTKADTHDEIL EGLNFNLTEIPEAQIHEGFQELLRTL NQPDSQLQLTTGNGLFLSEGLKLVD KFLEDVKKLYHSEAF TVNFGDTEE AKKQINANGTRPFEVKDTEEDFPR GPGDHREGAYDEAFRHV* |
| 4453 | 9950 | A | 4749 | 11 | 368 | GLKSLIN*LLAVYPREQTTEEVMR DPWVNS/GSGVAFDN/TE*QILDHLN PETTQLLVAMGFQADNLSVAVREQ LFSYAMATYLDLEHTLLKKRSTIRS QTLPPGDPTWPLYIEVCTFRLS |
| 4454 | 9951 | A | 4750 | 175 | 349 | PSVAGRPRRKGGRQPAQTRAVGI AGTEPPLYLGLWGPVGVDQG*QP ASFPGPPQVPKAPSNTKEA\SPSNA HSSSLGRLPSSPLPRPASNTGSLSPR QGTMTTL*GATHLPQHSD*EESTRE SPPPTLEQPLPPSVQLIRMPCPPLPVT Q |
| 4455 | 9952 | A | 4751 | 2 | 354 | ENCQINNLRFHRLRKP KKEEYTKPTA SRRK*IVNIRIERNGIEQKNNRTSSSS SSSSSSSSSSSSLTFR*MDGRRSSSSS SSSSSSSSSSQ*QRK\KTRLIKI*NERG DITADLTEIK*LLILQKLNNY |
| 4456 | 9953 | A | 4752 | 121 | 363 | WRDFKTKTVIRAK*GYLIITG*NHQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | EDTTVINMYAPKTAPKKYMKQKL TDWKRAV/DSKTTAGDLNILLIMD KTKQKINRV |
| 4457 | 9954 | A | 4753 | 178 | 439 | GPALINALLKWRIPSGEDREP*GRD WEKEKE/R*LEEGRERGGKGEGGK RRNKGRKEGREERGKGEREEGYIM CIHGIGNRSLAVLGA |
| 4458 | 9955 | A | 4754 | 193 | 355 | GLFSIEEH*HDSTHLGINTLALISRLFI EK*LLKRVYQVTQACELYAWNPN DQCLPPPLVRPVQHRGAYPGEDWQ IDYTQMPCKGFKY*LVFIDTFTVWI EAFPTKIEKAIV |
| 4459 | 9956 | A | 4755 | 3 | 227 | NIKIGKEEVKLSLFAGDVYLEKPKD STKKLLELI/NFSKVAAY*INIQKVA FLYANSE*SEKEIRNIIPFTIAT |
| 4460 | 9957 | A | 4756 | 115 | 487 | CSLCFVAEWSPWCGWTQLIYPW*/E/ ITHSPVHTQRLGLETHRTAEMRLFS FSLFFFLRQSFALVTQPGVQRCDLG LLQPPSPGFK*FSCFSLPSSWDYRHA PPRLANFVFLVQTGF\SMLATLVSN |
| 4461 | 9958 | A | 4757 | 2 | 436 | GTEAEQPSYQPGLELPQGDQEEP*G LAGKTGLGPRFRPTTGGSGQTLEEV EGLSHSPFQSPGIPGEFEKARKIL*A GS*HNSC*ATE/GLGERPGGICGVSS SVSTQGPMP*CGQQGN*ALESCRG ATAALSEQSPASPSSRAARA |
| 4462 | 9959 | A | 4758 | 76 | 194 | |
| 4463 | 9960 | A | 4759 | 310 | 551 | SSKQSSAKPPFCLPNPGKVCRSGRS RT*GCNLQKGSPEKGRRFGHPPE WTIFPSVQRQQA*FSDSPPTNGIP GEWKG |
| 4464 | 9961 | A | 4760 | 1 | 1165 | LRWQREEGOKAGVHVGTMTQHLR PQPGAAVLPAALAPPPKHQFSLQAS SPSRLGRAGLAGGPSRAGLLC*WRR LSFLPSSFPSPRSWGARSRRRARGQ VGPREPAGRSAGDRGVGGRFGGPL ALSFFATGLLRASCAPAFQEVTVLG KAVQWRLEPGEPFTEG*ALAGTLG LGKH*QGRQK*GWG*PSLANARQ LGKPLQVLGWLGHVEGRPGRAVK VTGVRSWSCLPGSTGVGDRSRATQ LPAGP*VSLRVDQGEAVTGWGGRA GARGSPGRQGEPRHSARG*GPESLP LPVTRNSLVGGLSEN*ACPCR*QK ERLSIRGVPERRPFGPEPGRGPASC SGLPTTGGTEERRKEGKRAAAISKA ALPGWARLPDQPGPAATGSK |
| 4465 | 9962 | A | 4761 | 1 | 389 | EETLPLFADDMILYIIKKKQKTKKTT KESTKRY*N*MNVFGKVAGYKV NTQKSIN*QYTI*KVKLAS\FSSSPQK NKIGINLTKEIQNVYSENYKTLKEIK DLNK*ESIPCSQIRRFNIVKMTVLLK LI |
| 4466 | 9963 | A | 4762 | 1 | 346 | RACL*FQLLGRLRQGDGLSLGIRGC SGPGWHHHSPA WATEKDPVSKTNK QNIKH/LRKSPLSRDEKILREKREEE KILAYHYLEKSAIYSISFFFLTKHILN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | TPVCWFSSEHIIYF |
| 4467 | 9964 | A | 4763 | 2 | 468 | FPSLPSSFFSRFLFCITVMF*VLDPLS LSYLTLLIPHLKIEFNFEK/CVNH/CF LLMLLLLFLLL\CTY*MCLGPFYFLP CLSFSSVFHFLSLCCIIGNLFRYIFKFI NFELC\CYVLYT*DLFYF*KFSLVIF* IY*FFLSIMLSL*VFFHLKHFI |
| 4468 | 9965 | A | 4764 | 3 | 364 | RNLKLISEYCKISG*KVNIENQ\VF YISNGQVEFEIKNTIPL*AHT*KMKY LDINVTKYVQDPYEENYKILMKKIK EQME/NIPCL*/GRLNTKTSVLPNLE **ITAIPIKIPASYFVDN |
| 4469 | 9966 | A | 4765 | 1 | 755 | EESILEEVLEALTSAGEEKKIDRFFC IVEGLRHNSVQLQVACMQLNNGLG TSSGELEFKLHIKNEFMPCGLKEILP NLKCLKNDGLDIQLKGFDEHKKED LVELSHRLEDIRAELDEAYYVYNM VWSTV*ETRAEGYFISILQHLLLRN DYFIRQQYFKLIDECVSHIVLHRDG MDPDFTYRKRLNLDLTQFVD\CV QAKLKEFEKALELYKKEFEFTD PQENSR*NCAKKEAQIYGFNPNSK TF |
| 4470 | 9967 | A | 4766 | 12 | 321 | KSCDWAERLVTLV/WN/PYFKNLSN SYYKQLSPMGGYLNWAHTLTWEI IDNILDQLIFPKLQKEVG*ESWETVV ITNHRDLFSLWLHYLSAVKTPGINGI CQHNY |
| 4471 | 9968 | A | 4767 | 2 | 375 | MSSPLPSPWSPCLLPQAPGPTLPVP PAETLSVSPACFLRLPINSPSQ*APA WRQLTADWGGHSALGLPGCPGPSI TWPSHSASHLLPQRNQGPMLGYA HLPGHLPNTNVLPSGHTPALERPK |
| 4472 | 9969 | A | 4768 | 3 | 338 | QSLALSPRLECSGAILAHCHFC/LPG FT*FFCLSLPSSWDYRSPPT/RQLIF VFLVEMGFHHLGQAGLELLTL*SA HLGLPKCWDYRHEPPRPAQRPKLK NLK*LTTVARFTI |
| 4473 | 9970 | A | 4769 | 66 | 365 | LRDEQQHGGPWTSPLSRPPTGKRA RGRSACPQLTH*PGTAARKGASPGR SRALALPTRCPGPACGGREPRLQAR GVP/R*IPPRRGPHGAPSGLPPGPVG C |
| 4474 | 9971 | A | 4770 | 3 | 345 | KRGTPLAGEMAEGHCL\CLPLGTEY LTVNPIVHLFNSEIG*KIRPVA\KVR HVYSITASIFFTPLRCLCGEKHISGLR ARSGIVLSLELNHGIDSFAHM*SCDL ILIIITLLSYYI |
| 4475 | 9972 | A | 4771 | 2 | 352 | KRGKPLAGEMEEGHCL\CLPLGTEY LSVKPIVHLFNSEIGKIRPVAGGR HVYSNTASLFFTPLRCLGGEKHKSG LRARPGIVLSLELNHGIDSFAHM*FV DLLIIITLLSYYIPFR |
| 4476 | 9973 | A | 4772 | 1 | 296 | QRSVKISISENGNSHMEIVSFLIFCQ FLLHVFCSTIHYDCYIFLLI*YPINRQ CLFAY*YSDIKFYSDIN/ISYFLCLLC MSFYPLSTCIYMGLVFIF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4477 | 9974 | A | 4773 | 2 | 859 | GRWPTQPTSLOGGQTLGDVREAFS RRP*NGERQGAPPACPLPRSLGLWR PWGPLSVTT*NRSWSCYCWLRLV/ GWKGSRAVVKALGSPEAAWHLLG PDAALQPCHFSQPQRRRCRGRPPFLP LSGWAGPWECWPTCQAGRT*IPEG GGSC*GPQVNDLQRHTEENVLRC DLPHPALAAWGTVSPG/SHAPAQ*T EV*RSAQSSFRPQCPLTSPARGTPGS SRLLCGVPP/CGPLLMLCPLPVPEV GLGPFLRELLNTKKLNCFVNKQKV PNKPACHLGDGPSLPHQIC |
| 4478 | 9975 | A | 4774 | 158 | 517 | RCRSGYVDQVAGLFCFVLRQSLTF VTQAGVQWHDLSLQPLPPRFN*FS CIILLSSWDYRCMPCLANFGIFLR/E RGFTMLGMLVLNC*PQ/CDPPTSAS QSAGITGMGPPHLGLSCSIKK |
| 4479 | 9976 | A | 4775 | 1 | 165 | GSLLPLLFIILEVLAKAIRQEKSIGN EKEKV*LSLLTDHMI/YM*NPTVKK LTT*KLTT |
| 4480 | 9977 | A | 4776 | 2 | 516 | QNPCISERQYCCEKLPLERSSRPQDS AGQPVT/HAHCSLSSTVDLCPLLAT HRISCWH*QDEVQGGRD/SVDKGD LVALSLPAGHGDTDGPISLDVPDGA PDPQRTKAAIDHLHQKILKITEQIKI EQEARDNVAEYLKLANNADKQQ VSRIKQVVQKKNPAAQTIGQLD |
| 4481 | 9978 | A | 4777 | 154 | 406 | CTDIQGYPGSRSAQAGVQWHNL/ CLSLPSSWDYRRPLPRPANFLYF*ER RGFTVLARMVVIS*PCDPPASASQG AGITGVSHRT |
| 4482 | 9979 | A | 4778 | 1 | 429 | ARLETNSRSVAHGGVQCHDLSSQQ PPPPGFKGFSGLSLPSSWDYRRPPPC PR*F*YFY*RRGFTVLARMVVIS*PC DPPALASQSAGITGLSHCAR/LERES HSIA\RAGGQWFHLGSLQPPPPRFK* FSCLSLPSSWDHRCVPD |
| 4483 | 9980 | A | 4779 | 1381 | 1787 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 4484 | 9981 | A | 4780 | 1147 | 1553 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 4485 | 9982 | A | 4781 | 1456 | 1862 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVVIS*PRDPPTSA SQSAGITGMSH |
| 4486 | 9983 | A | 4782 | 889 | 1295 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSI*PRDPPTSA SQSAGITGMSH |
| 4487 | 9984 | A | 4783 | 743 | 1149 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSI*PRDPPTSA SQSAGITGMSH |
| 4488 | 9985 | A | 4784 | 2583 | 3580 | DRVSLLLPRLECNAILAHCNLCLS GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFCS/RD TVSLCYPGWSRVA*SRITATSA\PLG K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFYLYFHRDEGLCCPGWS* TPELK |
| 4489 | 9986 | A | 4785 | 1966 | 2372 | LEYVAHPLHQLLILNNFYSVLNEKY LVFFFLNMYMTFKCNLLFFLRPSL/D SVTQAGVQW/RDLGSLQAL/PLPGF APFSCSLPISLAYSHLPPHLANFLY F**RQGFTVLARMVSI*PRDPPTSA SQSAGITGMSH |
| 4490 | 9987 | A | 4786 | 3 | 305 | FFFLRKSL/GSV/TQAGVQWRGLRSL QPPPPRFKRFSCSLSSWDYRCVPP RPA/NFLYF**RWGFTTLARMVSI* PCDPPASASQSAGITGISHRAQPIKY |
| 4491 | 9988 | A | 4787 | 1172 | 1688 | VFFGVFVFVFVFVFFPKLTSGTIPWA SPEVMIYPPTH*VCEAPSPFYVFSH LFSVLQSPSHLVCLFLCSF*DGVSCLR QAGVQWRSLSLQPLTPWFKRFSC LSLPSGWHH/RRPANFCIF/M*RRGF TMLPRMVSISSPRDPPASASQSAGIT GMSHRARPQSSVFKQSFLSR |
| 4492 | 9989 | A | 4788 | 641 | 1074 | VLNLVEFV/TRELAFTSNVFFCFFVF FCFFLRSL/DSVTQAGVHWDLGS LQAPPPRFTPFSCSLPSSWDYRRPP RRPANFLYF**RRGFTRLARMVSI* PCDPPASASQSAGITGVSHRAPTN VNKAITNGLFTYFFNEE |
| 4493 | 9990 | A | 4789 | 7273 | 7925 | IVSLFLFILLVFWWWCFFFFFFFETE SCSVAVAQAGVQWHNLGSL\QAPP PGFTH/LFSCSLPSSWDYRRPPRP VNFFFFFFH*RRGFMTL\ARMVLIS *PQVICPASASQSAGITGLSHRVRQ GPHNLLTNQVNKFFFFFFLETESHV TQAGVQ*HDLGSLQSPPGKRFSC LSLLSS*DYRLPPPHPTHF/CVFLVE NGNSPCWPGWS*TPDLR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4494 | 9991 | A | 4790 | 156 | 391 | IPHSYIRKFYSFKMAILSP/KLIYSINA ISKKIK*AFLKKTDELILTFI*KGKES VLDKPILKKKNIVGLKICDFETYY |
| 4495 | 9992 | A | 4791 | 365 | 506 | GRHHACLIVDRALVFPS/CQVGRAA HFLPLPGPCPAWTPPSRSLRPGP |
| 4496 | 9993 | A | 4792 | 2 | 503 | LTHPAGARPVLLTTPESFEGPCFGTP HGQSLSQSAFSRGHSLGDTVGVGTG QVGS/LLSGGGVRAG/GAGGGGGA GFGSRLALKAAGERGEKPREPVPPP *QR\GPHTKAPWT*AGQGQPPGRAC SPG/PPAEPASQPLTPGPGRRLPGGK RSRRDRARGAARKMGLLFPLD |
| 4497 | 9994 | A | 4793 | 3 | 389 | FQDLIKR*KATIHTLWY*HKNRY/D IDQQNRIEN/SKHRLSHLIFDKGTRTI Q/YGREQLSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSP IPDIGFHNDFLNMTPKAQATTCK |
| 4498 | 9995 | A | 4794 | 27 | 285 | VFFFFFFLRRSLALLPRLECSGTIVF LVETGFYMLARMVIS*PRDLPALA SQSAGITGVSHRARPASFNFLTINILP PLLLWTF |
| 4499 | 9996 | A | 4795 | 12 | 336 | SPVQL*F*LFLVFC*LWSWSAVVYL GPLGTPSADAHT/AGLSKTPPHWAA RARLDDVFSRLTFSSHSLNMELVQD LTASAPMYSSTRDPP/CLGLPKCW DYKREPPRAH |
| 4500 | 9997 | A | 4796 | 74 | 463 | HISQHDSYQLQVLLASYKTASFLFFF LRQSL/DSVTQAGVQWRDLGSLQA PPPGFTPFSCPQSPK*L/SSWDYRRPP PRPANFFCIFIVEKECFTLLARMVIS WPRDLPASASQSAGITGMSHRARP AQVS |
| 4501 | 9998 | A | 4797 | 1 | 337 | KKLISGFNVIPIKTPANPCVKIDKLIL KFIWHCKARRIGKAMWNKIKYGGI IQ*DLKICHKVRIEIVWY*LQGRQ/I DQ/WEQ/IQSPEIDPNIYSHLTYDKSP TAIQRRIYPF |
| 4502 | 9999 | A | 4798 | 3 | 331 | KNYKTLLREI/KEELN*WKDIPRLW LRRLNIVKMSFL/SKFIYRLDSIPIK/ MPSRHLFL*KLILKQILKFIWEGKGP GIAKTILKKNKFGGFTLLNFNTYNK AANSRVLVLG |
| 4503 | 10000 | A | 4799 | 3 | 340 | INRLNIFTMAIFSTLIYRFNTIPIKIPA GFVEMDKLILKLWVKFAHGIGKT TLKKNRVP/PIKFSSSSSSSSSYWNE DRNINQWN*IDNLKINPCVCGQLIF NKDAKTNEER |
| 4504 | 10001 | A | 4800 | 46 | 195 | SPATLGRPEVGPDS*GPGDRDHAGL TMVKPPVFYLKNYWMRSGDRDHP G |
| 4505 | 10002 | C | 4801 | 353 | 442 | MPLLYVQRLFARTGLCATLFGMM SPLYV* |
| 4506 | 10003 | A | 4802 | 1 | 273 | FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPE*LGLQA PATAPG*FFVFLVETGLCKHNEKSP LSVQGRIYVLRNQKG |
| 4507 | 10004 | A | 4803 | 57 | 231 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4508 | 10005 | A | 4804 | 2 | 169 | |
| 4509 | 10006 | A | 4805 | 698 | 1231 | |
| 4510 | 10007 | A | 4806 | 58 | 2674 | |
| 4511 | 10008 | A | 4807 | 7 | 235 | |
| 4512 | 10009 | A | 4808 | 1 | 245 | FFFFFFGTESRSVAQAGLRTAVARS RLTASSASRVHAILLPQPPE*LGLQA PATAPG*FFVFLVETGFHLVSQDGL DLLTS |
| 4513 | 10010 | A | 4809 | 175 | 394 | NFLRYSHFKKCNRRPGAVVTPVIPA LWEAEAGGS/CRSGDRDHPG*QGE GKRGSLFKFQEVSGAPNKFWSWLPL |
| 4514 | 10011 | A | 4810 | 65 | 2712 | SGSGHCLAEAAASMGPGWGWKLRT VALLAAAGTAVGDRCERNEFQCQ DGKCISYKWWCDGSAECQDGSDES QETCLSVTCKSGDFSCGGRVNRCP QFWRCDDGQVDCDNGSDEQGCPPKT CSQDEFRCDDGKCISRQFVCDSDRD CLDGSNEASCPVLTGCPASFQCNSS TCIPQLWACDNDPDCEDGSDWPQ RCRGLYVFQGDSSPCSAFEFHCLSG ECIHSSWRCDGGPDCKDKSDEENC AVATCRPDEFQCSGNCIHGSRQCD REYDCKDMSDEVGCVNETLCEGPN KFKCHSGECITLDKVCNMARDCRD WSDEPIKECGTNECLDNNGGCSHV CNDLKIGYECLCPDGFQLVAQRRC DIDECQDPDTCQLCVNLEGGYKC QCEEGFQLDPHTKACKAVGSIAYLF FTNRHEVARRMTRTRSGYTSFIPNLR NVVALNTEGPSNRIYWSDLQSRMIC STQLDRAHGVSSYDTVISRDIQAPD GLAVDWIHSNIYWTDVSLGTVSVA DTKGVKRKTLFRENGSKPRAIVVDP VHGKHRPCT/WPGVLCTCQVTSAT* DVRATIRR*ML/WFPQRTLEKAHLV SGREKQEEIIRCLRVKVLTYEMQ DLGGG*TRL*ITQAKMNAENWL*L EEDKVFWTDIINEAIFSANRLTGSDV NLLAENLLSPEDMVLFFHNLTPRG VNWCEERTTSLNNGCQYLCLPAPQI NPHSPKFTACPDGMLLARDMRSC LTEAEAAVATQETSTVRLKVSSTAV RTQHTTTTRPVPDTSRLPGATPGLTT VEIVTMSHQALGDVAGRGNEKKPS SVRALSIVLPIVLLVFLCLGVFLLWK NWRLKNINSINFDPVYQKTTEDDEV HICHNQDGYSPSRQMVSLLEDDVA |
| 4515 | 10012 | A | 4811 | 49 | 361 | STSYPTGSHAFL*PQNVVDAETNS* HINNVLRLKIKLLEENTETKNCHD LGLSTDYY/SVTPKA*ATTTKIDKL ELIKIKNFCTSKDITYKVKRLLIGNNI CK |
| 4516 | 10013 | A | 4812 | 2 | 346 | EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4517 | 10014 | A | 4813 | 2 | 356 | EKSSLFNKWCWDKWISTGKRMKL VPPYISSSSSSSSSSSSSSSSSSSSSS SSSTEKNCHDLGLATDYY/SVTPKA *ATTTKIDKLELIKIKNFCTSKDIT*K VKRQLIGENSCKSF |
| 4518 | 10015 | A | 4814 | 1 | 357 | VRPHHTNKKRVRLR/VRVNIKVRD KVSTEVKDKIKNQAAVIVKLGVIK AGPWVRVKDWVRLEVKIKNRDQV RGEAEVRRIGQQLRTKTRPKLVNHP KRNGSIN*NHITVECYSTIKKQ |
| 4519 | 10016 | A | 4815 | 1 | 323 | PVRGTEQSNKSWASGLQPGWGAE QLAWGSFNLSKWPSGGGDPQPILLS RVQNMGRRLAR*EAPCQPQPLPSR RSSPVPHQHL\PPCHPCGASLSPALA WPPPPPSRS |
| 4520 | 10017 | A | 4816 | 1908 | 2324 | ILASSLRANPGFIRNFHLFFFFFFYFLR RSL/DSVAQAGVQWHDLSLQAPPP GFTPFSCLSLPNSWDYRRPP/RHHAR LISFFLFLVEMGFTMLARMVSIF*P WDLATSASQNAGITGVSHHTPRP VIKYLPSPPNLAG |
| 4521 | 10018 | A | 4817 | 1 | 273 | RPRRRYPHSWWFL/QEVAIFTLIEKV VFYYSHRLFLHPAFYKKIRKIHKKW TAPIGVISL*AHPIEHA VSNMLPVDP VNLQRSIRTVLHFHQ |
| 4522 | 10019 | A | 4818 | 3 | 293 | DHVSPGVQDQAGQYKTPASLQKQ KQKTNRHGSAYLWSELLGSLRQED HLNPGVRCSELLLGHCSPAWAAK *DPVC*KNKTKNLIAGGHPRFSWIQ |
| 4523 | 10020 | A | 4819 | 2 | 170 | KLGFIIKIDFSSVKDNVKGMRRAQAT DW/DFIKIKDFSSVKDNVKGMRRAQ TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN |
| 4524 | 10021 | A | 4820 | 52 | 228 | WASGHVVRPYRVLNNFISNQKMD KEDLSGIAEMFKTPVKELLIVL*TCL IVAFKSDNS |
| 4525 | 10022 | A | 4821 | 22 | 376 | TGTVIKIAWY*HKDRHMDQ*NRINS SETNPNI*SKVQRPFWRASSSSSS SSSSSSSSSSSS/SSSSSSSSSSSSSS SSSSSSSSFIQNTGINLTDGFLGNVF LDMTPKAQAKE |
| 4526 | 10023 | A | 4822 | 151 | 379 | SIPGIQSWFNIQKSINVFYHIVILNTQ HRSSSSSSSSSSSSSSSY*LMIKF/LNK LGIEGNFLILIKAIHGKPTVNH |
| 4527 | 10024 | A | 4823 | 3 | 479 | RDEVSPHCPGWSQTPGLKQSSCLGL PKC*AYRHEPLGL\ILFFH*ATQETQ ARAGWSYASHFVDERTEAQR/V*G TCPRSHANYVLEDLICVLF*DRVCS VAQAGVQWHDLSLQPPPPGFK*FS CLSLPSSWDYRRFATTAS*ILAF*VE MGVRHFARLV |
| 4528 | 10025 | A | 4824 | 1 | 57 | GKRYTRSDELQRLRRAHTGVEKKLV CPECSQRSMRSDRLTGHIRSHQNK GIH*SDELQRLRRAHTG |
| 4529 | 10026 | A | 4825 | 3 | 602 | VDKNHTLSLLCQPSHGDCSRFSAST CLIRSRFHFNFNTFKIF*KLGDSMLT AVSVARDCGMILPQDKVIIAEALPP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KDGKVAKINWHYADSLTQCSHPSA IDPEAIPVRL/CP**LRGSSNDSLFC NEWIILSDTGGIFK/HLVPKGSNLG VCVCSHECIATVF*KNLYYCFQLML HGTVFARMAPDQKTQLIEALQNVE |
| 4530 | 10027 | A | 4826 | 3 | 241 | TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR |
| 4531 | 10028 | A | 4827 | 3 | 241 | TSFSCLSLSSWDYRCPQAGPANF CIF/M*RRGFTALARMVSVS*PRDLP ASASQSAGITRVSHRTRPLV*CFN*A LFR |
| 4532 | 10029 | A | 4828 | 2 | 321 | KAVLRRKFIATNT*KK*TSQIKNLL KKLQEKNKFKPKVSRRTIQRSEQK *IQTRKPGEKINKTKGSSSSSSSSSS SSSSSSQREDLNQIGNEREDITTGTT EIQ |
| 4533 | 10030 | A | 4829 | 132 | 290 | LVTSE***IYQIFFFSPEMESHVSQA GVRWSNL\SSLHPLPPGFKRFSCFSL |
| 4534 | 10031 | A | 4830 | 645 | 1201 | GGRDLLRTHSVGPSTPQTIPVLTTPG *CACTQDVPSPHS/PPMKELWPGA PQGSPGRLSPQPPH*RSPHSPTLW PAL/PGLASTEGWGAIALYILEKNW GREGLNLPPA*PFCPPQSPHGS LVF PSK CASREAPTSNPCLQPQIPRLPSR PKAQ PAPHLGGA AHTRISAGVAR VCAGAFGGQA |
| 4535 | 10032 | A | 4832 | 115 | 454 | TMMTSWINCFRKG*DDVEHHALHI NLRGKKFILFLPIQEGLTRGRKQ*AN TVGHFQLGFRLYKISGLEKLKLSKL STQWLLKPLHPDQL*TRAELLG*ES LDKYDQDPEALIR |
| 4536 | 10033 | A | 4833 | 1 | 638 | ERQSVPGFKASQDRLTLLVRAYTN Q*LKLRLPLIFHFENPRALKNCAYS TLVLCQWNNKA WMSAHLFTGW LTKYFKLTIETYCSEKTPFKILLFI DNLAGHPRALMEM*KEMNVFMPA KTTSIMLPLIASSFNYSYLRNRIHRTF VVVAQSWLQCPTTAISDIQIGPVAM GLLLIPSAFVLCWLSIQVSKLKH HSHHSYFLRFWRLTA |
| 4537 | 10034 | A | 4834 | 2 | 6053 | KEILQEYLEISSLVQDEVVAIHREM AAAAARIQPEAEYQGFLRQYGSAP DVPPCVTFDESLLERGEPELGELQL NELTVESVQHTVQLLGKRQVLQEA LQGLQVALCSQAKLQAQCELLQTK LEHLGPGEPPVLLLQDDRHSSTSSSE QEREGGRTPTEILKSHISGIFRPKFS LPPPLQLIPEVQKPLHEQLWYHGAIP RAEVAELLVHSGDFLVRESQGKQE YVLSVLWDGLPRHFIIQSLDGSRL RMEAADPGSPALQNLRLGEGGFP IPLIDHLLSTQQPLTKKSGVVLHRA VPKDKWVLNHEDLVLGEQIGRVPQ RGSNSQRAWVRGPNTGAPHPGVGS RMGRKRREL RDWEGRGRSPRFQ GNFGEVFSGRRLRADNTLVAVKSCR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | ETLPPDLKAKFLQEARKLKQYSHPNIVRLIGVCTQKQPIYIVMELVQGGDFLTLRTEGARLRVKTLLQMVGDAAAGMEYLESKCCIHRLAARNCLVTEKNVLKISDFGMSREEADGVYAASGGLRQVPVKWTAPEALNYGRYSSES DVWSFGILLWETFSLGASPYPNLSNQQTREFVEKGGRLPCPELCPDAVRLMEQCWAYEPGQRPSFSTIYQELQSIRKRHRPRCSSSAAPAHMLTALHSPGLLPASTLPAGCSAVSSLCPCCCQGFLFRAETIKPLVPTHEHSWHVHSSGRQVSEGTSAGNIEQARKGKGLEEC AVPTGGSTPLPEGRNDRDLRLPGPEPASEAGGPARGRRTERSGCPGAQLGPRQRPPEQGATGERAPAFACVAACTRAAVPGRVCVEASMKLKKQVT VCGAAIFCVAVFSLYLM LDRVQHD PTRHQNGGNFPRSQISVLQNRIEQLEQLLEENHEIISHIKDSVLELTANAEGPPAMLPYYTVNGSWVVPPEPRPSFFSISPQDCQFALGGRGQKPELQMLTVSEELPFDNVDGGVWRQGFDISYDP HDWDAEDLQVFVPHSHNDPGWIKTFDKYYTEQTQHILNSMVSKLQEDPRRRFLWAEVSFFAKWLVGNGQLEIATGGWVMPDEANSHYFALIDQLIEGHQWLERNLGATPRSGWAVDPFGYSSTMPYLLRRANLTSM LIQRVHY AIKKHFAATHSLEFMWRQTWDSDSSTDIFCHMMPFYSYDVPHTCGPDPKICCCQDFKRLPGGRINCPWKVPPRAITEANVAERAALLLDQYRKKSQ LFR SNVLLVPLGDDFRYDKPQEWDAQFFNYQRLFDFFNSRPNLHVQAQFGT L SDYFDALYKRTGVEPGARPPGFPVLSGDFFSYADREDHYWTGYYSRPFYKSLDRVLEAHLRGAEVLYSLAAAHARRSGLAGRYPLSDFTLLTEARRTLGLFQHDAITGTAKEAVVDYGVRLRLSLVNLKQVIIHAAHYLVLGDKETYHFDPEAPFLQVVGWEEAEPMMVLPFRLTEFQDDTRLSDALPERTVILQDSSPRFVVLFNPLEQERFSMVFL LVNSPRVRVLSEEGQPLAVQISAHWSSATEAVPDVYQVSVPVRLPALGLGLVQLQLGLDGHRTLPS SVRIYLHGR QLSVSRHEAFPLRVIDSGTSDFALS N RYMQVWFSGLTGLLKSIRRVDEEH EQQVDMQVLVYGTRTSKDKSGAYLFLPDGEA\SPTSPRSPCCVSLKALSQRWFRTMSTFTRRS GFTICQGWR GCLWYHPWWTSGTTSTRSWPCTSIQTSTAR/VIFFTDLNGFQVQPRRYLKKLPLQANFYMPVMAYIQDAQKR LTLHTAQALGVSSLKDGQLEVILDRRLMQDDNRGLGQGLKDNKRTCNRFRLLLERRTVGSEP DFFSKLAAMFR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GLIFHSSRSNGNREVQDSHSTSYPSLL SHLTSMYLNAPALALPVARMLPG PGLRSFHLPLASSLPDFHLLNRLTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFDC GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG |
| 4538 | 10035 | A | 4835 | 1 | 6606 | MGFSSSELCSPPQGHGVLLQMQEAE RLLEGMRKWMAQRVKSDEYAGL LHHMSLQDSGGQSRAISPDSPISQS WAEITIQTEGLSRLLRQHAEDLNSG PLSKLSLLIRERQQLRKTYSEQWQQ LQQELTKTHSQDIEKLKSQYRALAR DSAQAKRKYQEASKDKDRDKAKD KYVRSLWKLFAHNNRYVLGVRAA QLHHQHQQHLLPGLLRSLQDLHE EMACILKEILQEYLEISSLVQDEVVA IHREMAAAAARIQPEAEYQGFLRQ YGSAPDVPPCVTFDESLEEGERPLEP GELQLNELTVESVQHTLTSVTDELA VATEMVFRREQEMVTQLQQELRNEE ENTHPRERVQLLGKRQVLQEAALQG LQVALCSQAKLQAQQELLQTKLEH LGPGEPPPVLLLQDDRHSSTSSSEQR EGGRTPTLEILKSHISGIFRPKFSLPP PLQLIPEVQKPLHEQLWYHGAIPRA EVAELLVHSGDFLVRESQKQEYV LSVLWDGLPRHFIIQSLDGSRLRM EAADPGSPALQNLRLGEGGFPSIPL LIDHLLSTQQPLTKKSGVVLHRAVP KDKWVLNHEDLVLGEQIGRPVQRG SNSQRAWVRGPNTGAPHPGVGSRM GRKRRREL RDWEGRRSPRPFGN FGEVFSGLRADNTLVAVKSCRETL PPDLKAKFLQEARILKQYSHPNIVR LIGVCTQKQPIYIVMELVQGGDFLT FLRTEGARLRVKTLQMVGDAAAG MEYLESKCCIHRDLAARNCLVTEK NVLKISDFGMSREEADGVYAASGG LRQVPVKWTAPEALNYGRYSSES VWSFGILLWETFSLGASYPNLSNQ QTREFVEKGGRLPCPELCPDAVFRL MEQCWAYEPGQRPSFSTIYQELQSI RKRHRKHRAKTERKGTRGMRICTD RRQHFPFARGAQRQRPKATWAGAG FRGWRTRAEPQRSAPAARGPAGE LQQRAEQGATGGRAPAFACVA AACTRAAVPGRVCVEASMKLKKQVTVC GAAIFCVAVFSLYLMLDRVQHDPT RHQNGGNFPRSQISVLQNRIEQLEQ LLEENHEIISHIKDSVLELTANAEGP PAMLPYYTVNGSWVVPPEPRPSFFS ISPQDCQFALGGRGQKPELQMLTVS EELPFDNVDGGVWRQGFDISYDPH DWDAEDLQVFVPHSHNDPGWIKT FDKYYTEQTQHILNSMVSKLQEDPR RRFLWAEVSFFAKWLVGNGQLEIA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | TGGWVMPDEANSHYFALIDQLIEG HQLERNLGGATPRSGWAVDPFGYS STMPYLLRRANLTSMLIQRVHYAIK KHFAATHSLEFMWRQTWSDSDSTD IFCHMMPFYSDVPHTCGPDPKICC QDFKRLPGGRINCPWKVPPRAITE ANVAERAALLDQYRKKSRLFRSN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFFNSRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTSTRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSLAGRYPLSDFLLTEARRTLG LFQHDAITGTAKEAVVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVVGWEEAEPMMVL PFRLTEFQDDTRLSDALPERTVIQL DSSPRFVVLNPLEQERFSMVLLV NSPRVRVLSEEGQPLAVQISAHWSS ATEAVPDVYQVSVPVRLPALGLGV LQLQLGLDGHRTLPSVRIYLGHRQ LSVSRHEAFPLRVIDSGTSDFALSNR YMQVWFSGLTGLLKSIRRVDEEHE QQVDMQVLVYGTSTRSKDKSGAYL FLPDGEA/SPTSPRSPCCVSLKALSS QRWLRTMSTFTRRSFGTICQGWRG CLWTYHPWWTSGTTSTRSWPCTSI QTSTAR/VIFFTDLNGFQVQPRRYLK KLPLQANFYPMVMAYIQDAQKRL TLHTAQALGVSSLKDGQLEVILDRR LMQDDNRGLGQGLKDNKRTCNR RLLERRTVGSEPDFFSKLAAMFRG LIFHSSRSGNREVQDSHSTSYPSLLS HLTSMYLNAPALALPVARMQLPGP GLRSFHLPLASSLPDFHLLNLRTLQ AEHCLWAEALLHLRSLKALRPLPW ALSVIQEDTLPSAETALILHRKGFD GLEAKNLGFNCTTSQGKVALGSLF HGLDVVFLQPTSLTLLYPLASPSNST DVYLEPMEIATFRLRLG |
| 4539 | 10036 | B | 4836 | 114 | 255 | VQPRRYLKKLPLQANFYPMVMAY IQDAQKRLTLHTAQALGVSSLKDX* |
| 4540 | 10037 | A | 4837 | 1 | 452 | LDGRQLSV/SRHEG/FP/LRCIDS/GTS ELALS/N/RYMQVWFSGL/TGLLKS RRVDERHEQQVHMQLVYGTRTS KDKSGAYLFMPDGEAKP/TSRSP CCVSLKALSSQRWLRTMSTFTRRS FTICQGWGCLWTYHPWWTSGTTS TRSLHFSFN |
| 4541 | 10038 | A | 4838 | 3 | 3543 | QLGRLGPERRGGRALTVCEASMK LKKQVTVCGAIFCVAVFSLYLML DRVQHDPTRHQNGGNFPRSQISVLQ NRIEQLEQLLEENHEIISHIKDSVLEL TANAEGPPAMLPYYTVNGSWVPP EPRPSFFSISPQDCQFALGGRGQKPE LQMLTVSEELPFDNVDGGVWRQGF DISYDPHDWDAEDLQVFVPHSHN DPGWIKTFDKYYTEQTQHILNSMVS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KLQEDPRRRFLWAEVSFFAKWW NINVQKRAAVRRLVGNQGLEIATG GWVMPDEANSYFALIDQLIEGHQ WLERNLGATPRSGWAVDPFGYSST MPYLLRRANLTSMLIQRVHYAIKK HFAATHSLEFMWRQTWSDSDSTDI FCHMMPFYSYDVPHTCGPDPKICC QDFDKRLPGGRINCPWKVPPRAITE ANVAERAALLDQYRKKSQLFERN VLLVPLGDDFRYDKPQEWDAQFFN YQRLDFFNSRPNLHVQAQFGTSLD YFDALYKRTGVEPGARPPGFPVLSG DFFSYADREDHYWTGYTTSRPFYK SLDRVLEAHLRGAEVLYSLAAHA RRSGLAGRYPLSDFTLLTEARRTL LFQHDAITGTAKAEVVVDYGVRL LRSLVNLKQVIIHAAHYLVLDKET YHFDPEAPFLQVDDTRLSDALPER TVIQLDSSPRFVVLNPLEQERFSMV SLLVNSPRVRVLSEEGQPLAVQISA HWSSATEAVPDVYQVSPVRLPAL GLGVLQLQLGLDGHRTLPSVRIYL HGRQLSVSRHEAFPLRVIDSGTSDF ALSNRYMQVWFSGLTGLLKSGSLC FLA\SIRRVDEEHEQQVDMQVLVYG TRTSKDKSGAYLFLPDGEASPTSPR SPPSCVSLKALSSQRWLRTMSTFTR RSGFTICQGWRCGLWYHPWWTS GTTSTRSWPCTSIQTSTAR/VIFFTDL NGFQVQPRRYLKKLPLQANFYMP VMAYIQDAQKRLTLHTAQALGVSS LKDGQLEVILDRRLMQDDNRGLGQ GLKDNKRTCNRFRLLERRTVGSE VQDSHSTSYPSLLSHLTSMYLNAPA LALPVARMQLPGLRSFHPPLASSL PCDFHLLNRLTLQAEEDTLPSAETA LILHRKGFDCGLEAKNLGFNCTTSQ GKVALGSLFHGLDVVFLQPTSLTLL YPLASPSNSTDVYLEPMEIATFRLRL G |
| 4542 | 10039 | A | 4839 | 2 | 438 | FVPAKVAGAAEPDEDGGRSLRDC GDYTPSERLGPKGAMLWFQGAIPA AIATAKRSGAVFVVFVASDDEQSTQ MAASWEDDKVTEASSNSFVAIKIDT K/QMHLLKSETSVANGSQSESSVST PSASFEPNNTCENSQSRAELCEI |
| 4543 | 10040 | A | 4840 | 1 | 1608 | |
| 4544 | 10041 | A | 4841 | 1 | 3117 | MAPEWRPGTTASLPSGPGARSVC RSPEAGSASVFVRLCGPRNLGWFGP HLRLRTSAHARQRHPKTRASAREN TSRHSRNPSVSVQDLLSLASRCAG SIPITLESCLPVGLSKDVWPLTIEPKV KVFIFFNLKLPDCPSTMKNPASLLFSL FEGEWAI AEVLSDIWCTGVLAINK DQVLTIGFDINEFLSCSSSSKKSMSC SLTGSLALQPDQQQDHETDSSPAS AYQRIWEAFANQSRAERDAFLQDT FPEGFLWGASTGAFNVEGGWAVG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | GRGVQPKHVKEAFRLLNKSIIRVET PDVNLQDEEEIQMEVDEGAGGING HADSPAPVNGINGYNEDINQESAPK ASRLGFSEYCRISNLIVLHLRKVEE EEDSALKRSELVNWYLKEIESEIDS EELINKKRIIEKVIHRLTHYVEYFSS LHASQITHYKVFLSWAQLLPAGSTQ NPDEKTVQCYRRLKALKTARLP MVILHHQTLPASTLRRTAFADLFA DYATFAFHSFGDLVGIWFTFSDLEE VIKELPHQESRASQLQTLSDAHRKA YEIYHESYAFQGWLAFTHMSQTLA NKIRVRGMAQESCSHGSSVGYLQH PGSEQVQFPRTTSPCSSQLQGHQC TAGPPPPPGGGMVMMQLSVPNNPQ SCAHSPQWKQNKYYCDHQRGQK CVEFSSVDNIVQTSLNCTDPVVCVP SSFFIGDSGIPLEVIAGSVSADELVT RIHKVRQMHLKSETSVANGSQSES SVSTPSASFEPNNTCENSQSRNAEL CEIPPTSDTKSDTATGGESAGHATFL FREPSGCSQDQPAEDLNIRVERLTK KLEERREEKRKEEEQREIKKEIERR KTGKEMLDYKRKQEEELTKRMLEE RNREKAEDRAARERIKQQIALDRAE RAARFAKTKEEVEAAKAAALLAKQ AEMEVKRESYARERSTVARIQFRLP DGSSFTNQFSPDAPLEEARQFAAQT SVRVTSSEPPNPASSSKSEKREPVRK RVLEKRGDDFKKEGKIYRLRTQDD GEDENNTWNGNSTQQM |
| 4545 | 10042 | A | 4842 | 3 | 790 | GARGTFLSPASVESSVLLCLLVPHP VLSRGPPASPPSSYHPSLPGGG/GGQ *PLPEYGLESSEQN*GLSPGEDPGNP GGPFWGSGAPAGSLMEA*GNKRDA PPPPGDPSCSAPC/GDPPGMQGIQDS LPCHTASQKGGAFPGMAPGRVL HQQGPL*GPSRLSQESPSAGPPMPQ LPSWVLCQVRPRAWGCWEPKGPPG TQFPPRFPDPSGTPCPPGYLEIFLLDP IPPRNWLAPLAAAAQ*/PWGRWE MPMALPRGGLPLYT |
| 4546 | 10043 | A | 4843 | 1 | 1026 | |
| 4547 | 10044 | A | 4844 | 1 | 722 | MALEQRLKGGSGAALRSKAFPAEG TAGAKALQESDWSIGGAVSKPVF VQSVRELVADPCASNPCHHGNCSSS SSSSSDGYLCICNEGYPNCEQAL PSLPATGWTE/CHGTPTASACSCYS GA*/Q/SCLALRQR*HCLPGSRKQG/ KSCRNEMGSSGGDPYCLWECQF* QLCGWPPGIL*SATEHLSQDSARCH CLTDFALEGHGHIPTVLPHRWTKC DPPSGFRGTGPPGGDARLGE |
| 4548 | 10045 | A | 4845 | 2 | 2028 | CSPAAPRRPVRSCCPRWPCCCCSSE RGPEAAPWPTRCPPRPCL/LPGPCAA QPCRNGGVCTSRPEPDQHPAPAGE PGYSCTCPAGISGANCLVADPCAS NPCHHGNCSSSSSSSDGYLCICNEG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | YEGPNCEQALPSLPATGWT/AIHGT PTASACSCYSGA*QNPAASLSNGDTP AYLAAENRAESCRNEMGSSGGDPR YCLWECQF*QLCGWPPGIL*SATEH LSQDSARCHCLTDFALEGHGHIPT VLPHRWTKCDPPSGFRGTGPPGGD ARLGE*SLY\CFVNDVSVTKS/NCGFA LNSGGEVSTCVPGESHANDLECSG KGKCTTKPSEATFSCTCEEQYVGT CEEYDACQRKPCQNNASCIDANEK QDGSNFTCVCLPGY\NGELCQSKID YCILDPCRNGATCISSLSGFTCQCPE GYFGSACEEKVDPCASS\QNNGT CYVDGVHFTCNCSPGFTGPTCAQLI DFCALSPCAHGTCRSVGTSTYKCLCD PGYHGLYCEEEYNECLAPCLNAA TCRDLVNGYECVCLAELYKGTCEL YKDPCA\KSACLNGATCDSGLNG TCICAPGFTG*ECDIDINEC/ATVTP CHHGGVSLGDQPNGY\TCHCPHGW VGANCEIHLHWEVPGTWAESLTNM PRHFPLTFIHWEVPLRGPFPYADHP DRGDLPHQPH |
| 4549 | 10046 | A | 4846 | 1 | 703 | TISCPAVRSRRPRRISCLSCPGGGGA ASGLQRAAGGTGLSWVPAGLRVCC SQRSWRPAKEEQPVQTPRRTGKGG EISDMKPYKNKNEGNLENGKPEDE V*PDDEGKSY*EEKPYA*GNTECEG KLKADGEPGDEGQLEDNGSQEKQG KSECEGKPGEGKPAQAKPESQPR AAEKRPA*RLCGPGKAKK/NKPDQ GDRITFPQGLSGGLTGKASEQ*GDD ERMWRCVKGSRGA |
| 4550 | 10047 | A | 4847 | 180 | 866 | GAYVHGGRGGLCVQSLFQGVSSSDF CPPIPTLVPTLRPRAPCLWCTQDPAR PPCQSQRRLGPFQGVAGLKPSPGLL PNILLPESPSKRFNHGQLPVPQTVFG GGGSRGPPLLVPPLPLFVFPFCGCF LSQPRGHRSPSSP*EEG*STPLLSVC HSHTDLWGLSWAVPAGWTGPSALF SPQAVNRLPITRPAPTHPHSFPREAP GRW*TPLPTSQSLLFYGKDLPVK |
| 4551 | 10048 | A | 4848 | 112 | 679 | KI*NMWCYSDTGQFNVKLSVLL*I IYIFNKILSSFLVKTGKLSLKS VN/NK QQSRITKTSKENKRGGMFMR*DIKTF YVFAVIKSVLYMQI*ID*WKIIESSET DLHISSHLIFDKDNKMEKSLKK\WDI VYSSHRKIINLDL*HIPYVNINMIWN IDLKIKRFF*IAT/ENIFVTFSNVGND FLKYQLKSKIKKLKMRMVVYQMV P |
| 4552 | 10049 | A | 4849 | 33 | 394 | GSVWHHPFEGALRGPIPGAAGKPG LGTPSHPGLSPHPAACAACPRLPGL CSCAPGSAPLRLRP*/PAPCGSSDS VPRTP/GRRGLGSPGPPAPAAPKAE* LLQGGEFFSDPQPLAPEPRQLR |
| 4553 | 10050 | A | 4850 | 2 | 269 | LSGVCTVHIRGVCVWAGGNPSGTE LPGPLPPRPSASPPHPPQ*GVALP\ |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | Se q u e n c e N O: in U S S N 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|---|---|--|---|
| | | | | | | PVLFCFLVLPHPPTPNLIYPPCTVPFS PLPAPFAFFCW |
| 4554 | 10051 | A | 4851 | 1 | 543 | LLSKWIIITPSGAGSGDPPPAASPRR KQRMKIMKTTRSQTTPGRAPAASA SSPTL*TPGRDLESRLRP*PTNLPVR TPPGTAAVCPLLHRP/PQKAPVLGP ARV*ERGE/DANATPKREGLKRA/PP NDTLDFLWLGTPSSTKIKWTRPPAV EPLLVLHPTPTLPPLPVVPIVTQRVE YQGRFF |
| 4555 | 10052 | A | 4852 | 831 | 1301 | FFVFTFKYKNTILLCVINQGPSSKNL FFFQGRDIHQFILSFVFRAGHLVPSQ ASPTSKRPKPFSLIPNPYLLS*FPLLIE KLVINFLKKKFPTTRASP*PNQSTSR SSPFSYPGRRVPPLQTSSVPELRTPY WTGAPPLNGSSGYVSPTLPPPLMH |
| 4556 | 10053 | A | 4853 | 1 | 1222 | |
| 4557 | 10054 | A | 4854 | 2 | 563 | AHVIIYRFSMH*VITDVIPMLEVRSV YEINDVGTPEGEQ\TPPLTPVGGSN PQPIPAQSHPTSSSSSDGLRDNVPW LKVKNSPLKQSPGYQTELVIQLVW VGGEPPQIASLAVNSSYGLVDFGN CNGIAMVDYLQKAVLLNLGTIELY GSNDPYRREPRSPRKSQRPSGAGLC DISEGLVPSKA |
| 4558 | 10055 | A | 4855 | 648 | 1377 | EYLGHWELQKRSLSPATGGGQG QLGAEGGP/GPGGGAAPAHLLAPN QACGVGLIDWRPRWTRGGTAAAG ARTPNLNPAAALTP/GRHSCVSVKK GSESELSRRR/TLPVVSPPGGGGCE MLRPDPASSP\SSQTP*PVPGAQAQT LALSCPPNSCPAKEVGAAGF*APLH LLSPSVGEGGGASGSTPKVSSFP GGPLHSP*Y*PGPENWEGGDEGPL SHPARVPAAQSETECVPTESPQ |
| 4559 | 10056 | A | 4856 | 3 | 394 | SQAPS/GVAAHTPLS*AWTQPWNS IHMALASTRPNMPLRSGPA/CMPQL QLQELFTRSLVESELRIAPSEYPDES PIEQLEERRQLLEQPISLDVMLEPYI LRRSKLDLLYTSDSDLQLYKEQGE GQGDR |
| 4560 | 10057 | A | 4857 | 3 | 666 | SLLPKIFIGCLRRASSGPGAGNMLGS PSPQPLVSILGIAESWSTLPQGQPPA NPEAWAGPAGAKTDKSKT*GHFT ETLPNVPKKDPLQLGA*KPGGSKPS EE/VWSQ/SPGPWLRNSGFFPPLNP RWGPFSTLWERF*NCSQPFRLRN PPVPL*GVLRASNPWPPHPHHPA NMPPAPPRVLRSSSTSAPPPWGCT QGPRGARAGA*AGAASS*SRGR |
| 4561 | 10058 | A | 4858 | 3 | 361 | FFFFRKWVNIFANYM*KKLILKIYQ QL*KLNHKVQ*LDL*MNKQNFHQK TTQM/AKKHLTGCTKLLICREMKK KTQ*QRNHLTPIRMATYFLKNAN/C W**CNKNETHVGCWWKTKM*SLF |
| 4562 | 10059 | A | 4859 | 3 | 397 | DQPTDIILDEQ*LelfHLRTGIRRG PVSSLPFN/IRAIRQEK*IKGIQLGKEI |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | KLALFADMILYLENPEDS/AQKL/LR LINNFSQVSGYKINAQKLGAFLYTN NVQAE/SQIKNPIPFTVAIKKLKYLKI HLAKE |
| 4563 | 10060 | A | 4860 | 2 | 328 | AHIDAVNEAMRLLLEHGFHAPTMSW PVSGTLMVEPIETEDHA*LDRFWDA LINLLQGIADIEDGRICPRVNPLKMS PHSLTCVTSSHWDRA\YSEKGAAFP LPFVKPENK |
| 4564 | 10061 | A | 4861 | 13 | 410 | NKMRRQATDRDKMLAKDTFDK\GT LEIYNQFLKFNNKKMSIPIK*WAKN L/NSHLTREDIQVANKPMKRCSTSY FIKEMQIKAMTRSRCADIKMAKIQT TDDIKC*RTCTRSTNFPFPALHLFYQ LTFRKSISH |
| 4565 | 10062 | A | 4862 | 3 | 293 | DKGLKGFRGFPTFTSFGQPTWLGLG LDLPEPGN*GPGFGCGP/NSRVGPTL SNLGPGERGPPGPPGLGV*ALKGK RADKKGGASFFPGF*KFPVGLP |
| 4566 | 10063 | A | 4863 | 125 | 366 | GIPGERRLEPPG/PKGPPLSPQIKGN NGPGPQN*VFFGGFKTKVPFGAQQ GS/GNPGPKPIFPPPGPKGRKYRVGP MAPPLQ |
| 4567 | 10064 | A | 4864 | 79 | 336 | HIATFNALSYVQASKRDKKFFACAP NYSYAVLCECLSSSIHLSSACSHVH C*RHDDALLWQPHGSIIRDDMR*HI ATFNALSYVQASKRDKKFFACAPN YSYAVLCEC\HRRVFIYRQPAPMST VFYNRKDCLO/TVDRMLIHKVASLK TNDPILSIQAPK |
| 4568 | 10065 | A | 4865 | 2 | 512 | KIQIASIRNEIGH/LLTDATYIQRRLR E*CGQLQANKFDNLNGRDKFPGRH KLPKLIQKEMEAGRSGPLSPRVLG LQA*ATVSGLTGKFYKTCKEEIPIL TILFQKTEKGTLQSS*EETSTILIPNQ EGKKNFQNGCLSMDPGTGKVPLTK ILVNQIQQSVIHKDNISI |
| 4569 | 10066 | A | 4866 | 466 | 1451 | EVCGLKKARISLFFF*DGVSLLCCPG WSAVAQSRLTATSASRV\K*FSCLSL LSSWDYKRPPRPANFLHF**RQGF TMLARLVIS/WIS*SVPPWPPKVLE L*AKAGDSLEPGSSRLQ |
| 4570 | 10067 | A | 4867 | 3 | 379 | NKSCQGPRTSFASAGWALKNPRWQ EQKEGLGKAGRPSGMNSSASSPTPG RKRELGMGSPSLRSPP*CE\GRSDR LG*PP*GGQGGGGH GAPSTPGPGG\ GPGDFHSKPPDPSLVPRPTEARGSP GP |
| 4571 | 10068 | A | 4868 | 2 | 1718 | SEGAPPRRGAWGGPPARSHTLAPT PLPP/GPLSLCFACKWLGVDRD AG*LGSQKAGGRGHPGMGQGKGT PPAHAW*PTGWCTGPK*KLGFLCPF HIPVSLACFLLSCAASDFSVLTWQ LWGP*EPPTEGGHSPFPSCRC/HRQE EGFLPVWQSPRQRPRMRPDSAPPST SARASKVGPGRGLPLNFG/QRPNL TPYGPAPALALS*PPQRWEELAEGA |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | PGPQPPVASKGPFSS*PKVLREPAVE TSSCASAPLAVFVRGVHTCIGG*AP GLSGGHPLTVSF*IGGIEGLDCLSPQ *AWGPGLGLEVCCGSHQASPPGPG VLGAPCPPPPCPPQGG/PAQPVGPS/P SHHGGERE*RGRPHSKLPLPPGVWG GC*RIHSRGPPGLSQPLFCF*PRRLS\ PAQPA*SKGGSRLVLSFCFLLPGS* GTRASGRGHSPSLKPGPGRAGRQ\G ETRGS\GSPGE*GCWSQNWDRGPA GQPWATSRVSIVRGWRVPGVAGAG FLAVLPWAPPSEARWQEQADQNPSA FGPKWEAAFLPNLPCQGGQQRGSPSP PPPPGCRNGDPSQGLGAGAEYSLGP LPYT |
| 4572 | 10069 | A | 4869 | 253 | 451 | RWKA WFGREIKGNNPRCKRGGGK HGTG/EEIKGNNPRWKRGGGKHGT GGK/YKGNNPRWKRGGGKHGTGG K/YKGNNPRWKRGGGKHGTGGKL K/SNNPRW*REGGKHGSGGK/YKGN NPRCKRGGGKHGTGGKLK/SNNPR WKRA GGKHGSGGKFKEIIPDGSVK VESMER |
| 4573 | 10070 | A | 4870 | 2 | 269 | EGGLGLNRFPPPPGPPRRPAAACMS AP*PQR/HWPP/SPREEKASLNEPGG PGRGRGRGSGQLHGEGGPRGGE/R GNWPGGMEGEGGIDAPAS |
| 4574 | 10071 | A | 4871 | 20 | 312 | SVMNGTSICKCRANDETGLSPSPAG PKSRSRRLS*LWRPSAATDSGSPPT* PVPTSPPPAPTAPRPGSRAPSSPGLA PTLTGPGG\PLRPPPPAEEP |
| 4575 | 10072 | A | 4872 | 299 | 472 | KSISVATANPGKCLSCTNSTFTFTTC RILHPSDITQVTPR*/GVPGKSGASLL SSAVFS |
| 4576 | 10073 | A | 4873 | 1 | 3454 | MKHTLIPRIKNAQLQMSLAVPVNS LVCLGKILEYLDKWLVDGILPFLQ QIPSKESAVLMGILGIYKCTFTHKL ITKEQLTGKVLPHLIPLSIENNLNQF NSFISIIKEMLNRLSEHKTLEQLHI MQEQQKSLDIGNQMNVSEETKVTN IGNQQIDKVFSHIGADLLTGSDSEN KEDGALNVPPAGAKPTQQRPTDMS ALNNLFGPQKPKVSMNQLSQQKPN QWLNQFVPPQVSPATGSSVMGTQM NMIGQSAFDVCSNEDLPEVELVSL EEQLPQYRLKVDTLFLYENQDWTQ SPHQRQHASDALSPVLAETFRYMI LGTDRVEQMTKTYNDIDMVTHLLA ERDRDLELAARIGQALLKRNVHLS QNESLEEQLGQAFDQVNQLQHEL KKDELLRIVSIASEESETDSSCSTPLR FNESFSLSQGLLQLEMLQEKLKELE EENMALRSKACHIKTETVTYEEKEQ QLVSDCVKELRETNAQMSRMTEEL SGKSDELIRYQEELSSLLSQIVDLQH KLKEHVIEKEELKLHLQASKDAQR QLTMELHELQDRNMECLGMLHESQ EEIKELRSRSGPTAHLFYFSQSYGAFT |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me- thod | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|-------------|-------------------------------------|---|--|---|
| | | | | | | GESLAAEIEGTMRRKLSLDEESSLF KQKAQQRVFDTVRIANDTRGRSIS FPALLPIPGSNRSSVIMTAKPFESGL QQTEDKSLNQGSSSEEVAGSSQK MGQPGPSGSDSLATALHRLSLRRQ NYLSEKQFFAEWQRKIQVLADQK EGVSGCVTPTESLASLCTTQSEITDL SSASCLRGFMPEKLQIVKPLEGSQT LYHWQQLAQPNLGTILDPRPGVITK GFTQLPGDAIYHISDLEEDDEEGITF QVQQPLEVEEKLSTSKPVTGIFLPP TSAGGPVTVATANPGK\CLSCTNST F/TLFTTCR/IYLHPSDITQVTPSSGV PFHLSCG\SSGSSFHSNTAVNSPALS YRLSIGESITNRRDSNYNLSVGTME VGPKFLQER\GIS\AKVYHSP\SENPL QPLPK\SLAIPSTPPNSPSHSPCPSPL PFEPVHLSENFLASRPAETFLQEM YGLRPSRNPPDVGQLKMNLVDRLK RLGIARVVKNPGAQENGRCQEAIEG PQKPDSAVYLNSSGSSLLGGLRRNQS LPVIMGSFAAPVCTSSPKMGVLKED |
| 4577 | 10074 | A | 4875 | 1 | 638 | LA WGGKKGKASSDSGGLVDSISTL TPTPGDTNT/HSDLIVRGGAYGGQW AHGVLAQVQPSVGAETV*PQMGE *TDVCGSQSPHICSLTLRVGATML GKAR\WKPLG*TLPR\KIV\NSKATC SPGGTAKVSAAIRGLGRCRVVTPTA ASFHSS*\WLWVKTGGSRKKDSES WVNLTRTPIATAVPDMTTDSLGOIQ SIPGHPVLQPIDPGESL |
| 4578 | 10075 | A | 4876 | 31 | 448 | PKSLLSLLVKINYGYVVK*QATKAK LDNWDYIKLQSFCTTKIMNRVRRQ PAE*ENIFANQTSKGLISKIYKELK QLNSKKANNLIKWNSSDDLNR/HFSN EDIQMASRYMKK\STSQIIREMQIK TTMRYHFMPIRMTT |
| 4579 | 10076 | A | 4877 | 3 | 286 | KFTFKRHHHLQLLKRK*DS*V*T*Q MFMEQIKEDLSKQRDNCS*IGKLSI AKNIYVSNPG*FDAIPIKIPARFFYA FGLYCRNSVSLSPRLN |
| 4580 | 10077 | A | 4878 | 3 | 236 | ATHSTLPSFQGPVSLASMTVVGIDG KASRPLQTPVCQLDQHSFLHS/FLV IPTCPVPLL*GILTKLSASLTIPRLQ P |
| 4581 | 10078 | C | 4879 | 206 | 262 | MVAIGTGYRRPGLRFTLN* |
| 4582 | 10079 | A | 4880 | 2 | 756 | LTSSRGARPAPLRAPAR/LDPAFRAN PLRSYSGSLPTFPYLHCNMPKAC SPWRPAADMGT\PGARFTSPPDFQ GPARAPPDAAGTATLSKARAPLSGR NPFQGRPCPSQRKENSRRRTSPG SRRVTDGRLAGAPCSATPDSGI*T RLPFRIGRGAPEAIAPSLRNGARPSL RTD*PMFQLLGYNWNPSPVRPSKV LRLNICYYTP\SHAPAAAPPGPADFQ GPARAHRTPEPRRFRHGPLSRGE P |
| 4583 | 10080 | A | 4881 | 3 | 322 | MGSVTGPLYSGYKEEVVCCTLVEV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FPSLLQVSRNPRMPFDLGLIFCLG GQGFPRATTVSGHWPE*LSQSSSP KLRPPTL*SKPAHPGAAEALKAVPR TSAGAR |
| 4584 | 10081 | C | 4882 | 240 | 500 | MQNGLSGAYFPSVWAAKDSQERR RSPATGRNDSPRAPLPRSSARRPSK ANLHTLGQLKLSSRCRAPLRRAA RTRXSXDQXWRRXTT* |
| 4585 | 10082 | A | 4883 | 22 | 696 | CTFGSFPFGLSAWSFRASLPAPAP GPNERFRSPGAGGFWGVDAAGQPA PAEVLGTALRASAAPGCAD*NPKKI KWHPG/SFCSPGEGMEILQQVCSKQ LPPCNLSKEDLLQNPYFSKLLNL QHVDSEGLSLTLAKEQAQAWKEVR LHKTTWLRSEILHRVIQELLVDYYV KIQDTNVTSEDKKFHETLEQRLVT ELMRLLSPSQEREIPLLGLEKADLL E |
| 4586 | 10083 | A | 4884 | 1 | 594 | AVVHFRLPLPGPFILCLSGPRFPQP AAPGPNERFRSPGAGGFWGVDAAG QPSAEVLGTALRAPAAGLQVCF KGSAGGASGKRSSGRVIPA/MWPET VVALGNPWTVQTEGKVGAGEPVL HFDSSRAL*GSVSCENNL*NQFNRS SCSV*RQALRI*KTPSEHLKCLGPC SSVFNTSECRVENRSLNCPFTPCNL |
| 4587 | 10084 | A | 4885 | 2 | 326 | VKTAEFVNKWQKNSTKLWNSQAQI DSSSLVNQINDLRQTEIWMGDRIMN LESRIQMCDWNTSDFCVTPQYNE TEH*WKKVKRHLEGREENLT*IVK LKEQDFEASQ |
| 4588 | 10085 | A | 4886 | 2 | 373 | VLLTPEERTVVIALWRKVNVAALC R*GAWA**L*AYPWTHRFFESFGDI DSSDAVMGKPIVNAHGKNVLGAFS DGQSHLDNLLGTYSQSELHCDKL HVDPENFKLLGNVLVCVLARNFGK EF |
| 4589 | 10086 | A | 4887 | 3 | 332 | HLSIINLVNQLNSPLKAYTLPVWIP SS\RGPTICCLQEIHFAKNTRYKLKV KELSSSFQANEKEKHADKTGFKVPK L*REKNGHYIMIKRSVQKENIYIYM FLIADPDIC |
| 4590 | 10087 | A | 4889 | 1 | 304 | HSCSSMRMPPLPTPPP/IVLCPPHPSP LIKALVSSKPP*VPSAETWPVAAL GA*VPAVLGWPLHTENVLPVPPPL EMPRIQWHFMLCSFPQRSRADEST |
| 4591 | 10088 | A | 4890 | 1 | 254 | RPRRQFGIEGSFLNQIKNIYKKSTAN VILYVDRLNAFSLISGSSSSSSSSSS SSSS*LPVNIIRQ/EKVI*GMQIVKEE LNLSL |
| 4592 | 10089 | A | 4891 | 310 | 415 | SQYFGTLRRVDHLRSGVRDQPGQL GKTPS*PQVIHPPQCPKVLGLQYYH FLFFLRRL/DSVAQAGVQWRDLGS LQRPFGFTPFSCSLSPSSWDYRRPP PRLANFFVFSVETGF/TVSARMVIS *PRDPPASASQSAGDTGVSQAPV |
| 4593 | 10090 | A | 4892 | 2583 | 3580 | DRVSLLLPRLECNGAILAHCNLCLS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GSSDSPASASQVTGITGKCHHTQLIF VFLVEMGFHHIAQAGLELLTS\DSPT LASQSAGITGVNHHAWLFFFC/SD TVSLCYPGWSRVA*SRITATSAIPGL K*FACFSLPSSRDYRHVPPHPGNFCI FGRDEVSPCWPGWF*TPDLR\YPPA SASQSAEIIIGVSHHTWPQEVFLFLNL FIYLRWSL/DSVAQARVQRRDLGSL QAPPPRFKPFSCSLPSSWDYRRPPP HPANFFVFLVETGF\TVLARRVLIS* PRDLPASASQSAGITGVSHHTR/LIF/ NFFETGTHSVTAAVQWYTI/GSLQ PRTPELK*SSHLILTSNWDYRCTPPC PPNLFIYLFYFHRDEGSLCCPGWS* TPELK |
| 4594 | 10091 | C | 4893 | 40 | 180 | MSFEAEIVLSPDRTTALHPGLQIETL SHIIIIILSTISFHQLLH* |
| 4595 | 10092 | C | 4894 | 4827 | 5060 | MWIYFWTLNSVPVIYMSLMSIPHY FDYCCFIVSDIMLPEITFTFILLMV ALAIRGPLHFRRHFRJNLSIATKNA* |
| 4596 | 10093 | A | 4895 | 2 | 311 | FILHVCDKLILFVSGDTFQTVSPRFL APRTFLAPLQNP*PLSPCAVHISFSRP LPARSPLPP/PRPPPPPTCSTAIPATH NPILTTHTSTPPPTLPTINLTSSP |
| 4597 | 10094 | A | 4896 | 2 | 374 | DLTPKV*SRKGKIGKLDFTKTFW SAKDHVKRLKRQTTDWEKIFLNHIS NK/GLLSRIYK*LQTQY*KTPSNPI/K KTAKDVKEHFTEEDIQMACNPMKR CSTSLAVRELQIKTTVRYLKIEFNF |
| 4598 | 10095 | A | 4897 | 1 | 684 | |
| 4599 | 10096 | A | 4898 | 1 | 1349 | |
| 4600 | 10097 | A | 4899 | 1 | 821 | MLQTWSGYDNPRVTQKVPPFQLNC LPMTVVLLILYAEVATDWNRVGLT QGQLLHSLRLDPWSGLTQRTFPTGA MEISPDYLPPEFIVENTERIDEREKG REQPPKKTENKAWPKMLKGKKA KGKKVAPAPAVVKKQEAKKVNP LFEERPKNFGIGQDIQPKRDLTRFVK WPRYIRLQQRAILYKRLKVPPAIN QFTQALDRQTATQLLKLAKHYRPE TSKRRRLLAQAEKKAAGKG/VRPT KR/PPVL*AGVNTVTTLVENKEAQL DLYCAI |
| 4601 | 10098 | A | 4900 | 1 | 868 | GTRPKMPKGKKAAGKKVAPAPAV VKKQEG\AKKVVNPLFEKRPKNFG IGQDIQPKRDLTRFVK\WPRYIRLQR \QRAILYKRLKVPPAINQFTQALGP RKQATQLA*AWPTKYRPRDKAREG SRDLFGPGPRKKAAPKGTFTKRP PVPSKQ\G*TTVTTLGGGPRKASAG WWIAHDVDF\LELGLSFLA\ALCRK NGGSPYCIKKGKQDWGRL\VNKK TCTTGRLSHR*TSED/NKALLKLVE AIRTNYNDYDEIRRHWWGNNVLGP KSVARIAKLEKAKAKELATKLG |
| 4602 | 10099 | A | 4901 | 145 | 745 | RRRGTSQCNLITIVNHISEITVIMFIE CSLCIKVIRLFHILILLDFSSKPAPPPP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PCGAPGL*TATLLSRLRTARDLGTR L*ASPASPLCAVPSPAAAAFL/SLPLP LCPSSSSARELRSPTPGLSGQPAPAA SPGPG/PAG/PPPPPLAVRPRFAPHL QLCPGPPFSRPSVLPASSRCQPGLSA PSLPSSPRPPPLRGLGRS |
| 4603 | 10100 | A | 4902 | 94 | 432 | TFLFFLIFSSEYWKFKQKQYSLEKSL FVAYNHKDG*THFLKGNNQFIFSLA/ LFTLGDIIYCKDIFGRLGLQP/TDISS DSPFLSFSSSIYILTWGQARWLTPVI PAFWEAKAG |
| 4604 | 10101 | A | 4903 | 109 | 422 | FFEDGVLSRSVAQAGVQWR\NLSS LQPLPPRFK*FSCFSLRSRWDYRHA PPCPA\FVFLVETGVTLARMVLIS *PRDPPASASQSAGITGVSHCAPSRH SLS |
| 4605 | 10102 | A | 4904 | 3 | 364 | HEETAYDINILS**TQTFNMARLE*N CCNTIKSISEK/PTANSIR*AKKQEGF FQISGIRQGCLLSSFLFILEVLARGN R*DKN/GIQIGKKKVELSLFSETMRF NIWKRLWKPHITTRANK |
| 4606 | 10103 | A | 4905 | 50 | 394 | LSYSWHSIHLMLKIISWHFDGQFSA LVIL*LSVAVDTADYSHFLETASLL DFEFTVLSWFSSYL/TDMFLFTLVFS LAPFSIQLLNIGISQGSVLSPLLYAS ASGYMSLNIMYRH |
| 4607 | 10104 | A | 4906 | 49 | 366 | SGSSLAAVFWGPKGPAQAP/GPWAP WASPSGPDLPRLHPADPQRQLST VPLPLSRPPALSLIAPMALSHSCSNIP P*TPPPASLRPELTPARS/PPTR*SHS PPP |
| 4608 | 10105 | A | 4907 | 119 | 246 | FCFHHLNLPFLIF/NVCLCV*QSHS VTQAGEQWRNLGSLQPPPPRFKPF CLSLPSS*DYRHAPPQLADFCISSRD GVSPCWPGWSQTPDLR |
| 4609 | 10106 | A | 4908 | 1 | 280 | ESRSVAQAGVLWRDLCSLQPPPPVF K*FSCLSLPSSWNYRCAPCPASFFV FLVEAQGFTMLARLVLS*PQ/CDPP TSASQSAGITGMSHCTWP |
| 4610 | 10107 | A | 4909 | 406 | 661 | SQTPDLR*SAHLSLPKCWDYRR/AA TAPGQNISFKLPNPWEKAKHLMKS T*RLKHFTNFALFV*NCIDD/WMEF ALVAQAGMQWHDLGSLQPLPPQFK WFSCAPASPKCWDYRREPPCPANFF FFLYF**RLGFTMLARVVSNS*PQ/C DPPTSASQSAGITGMSHCAWPPFFF LFFSFFFETGSHCVAQAGLK/PLKLK RSSCLGLRKCWDYRREPLRLAPSW TFRM |
| 4611 | 10108 | A | 4910 | 3 | 459 | ELRDGEKVLDLCAAPGGKLIALLQC ACPGYLHCNEYDSLRLRWLRQTLE SFIPQPLINVIKVSELDGRKMGDAQP EMFDKVLVDAPCSNDRSWLFSSDS QKAS/W*DKSKEEFAFFYRLGC*GL QLRPLRPGGILVYSTCTLSKAENPR CDQ |
| 4612 | 10109 | A | 4911 | 1 | 95 | TPKVHASWQK/MAD*SGQCPVLQIP |

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|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | LSSLMMQ |
| 4613 | 10110 | A | 4912 | 253 | 1531 | SWKLAEKVWEAQLPGFPSPQC RCGRGQSRQVRCVGNNGDEVSEQ ECASSPPQPPSREACDMGPCTTAWF HSDWSSKCSAECGTGIQRRSVVCLG SGAALGPGQGEAGAGTGQSCPTGS RPPDMRACSLGPCERTWRWYTGP WGECSSECCSGTQRRDIICVSKLGT EFNVTSPSNCSHLPRPPALQPCQGQ ACQDRWFSTPWSPCSRSCQGGTQT REVQ/CA*APTRPSAPDALLNCGPPG SAPVNSQPC/MPAP**SMARDSSSTF APWVGTGPGFCVLPLLTQPPVCRSL RTCPGSGLPRIPPERGPGHLHGFLCH HRSPIGLGPLWNPLGSSSLFPLGQQ GMSSR*TEGVGKVNGTQSDFSGT GQAHVGGCDGVCCTYCLRCCFWG LHGICVWSNVYHFSKRRLHRTLEG TRPVFLEDFS |
| 4614 | 10111 | A | 4913 | 131 | 355 | STADTLP**TPKLSPQLMDTILPSQS VAMFHT*DHSAPTGTGAPPHHTPS RPLNTRGPTEEFSPRPPPQHRPSSC |
| 4615 | 10112 | A | 4914 | 3 | 420 | QQPPTRLD*GPKQLMPHSPHNPHIT* NPAVLSLPPQTKLLGPPVVRGPLLIR *SPQLLPACPL*RSTRPGTLKPKAT PA\PPPTTVHKPVASLRSHLRADGPG APPHTTSPRPLNTRGPTEEFSPRPPP QHRPSPPTK |
| 4616 | 10113 | A | 4915 | 11 | 375 | |
| 4617 | 10114 | A | 4916 | 3 | 260 | |
| 4618 | 10115 | A | 4917 | 3 | 208 | |
| 4619 | 10116 | A | 4918 | 1 | 422 | |
| 4620 | 10117 | A | 4919 | 127 | 4348 | GASISDIQTETTEEDSVLLMHTLLAA TKDSLAMDPPVVRNRPKSKTKKAPI KTITKAAPAAPPVPAANEIATNPKPI TWQALNLPVITQISQALPTTEVTNT QASSVTAQPKKANKMKRVTA QGSQSPTGHEGGTIQLKSPLQVLKL PVISQNIHAPIANESASSQALITSIKP KKASKAKKAANKAIASATEVSLAA TATHTATTQGGITNETASIHTTAASI RTKKASKARKTIKVINTEHIEA LNVTDAAATRQIEASVVAIRPKKSKG KKAASRGPNVSEISEAPLATQIVTN QALAATLRVKRGSARKAATKARA TESQTPNADQGAQAKIASAQTNVS ALETQVAAAVQALADDYLAQLSLE PTTRTRGKRNRKSKHLNGDERSGS NYRRIPWGRRPAPPRDVAILQERAN KLVKYLKVKDQTKIPKRSMDLRDV IQEYDEYFPEIERASYTLEKMFRVN LKEIDKQSSLEMLISTQESSAGILGTT KDTPKLGLLMVILSVIFMNGNKASE AVIWEVLRKLGLRPGVRHSLFGEV RKLITDEFVKQKYLEYKRVNPSRPP EYEFFWGLRSYHETSKMKVLKFAC RVQKKDPKDWAVQYREAVEMEVO AAAVAVAEAEARAEARAQMIGEE |

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|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | AVAGPWNWDDMDIDCLTREELGD DAQAWSRFSFEIARAQENADAST NVNFSRGASTRAGFSDGASISFNGA PSSSGGFSGGPGITFGVAPSTSASF NTASISFGGTLSTSSSFSSAASISFGC AHSTSTSFSEASISFGGMPCTSASF GGVSSFSGPLSTSATFSGGASSGFG GTLSTTAGFSGVLSTSTSFSGAPTT TVFSSALSTSTGFGGILSTSVCFGG PSSSGSFGGTLSTSICFGGSPCTSTG GGTLSTSVFSGSSSTSANFGGTLST SICFDGSPSTGAGFGGALNTSASF VLNTSTGFGGAMSTSADFGGTLST VCFGGSPGTSVSFGSALNTNAGYG GAVSTNTDFGGTLSTSVCFGGSPST SAGFGGALNTNASFGCAVSTSASF GAVSTSACFSGAPITNPGFGGAFST AGFGGALSTAADFGGTPSNSIGFGA APSTSVSFGGAHGTSLCFGGAPST LCFGSASNTNLCFGGPPSTSACFSG ATSPSFCDGPSTSTGFSFGNGLSTNA GFGGGLNTSAGFGGGLGTSAGFSG GLSTSSGFDGGLGTSAGFGGGPGTS TGFGGGLGTSAGFSGGLGTSAGFG GGLVTSDGFGGGLGTNASFGSTLGT SAGFSGGLSTSDGFGSRPNASFDRG LSTHGFSGSNTSTGFTGEPSTSTGF SSGPSSIVGFSGGPSTGVGFCSGPST SGFSGGPSTGAGFGGGPNTGAGFG GGPSTSAGFGSGAA\SLGACGFSYG |
| 4621 | 10118 | A | 4920 | 3 | 1380 | NMLGKYL*VKDQTKIPKRSHMLR DVIQEYDEYFPKIIERASYTLEKKFR VNLKEIDKHSSSYILISTQESSAGILG TTKDTPKLGLLMVILSVIFMNGNKA SEAVIWEVLRKLGL/RPGV*LGSLSA CCPCCPLAREDPRIASVWWSGGT GWGAGLGRGPRVLTCDVDDGQMV KLSAVSLLNVLCF*A*MLDRPSRIP DKEGIWVLNCLLLVAMCSLLSSLH* DCPMC*ERSPSMLGKWPLALNLGQ FLICGSWGLIFPNCQG*GIHSFGGSE GKLITDEFVKQKYL\EYKRVPNRSP P\EY\EFFWGLALPTTETSKM\KVLK FACRVQKKDPKDWAVQYREAVEM EVQAAAVAVAEAEARAEWFQHQH WLYLANPAPSNGASSSGPKFYCW PAVDPSTGVGFCSGPKHQVASSGGP STGAGFGGGP\NTGAGFGGGPEHQ WLWQVEPPVLPVAF |
| 4622 | 10119 | A | 4921 | 1 | 412 | TRMGLPDASRRRTCRMDPEGWQE AMSSA*GRITLQRLSTGPEGQGGRE KVGPEGGSNPQQPKAAGVLSKHL PGAPAQPPQRPPSSPPLAGPLTERV EKVCDFLDAAGDYLN/GTPG*PSPG ESPAAQDPPVPPWPP |
| 4623 | 10120 | A | 4922 | 117 | 295 | |
| 4624 | 10121 | A | 4923 | 1 | 3564 | |
| 4625 | 10122 | A | 4924 | 1 | 355 | LPGIEVLWQGPVVSKVIPVESIEEV |

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|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | CKSIKRAPVIWDTIHVN/DF*SALTP YQIVTTKFYFRIKKIVHWGPFPHSSQ KILSICEKYQWLSVPLTHNLTKFLSII VNYSRYHCKIPQLV |
| 4626 | 10123 | A | 4925 | 3 | 3145 | AAAEGELGAWRGNSGRPKIIGRAA EAENEDRTLGRLLPGNERSQPRSP MLLAPQLKAEAAADKGLAPVPPPF SSGHSGPCEREGERGQRGRGRSRRG AHLELKPSPLRAGAPTDRGRGGP AEVAAAGGRRMVQKESQATLEERE SELSSNPAASAGASLEPPAAPAPGE DNPAGAGGA AVAGAAGGARRFLC GVVEGFYGRPWVMEQRKELFRRLQ KWELNTYLYAPKDDYKHRMFWRE MYSVEEAQMLTLISAAREYEIEFIY AISPGLDITFSNPKEVSTLKRKLDQV SQFGCRSFALLFDDIDHNMCAADK EVFSSFAHAQVSITNEIYQYLGE PET FLFCPTEYCGTFCYPNVSQSPYLRT VGEKLLPGIEVLWTGPKVVSKEIPV ESIEEVSKIIRAPVIWDNIHANDYD QKRLFLGPYKGRSTELIPRLKGVL NPNCEFEANYVAIHTLATWYKSNM NG\VRKDVVMTDSEDSTVSIQIKLE NEGSDEDIETDVL YSPQMALKLALT EWLQEFVPHQYSSRQVAHSGAKA SVVDGTPLVAAPSLNATTVVTTVY QEPIMSQGAALSGETTLTKEEEKK QPDEEPMMDMVVEKQEETHKNDN QILSEIVEAKMAEELKPMDDKESI AESKSPMSMQEDCISDIAPMQTDE QTNKEQFVPGPNEKPLYTAEPVTLE DLQLLADLFYLPYEHGPKGAQMLR EFQWLRANSSVSVNCKGKDSEKI EEWRSRAAKFEEMCGLVMGMFTR LSNCANRTILYDMYSYVWDIKSIMS MVKS FVQWLGRSHSSAQFLIGDQ EPWAFRGGLAGEFQRLPIDGANDL FFQPPPLTPTSKVYTIRPYFPKDEAS VYKICREMYDDGVGLPFQSQPDIG DKLVGGLLSLSDYCFVLEDEDGIC GYALGTVDVTPFIKKCKISWIPFMQ EKYTKPNGDKELSEA EKIMLSFHEE QEVLPETFLANFP SLIKMDIHKKVT DPSVAKSMMACLLSSLKANGSRGA FCEVRPDDKRILEFY SKLGC FEIAK MEGF PKDVVILGRSL |
| 4627 | 10124 | A | 4926 | 3 | 251 | HERHELQMLVDAPCSDLAQELROS CATVQRLQHTLQQVLD/Q/REEVRQ SKQLLQLYLLALYNEVSLLS*QDIF NVALDVCMCRS |
| 4628 | 10125 | A | 4927 | 1 | 408 | GTSLNSLSKTKAKDLFIGDVIHNAG PHRDKKLKYYIPEVVYSGLYPPYAG GG\GLYSGHLALRLNHIADSVQF*P R*DPYTVR*LLKPSSAGYDPTFVLLI GTDGIYTYTPSSCENGLGSCEEPHL MSFRSYFHG |
| 4629 | 10126 | A | 4928 | 187 | 378 | LCQKTMSLFTHSFCFSVGRNMEGV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LMDVDCESVYPIV*ASN*GLASAEV GGSFEPRSLRPAWAT |
| 4630 | 10127 | A | 4929 | 26 | 121 | PDRTMGG\REQRQSPGAQRTFFQLL LSFFVES |
| 4631 | 10128 | A | 4930 | 3 | 867 | |
| 4632 | 10129 | A | 4931 | 1 | 558 | EVRVKCVKALKGGLYGIPLDTACL KLFTGRFKDWMVSMIMDREYSVA VEAVRLLILILKINMEGLVMDVDCE SVYPIV*ASI*GLASAVGEFLYWKL FYPECEIRTMGGREQRQSPGAQRTF FQLLL\SFFVESKSHFVTQGGSGQF SAHRNLCPLPGSGNFHVSASRVAGIA GAPPHTWLIYVFFS |
| 4633 | 10130 | B | 4932 | 1 | 1617 | MKNGVQWAEAGHDYVLDLVSDL ELLRDFPRQKSYFIVGTEGPAASRG GPKVVFGNSWDSDEDMSTRPQPQE HMPKVLDSGYSNHDGTNGETE AQRGTATHQGQPTMAAVSESDSLG EPAVPHKGLDCYLDLFDPLVLSYGD ADLEKPTAIAYRMKGGGQPGGGSS SGTEDTPRRPPEPKPIGLDASTLAL QQAFIHKQAVLLAREMTLQATALQ QQPLSAAALRSLPAEKPPAPEAQPTS VGTGPPAKPVLLRATPKPLRPAPLA KAPRIPIKPVAAPVLAQDQASPETSL HRDAATVTQMHLTGQGRLLSLLD DSSLHLWEIVHHNGCAHLEALSFG LPSRPGFDGASAPLSLTRVTVLLV AAGDIAALGTEGSSVFFLDVTTTL LEGQTLAPGEVLRSPDDYRCGKA LGPVESLQGHLDPTKILIGYSRGLL VIWNQASQCVDHIFLGNQQLSLC WGRDSSTVSSHSDGSYAVWSVDA GSFPTLQPTVATTPYGRACTPVAHD HIDELVRGAVFSEKHFCIEDL* |
| 4634 | 10131 | A | 4933 | 1 | 811 | HASAGAGCWHLPGIIEGAAQKGGR GRQVIAVARTADVIIMMLDATKGE VQRLLEKELESVGIRLNKHKPNIFY KPKKGGGIFNSTVTLTQCSEKLVO LILHEYKIFNAEVLFREDCSPDEFID VIVG\NRVYMPCLYVYNKIDQISM EVDRL\ARKPNSVGSSSCGMKLNLA DYLL\EMLW\EYL\ALTICILHQGRR RDRRARFSQDAIILRKGASVEHVCH RIHR\SLASQFQVTPWVWGAPAPSY S\PAQAGGALTH\TMEHEDVIQIVKK |
| 4635 | 10132 | A | 4934 | 1 | 431 | QRFPAAFGPGARRDAPPHSPPAEC RAHAATWRLKPRPHRPHSLTAPLP VHWAGTTEPLSPRPATGTESARRC ISGDTQSFLRLARPCRQPGPS*DRC RPGVVSCLDREKNAGHWLSMAFS LLWVLATQHCLHPEESLTM |
| 4636 | 10133 | A | 4935 | 56 | 252 | GAQERGCPREKHGNAELAEGVLIL RGRGKPPSASLAGRE*I*SRGPEWK VTVNQTAKAKERTGP |
| 4637 | 10134 | A | 4936 | 81 | 896 | CGLVTPACLDPWVGIAPLPDTLIVL RGGGSALLPAPIPPVTLEEKQTLTRL LAARGATIQELNTIRKALSQNGGG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LAQAAYPAQVVSLILSDVAGDPVE VIASGPTVASSHNVDCLHILNRYG LRAALPRSVKTVLSRADSDPHGPHT CGHVLNVIIGSNVLALAEAPAAGRG TG\YQAVVLSAAMQGWGTPAAHR DDRYQCHGHPPLVPAASVMA*VTF WEFRGGLQGQGQMAEQARLADGG FPLPLRMRTSPSASSAFPCFSLGQPL S |
| 4638 | 10135 | A | 4937 | 100 | 332 | NKPQPQLLYRIKLTSTPFHPIQKVGL RQMIDLNIPPRIKLLLENIK*YLSDL GV\TK*KLTGFNFKIKHFCSPSSC |
| 4639 | 10136 | A | 4938 | 692 | 900 | NKLLWLGAVTPACNPSTLGG*GGQI MRSGVRDQPVQHGE\TWSLLKIQKL AGHGWPAPGSPSCLAGLRQE |
| 4640 | 10137 | A | 4939 | 87 | 322 | ARLVQNTGAQLKEVQYKLFQGLF FE*/QSHSVAQAGYSAVIIAHCNLSL LGSSDPFFSAS*VAGTTGMCQHAW LIFDR |
| 4641 | 10138 | A | 4940 | 91 | 356 | GHAFLFGGYSSSHWPSTYPPHAPV PPPPPSPPYPSLPPFHSPLPIKPFPLPP /SPSPSPSL*SPPTPPPTLLIPSPSPPP ASPPLQ |
| 4642 | 10139 | A | 4941 | 2 | 332 | CGGPPGSPDTRGGSLIPQGV*AA/GP MEQVPLVAPSSAIPA VPGSLSGTPSH QPVLGTHTPSCPGLTYIPPESEL DCPAPGRQRPCPGQTPLPTPCPPSFI FSKQPR |
| 4643 | 10140 | A | 4942 | 637 | 1560 | VWQLDKSMRAAQPWAPAGGAAGS EWAGLKR\RLGWSSFSFAAAQSPL ELLGHPQSPWPSEAPWKACQVSF QGT/RVAASYHNAQHGTERQHSSC *GLGS*/CNSPTWARLSTHCPQ/HSR NTPRTQHCPHYPPRGLAKRWLCGE GPNPYSHPLREGPLRRRVGRGMGK EVHLFYRAWHSGIHFPS/TPSRTSHQ DSPHLEN*TSPLIDLTPTWAPPMCK RIL*KCTCNSLPQKPSMALQCI*NEI NKTSTTSPT\CLAPH*APATLACSPF LQPAELLISGTLHVIFHPPRTLFPKS RTGSFLSSPQVSV |
| 4644 | 10141 | A | 4943 | 2 | 335 | ALHPTLTLDLYFTIYTKIHST*IVDL DVKPKTLKLEESIR/VKLCDLRLSK ISWILKAQSIEEQDTDWDLKT*NNY SSNGTVKRIKRQVED\WHKVFARRI SDTGLVSRISC |
| 4645 | 10142 | A | 4944 | 2 | 345 | FFFFFFETESRSVAQAGVQWRDLSS LQAPPPG\SRHSLASAS*VAGTTGVC HHARLIFVFLVETGFHHVSQDGLN LLTS*SAGLGLPKCWDSEKLFFFFG DKSFRFCCPGWSTMV |
| 4646 | 10143 | A | 4945 | 178 | 388 | RREPLHPANLLLFFFFFFEMESPSVA QAGVQWRDLSSLQAPPPGSCHSPT SLS*VAGRLRNKNCLNPDAW |
| 4647 | 10144 | A | 4946 | 546 | 850 | FSVLFFYFESESCSVLQAGVQWRDL GSLQPPPPGSSHSPTSAS*VAGTTGT CHHTQLIFIFLVETGFHHIGQASLKL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LTS*FAHLGLPKFWDYRCEPPHPA |
| 4648 | 10145 | A | 4947 | 169 | 358 | GNGFLFCTQVEVQGAFL*YLNLLAP GVK\LFSLTLLKPWDSGTFPTFSFN FFIYLAKEGFGNG |
| 4649 | 10146 | A | 4948 | 1 | 145 | ANSAAMP\SLGCSASSGLVFWPQGL YLLGVVS\VSPLPPTPTTVTFPEQI*LL SPQVSSSPVSEGSSQHHPA*SLRPFHV PRS/SPVSSLQPFAPAKSPGPSATCAF SAPSL\LLTLLASGDSSFWGPGPIQM SAGGSIVMCS*GLVFWPQGLYLLG VVS\VSPLPPTPTTVTFPEQI |
| 4650 | 10147 | A | 4949 | 1 | 295 | GTSSRLRLHRTDELTA\PSIYRSTKST LDGSLAANEREPFTLGKKPPFSDKP SIPAGRSLGEHLPKIQKPPLPPTTER HDWSRRLAGKKPPVPKHGWVP*/R EDDNE*DELTA\PSIYRSTKSTLDGSL AANEREPFTLGKKPPFSDKPSIPAGR SLGEHLPKIQKPPLPPTTERHDWSR RLAGKKPPVPKHGWVP |
| 4651 | 10148 | A | 4950 | 119 | 1036 | HASCLKTQALQECSVG\GGGLPVVS PAGPPRCFCPALPAAALALQGTFFPA TGG*A\WGLSSPDWTFSTKKLVMS ARSHGEGGAQGPATLTGPPGEGAL RASQ/PGTAGSELRHRARGPAQICST RTR\PA\WWT*SLPPPGHSRAVGF RCGPASP\GVPVNA\VALPPSTCGE ESRLPQEEGGIHMA/PGTPLCSGDCI CCED*PQSRSGQFGADSL*RAKGGT LPSGPSARRRSPL*ASESASCCRRAS SIGPPAAQGERADSRALGTAPPGE LALRPTPGGIGTPPAGGSEDISREVD PAKRHGLGA |
| 4652 | 10149 | A | 4951 | 2 | 1262 | GSAAGSTYEPSSMRLEALQVLTLLA RGYFSMTQAYLMELGEVICKCMGE ADPSIQLHGAKLLEELGTGLIQQYK PDSTAAPDQRAPVFLVVMFWTMM LNGPFSRFSADSEHPTLQASACDAL SSILPEAF\SNLPNDRQMLCITVLLGL NDSKNRLVKAATSRA\GVYVLFPC LRQDVIFVADAANAILMSLEDKSLN VRAKAAWSLGNLTDTLIVNMETPD PSFQEEFSGLLLLKMLRSAIEASKDK DKLSTISIYYFNGQENRKEKNWNER EYKLEIPYELCTEVD\AINKWTAPWT SQAYNALTSVVTSCKNFKVRIRSAA ALSVPKGREYGSVDQYARIWNAL VTA\AQKSEDTIDFLEFNTVSSLRTQ ICQ\ALIHLLKLG/RSASDLP\MKET LELSGNMVQSYILQSLKRSRIGR |
| 4653 | 10150 | A | 4952 | 52 | 730 | KSACDALSSILPEAFRNLNDRQML CITVLLGLNDSKNRLVKAATSRA\L GVYVLFPCLRQDVIFVADAANAMV MSLEDKSLN\RAKAAWSLGNLTD LIVNMETPDPSFQGRVLWSPAENG YDQALEASKDKDKVKRHA\VRAL GNLLHFLQPSHI/GKTPHLQKFI*GSL SRALN\LLF*QKLAMKVRWNACYA MGNVFKNPALPLGTAPWTSQAYNA |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | LTSVVTS |
| 4654 | 10151 | A | 4953 | 3 | 363 | HELEFEIKNTIPFILAP/N/NIKYLGIT/ LTKYVLYLN/DLYAENYKTLMK*IR DLNGDPLSCKVKNLIKINKYMK\EIL CSRIGKDSNIV*VSLLPQL\ACRLNAI PIKIPANHFVEVN*LILKFI |
| 4655 | 10152 | A | 4954 | 179 | 438 | ENIMSKTSTENCTKQCHFVHVN*Y SIFFFFLRQSL/DSVTQAGVQWRHLG SLQAPPPGFPTFSRFSLPSSWDYRCP PTSLANFFCILVETGF\TVLARMVSIS *PRAPPASAS*SARCKLHLPGSHRSP ASASPVAGTTGARQQA\WLIFFVF |
| 4656 | 10153 | A | 4955 | 1 | 264 | QFPKPSPRGP/TPTKSLFHILSPPNQ*I SPPP*QLPPSLYQIPPTIRLSPLPLAES PSPLSVGLGGPLGWVGQLLCLSPFG GPKHVEV |
| 4657 | 10154 | A | 4956 | 3 | 369 | HERHELVKEFNKVSGYKINAHKSV ALLYTN/DDQAENQIKSSTPFTIAAK SVK/YLGIYLTKEVKDLYKENYKTL LKEIVDNTNKRKHIP*P*MGRINIVK MTTLPKAIYKFNSMPIKISPSHFG |
| 4658 | 10155 | A | 4957 | 2 | 338 | GCWDN*ISTCKRMKLDCSMLHMK INSM/WIKDVNIKSSSYEK\NIGVNL DNVLGNNGFINMMPKAQASKEKIIN WDSAKLK/IRK*RQLTEWEKLCANP IYSHLIPVLCYLYLV |
| 4659 | 10156 | A | 4958 | 42 | 447 | IELVTVLQFYRAFYLFERYAGFLFY YYFLFFVEIRFHYIFQAGLS/ELLGSS DPPTSGLPKCWDYRR/DHRTWPDM QDFLMFHIFPKLFSFPDMCFLASE*P SANTWLLL\VVQSSFSLLSHTYHPPG KASTLWFS |
| 4660 | 10157 | A | 4959 | 377 | 1220 | FRKVVP LAESHPAVPG\GKVRTSR PKSPRALPT*/PGLFNP GCQRETPSP LG/PPGQHP/VPGQLNSKRKQIPHNE LVEQTLRSGLTSAQPAHPTGGYSCS KL R P G P L P N P N G L C R C S D G R I P G D R EPLALSRT*IHLRACTGPDAAAQVL PGLLPCPHLPHLSGMFDSWLAPP LPDPCQRPTPPQAPSSEANNQRSQA PGCGPHSLRDSSELQGQCPGAQAF RGSGLFQLTQLTGPLHGTR*RLSPK NSQALKPHM*AVGRILHWPPAARP GNSGRYPDD |
| 4661 | 10158 | A | 4960 | 3 | 353 | HEVPAKGPRPHLTDCPTTQDFLPGF SPRPASGPPPSLSLRLFQQPG*TVW SPGPPCPVVPDCTSASGQVPFLPPAF RFKNVF*PSRPSGTRGGP/PP*VCTS R/PLP*TSEPQPQPG |
| 4662 | 10159 | A | 4961 | 301 | 343 | TRMAHFWS*STKPSPMGPIQWSHM PGAFSE/SSSCHSHSAFLPPYFSGPS NRPPIRALCRNLPLPLPNKPRAPSAA DEDNSLNVEWYVPYITRQA*AALI KINQDGTFLVRDSSKK |
| 4663 | 10160 | A | 4962 | 2 | 319 | ARGPGPSGKSGARSGLGNTPRRG AGLGRVPWSLCY*EGVESGRPEGA GPGTSPGVGFIGAYHGRGVTKVGG |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LPG/GQACGVWSDPKSPGEPVEPIPG GSWPPQREP |
| 4664 | 10161 | C | 4963 | 109 | 372 | MQAWINIRKSVYVIHCVNKIKXXX XXXXXXXXXXXXXXXXXXXXXXXXX XKLRLRLPQPVKGHLQKPMADIPN GKKLKASTTKIMNKTSS* |
| 4665 | 10162 | A | 4964 | 3 | 990 | RTLRECYK/HI*ANELNNLDEMSKL KDA/TLLQLTQEEIETLKYNNEIE*I M/NKLPTKKSPGPHGFTG*FYQMFO EEFTPILSRL**KIKEEGTVPNLLYEV /SIIMIPKPKDKITRPVSLMIIGAKIFK QNI*HTQVYAHIHRIYVYHDHNGFM QAWFNI*KSVYVIHCVNRIKDKNH MIVSIGA/EKAFDKIQHPFMVKTCT QERTF/FILLKGIY/NKPMADIPNGKK LKA\PLRSGTRRVPDFRWKQ/CP LPLLFSIVLEVLARAVRQEKEIKGM QIRKVVKLFTDGMILYVEKSKESTI KTSKLINRFNKGSEYKANIKK*VVF L*SSNQQT |
| 4666 | 10163 | A | 4965 | 3 | 314 | HENDSNPETDNRQEGPSQENIGRVS D/MAFVPSAWTASGGVAWGNPGES GSRTGGVRAETLAPRLQV*PAHLIG HPRSNRGQGRPPWKAGKLKGCQEV LFRFAAF |
| 4667 | 10164 | A | 4966 | 2 | 329 | ARGEERKAFRCIYDCVIHE/CEECR KAFRCIYDCVIHERIHNGEKLIEC*E CETSLSSNSVLIQHQRHTAEKPYEC NECGKAFHRTSVFLQHQRFHTGEQ LYKCNECWKTFRCSSRFIVHQRIHN G*KPYECNECGKAFHRTSVFLQHQ RFHTGEQLYKCNECWKTFRCSSRFI VHQRIHNG |
| 4668 | 10165 | A | 4967 | 61 | 533 | WTEPVRHPDIHSQKREPSLMPPTVT GPGTTNMLFQPHRGPEKSRVPLHSS SSSSSSSSSSSSSSSPKTF/FGAPK/LP PSAPTSPDLAQAS*GLKSWKPWSGE RRFGCSKORRALPTAS*FQGQSHAA PETPSYVGQDQSPSPGG*RPSTSPEG DSCFP |
| 4669 | 10166 | A | 4968 | 22 | 482 | GKGP GPPGGVCKSTLPPAKPWRGPP HLPLPLGL*EKALPRALGQWEGRES FWDQPGKLPLQN/PPRSLGVAMGT QAVEIPDGRPLDLSPTPAHSFSFLAL KPLLGEARVHFRASAWPLPTRAWT LDLPQLGWGFWDCLMALESRSSG ESPSLL |
| 4670 | 10167 | A | 4969 | 146 | 1299 | GAPGPWPTGTTWLPGAAGAVPDGP FLLPSSAALSRTAS*FSQPPPVPAL TVPWPRCGC*TSCPAVPQSP/GLPR TLVPACRGLPLSSVPSSPASRPKLPL HSPSSWSIPPEGSWGPLPTTLPLPWG L/PRLQSREHKPALSAATWQGLVVD PSPHPLLAFLPLSSAQVHF*PGLRSW VGPFGLRKQP*HTGLSSLTTGCCP AWLTSWPRISQSERKAHP*CLPL*Q ALSPPISYFNLTVDLRNRDYHSASS SSSSSSSSSSSSSSSRRLSWSPKHHPL |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | LPSFILSWPQGIPRGLKNPGKTRGGL GWWKKGFLANWLSKKPRRKKGPS FPPLVL*FQGPRALPVPRNPHPKLG ASSQSPSPWWGKRPKPKSPGNGTS WLPPK |
| 4671 | 10168 | A | 4970 | 298 | 954 | QVQGHEDFLGARNTTLCSSFSCPGP GILGAEILETVGWCEKVCMLRAEK GSPHCFVIPGPEPCSPRNPNLAGAGP ESKPWWVEAKQKP*SGLLLPLVVFS VPRS*NCEPGVGERSGRGVHLGFLQP GYP*PHQGFWEILQGQLSRLFPNSSL PPH/MPLKPQQKSHSSHKQKGRGKN EEKTLCQVICRQRMGLVP*QHPTPC GAPSPHPHPQTPPKQVPYL |
| 4672 | 10169 | A | 4971 | 4 | 410 | PIERPHELKHRLPHVQKLVEDVGDG VIPAALEEGQAGWSHGFLVFLVEIK SAEGP/PGPADSRVRGVRPQRSQSA GPA*RAGRQDGVCRSLGQGRGGGR ATSLVLHPPGYPGCWFSVGVPSLPQ YTGIRSSSPRTRG |
| 4673 | 10170 | A | 4972 | 148 | 268 | LQPR*PLTCAPPPCPVQTQTHPISVS QTLLGLEFCCSLSL |
| 4674 | 10171 | A | 4973 | 397 | 1449 | RSHPSGTGRRTSRLESWFLGVSCKK SKVREGPLGPA**AG*RGVRPQRSQ SAGPA*RAGKRQDGG/SPEPRAGVG GEVGTQSP/GPSGASGYPGMLVSKP VGGTSASWLPAGCPIPS*LS*QRSQG SPSSCLIGHLLALWAAFGLVTSPLP QYTGIRSSSPTA*ATVQGDGSHKGG TGGTGLGRGRNTQPDACGRGHR SPTR/RPHGNPNGNTGCAEGGQARS LLPKLAPKLPGWVPSVPVAVGPGD FGWRQAQYQSSLWDLSSPRNTLGR SATSAGPAPPALLGAGSGRSSGTSP AAPGCSSRCHCWASAPAGVSGGPG\ GRGAEAPPSPTLAQRGSPPG\AAIFP PACGIPP |
| 4675 | 10172 | A | 4974 | 2 | 637 | ARAKEV*DLYTERTK/PLLKEIKEDR NKWKHTSCLWIARLNIVKMSILCKL VHRLSAITIKI/PCWLCLAEIDKLILK/ FIWKFK/RSRVAKTVLKKKRVRL TLNFKTYFRVTVIKIEWLWQKD KYIDQWNRIKSLEINSYICGLLIFYK SAKTIS*ENSVSWYLDNWIPTCERM KLAPYIYKKIK\WIKDLNIRAITVKL IKENIGPGARL |
| 4676 | 10173 | A | 4975 | 254 | 590 | KARYILPDLMIGLDFFFFLGETKFP FAPQPGGHQGDG* LTPPRSGNYRLGPPPLNFFVF*KKR GGPHVGQTGFELLT*KDPPPLASQR AEITGGTHHA |
| 4677 | 10174 | A | 4976 | 103 | 378 | CFLYSICRGADTQRRFKLSDSLINST ECLHVHCRGLEISLADCAYT*ILTK GNHNPLS*YTFMRN\AKQPVN*YHR CTETFSLTRMELLVSV |
| 4678 | 10175 | A | 4977 | 2 | 327 | RQCLALWPRLECSGVIIAHHSLHLL GSSDPPTSAS*VAGTTGMHHAQLI/ LFWVLIDTG*CYVAQTGLEPLNSGH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | PPTSASQSAGIIGLRHRAQPCVFQSS QKRGPELF |
| 4679 | 10176 | A | 4978 | 19 | 1009 | KTTQQQNLFFSSAHETFTNTDHL GHETSDFDMF*HIQVI*STFLYHNVIK LEVNSRKISGKCPNMWKLNTVLS NTKIINFLDNKQNETIKI/RAETNELE NR/RTEKIN*TKM*FFEMINTIDKSL AR*SRGKRHKLLISGMTNVVSHCVS LPTLFLFQSCFDYILTTLHFLINF/QN RFNNLYKMIRGY*QLYKN*FDKLH EMKNFL*/RY*LPILTQEEI/S/HLNSPI YILKIEIVVLNLPNTKTYW*TLKF/EE MIPIVHRLFQKQETLPNPFYEVSITPI PKI/QD/D*TKENFRPISLVDKIPSK NLSNYICSLNASHPQRSTDPNLQ NF |
| 4680 | 10177 | A | 4979 | 3 | 358 | STSNAYHSNSLHQQIKEKKNHTILSI DAEKAFYKIQEPLLAITL*NRNSGN/ FLNMLMTTY**PKVNVILIGNITIPY* YFAFLP*KLRTQSRSLSSLFIVLK NPANVTVISINIKRK |
| 4681 | 10178 | A | 4980 | 3 | 341 | FFETESNSVAQAGVQWHDLGSLQP PSPG\SSNSPASASRVAGITGACPNV QLISVGFLFFVFWFFFETESLSVAQA TGVQWVRSWAYCNLRLPGSGRFLC LCLPSSWGLQGV |
| 4682 | 10179 | A | 4981 | 658 | 1001 | LILSARPPKGEKGSFLLAEFSSYFHS GLFSSARSFFFFFFFETESHCVQA GVQWLDLGSLLQPPPG\SSNSPASAS QVAGTTGVCHHAQLIFVLLVETGF HHVGQAGLELLTS |
| 4683 | 10180 | A | 4982 | 53 | 394 | PQSGFWFIYFSKQGCFFVNILNIC SFVLFFFETESCSVAQAGVQWHDL GSLQPPPG\SSDSPASASRVAGITG ACHQTWLIFVFLVDMGFRHVGQAS LKLLTSGFKKWVT |
| 4684 | 10181 | A | 4983 | 66 | 516 | HFYQFFPHFSGRMDLWSSLLCHFF MTSQFVTFVLLYFIFVYILSV*LD F*MRKQT*LISG*ASI*YRYV*LQNL YVLKLYITPLSL*AHVLIYL/CYLKS ESHSVTQAGVQSHNLSSLPPRFK*FP CLSLPNG*DYRNVPPHPANFCIS |
| 4685 | 10182 | A | 4984 | 3 | 324 | HENRMKYEISINMWKLNNIFLNKL WVKEITSRLQKYFECSENKTTTYQK L*DAKIKMNQCQGYLWVFMALSA* ISKRKRLINYL SFYLSKLEK*EPTK PKASSRKVV |
| 4686 | 10183 | A | 4985 | 108 | 277 | ARVIRANFCIFGKDRVSPCCPG/W/ SPELPGLKRSPSLSPKCDWYP*AT APGQHPYS |
| 4687 | 10184 | A | 4986 | 29 | 454 | |
| 4688 | 10185 | A | 4987 | 116 | 424 | |
| 4689 | 10186 | A | 4988 | 1 | 1217 | PPTTCTPACQGLSGAAMKSLVLLC LAQLWGWSAPHGPGLIYRQPNCD DPETEEAALVAIDYINQNLPGYK HTLNQIDEVKVWPQQPSGELFEIEID TLETTCHVLDPTPVARCSVRQLKEH |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | AVEGDCDFQLLKLDGKFSVVYAKC D\SSQDSAEDVRKVCQDCPLLAPLN DTRVAHAEKAALAAFNQNGSN FQLEEISR\AQLVPL\PPSYV\EFTV SG\TDCVAK\EATEAAKCNLLAEKA IMAFVKATLK*ESLGGGRRLLQCTCT VF\QTQPCDLHSPNPEGANEAVPTP V\VDP\DAAPPSPPLG\APGLPP\AGSP PELPCFYWAAPP\G\HQLHR\AHY\D LR\HTFHGVWVFIGGHPSGRKCSHP PGKHGTVGSSLVFWCCCCLGPVVP SIVPG\RIRHFKVLG |
| 4690 | 10187 | A | 4989 | 1 | 443 | KKFVIPDFEFTGHVGRIFEDVKELT GGKVAA YIPQLAKSNPDLWGVSLC TVDGQRHSGHTKIPFCLQSCVKPL TYAISISTLG/DYVHKFVGKEPSGLR YNKLSLNEEGIPHNPMVNAGAI VVS SLIKMDCNKA EK FDFVLQHLNKK |
| 4691 | 10188 | A | 4990 | 3 | 217 | ATKRKKKMKDKDKA\KLEAMGTS KTNEEDKRRGLDKRTPDQAAFEKM QEKRD FSRHLDTLTEHYDIPKVHH |
| 4692 | 10189 | A | 4991 | 3 | 475 | AATESGMVAYYQVQKGPLKLKG VAKLGVT\K/RVRPEGPRDSVFIPLPK FLGTPGPDPPTRLLMFFSRKKKKK DKDKAK\LEAMGT\SKKNEEEKR RGL\DKRTPAQAAFEKMQEKRHME RILMKA\SKTHKQRVEDFNRLGTL \TEHYDIPKV\TWTK |
| 4693 | 10190 | A | 4992 | 783 | 5158 | PDKSGRRRDVEGGVCCFLSLLRNSR YLLSTHILERGKASLCHPGWNAL VPSPLTAASASWVQVILLPLSLPSG WDYSLHLEELTGESPTSERAFNYH PTTCLRRKILQDSEHTASTRGPMTL DRPGEGATMLKTFTVLLFCIRMSLG MTSIVMDPQPELWIESNYPQAPWE NITLWCRSPSRISSKFLLKDKTQMT WIRPSHKTFQVSFLIGALTESNAGL YRCCYWKETGWSKPSKVLELEAPG QLPKPIFWIQAETPALPGCNVNILCH GWLQDLVFMLFKEGYAEPVDYQV PTGTMAIFSIDNLTPEDGVYICRTH IQILPTLWSEPSNPLKLVVAGLYPK PTLTAHPGPIMAPGESLNLRCQGPY GMTFALMRVEDLEKSFYHKKTIKN EANFFFQSLKIQDTGHYLCFYDAS YRGSLLSDVLKIWVTDTFPKTWLL ARPSAVVQMGQNVSLRCRGPVDG VGLALYKKGEDKPLQFLDATSIDD NTSFFLNNVTYSDTGIYSCHYLLTW KTSIRMPSHNTVELMVVDKPPKPSL SAWPSTVFKLGAITLQCRVSHPV EFSLEWEERETFQRFVNGDFIISNV DGKGTGTYSYSYRVETHPNMWSHR SEPLKLMGPAGYLTWNYVLNEAIR LSLIMQLVALLLVWLWIRWKCRRL RIREAWLLGTAQGV TMLFIVTALLC CGLCNGVLIETEIVMPTPKPELWA ETNFPLAPWKNLTLWCRSPSGSTKE |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | FVLLKDG TGWIATRPASEQVRAAFP LGALTQSHTGSYHCHSWEEMAVSE PSEALELVGTDILPKPVISASPTIRGQ ELQLRCKGWL AGMGFALYKEGEQ EPVQQLGAVGREAFFTIQRMEDKD EGNYSCRTHTEKLPFKWSEPSEPLE LVIKEMYPKPFFKTWASPVVTPGAR VTFNCSTPHQHMSFILYKDGSEIASS DRSWASPGASAAHFLIISVGIGDGG NYSCRYYDFSIWSESPDPVELVVTE FYPKPTLLAQGPVVFP GKSVILRC QGTFQGMRFALLQEGAHVPLQFRS VSGNSADFLHTVGAEDSGNYSCIY YETTMSNRGSYLSMPLMIWVTDTF PKPWLF AEPSSV VPMGQNVTLWCR GPVHGVGYILHKEGEATSMQLWGS TSNDGAFPITNISGTSMGRYSCCYH PDWTSSIKIQPSNTLELLVTGLLPKP SLLAQPGPMVAPGENMTLQCQGEL PDSTFVLLKEGAQEPLEQQRPSGYR ADFWMPAVRGEDSGIYSCVYYLDS TPFAASNHS DSLEIWVTDKPPKPSLS AWPSTMFKLGKDITLQCRGPLPGVE FVLEHDGEEAPQQFSEDGDFVINNV EGKGIGNYSCSYRLQAYPDIWSEPS DPLELVGAAGPVAQECTVGNIVRSS LIVVVVVALGVVLAIEWKKWPRLR TRGSETDGRDQTIALEECNQE GEPG TPANSPSSTSQRISVELPVPI |
| 4694 | 10191 | A | 4993 | 1 | 369 | GTFQLPKPIFWIEAETPALPGCNVNI LCHGWLQDLVFM LFKEGYAKPVD YQVPTGVTMAIFSIDNLTPEDEGVYI CRTHIQMLPTLWSEPSNPLAKLVVA GGCGLWLLASGNCCPRYHGWS |
| 4695 | 10192 | A | 4994 | 183 | 429 | ISIKSMKLISDYKYCIYIYRYHRDVI RLGIIDIYSVLHPTSAQYTFSSLHGT LTTRDNILGHKT LNKFKRIEIRQYL FSDQ |
| 4696 | 10193 | A | 4995 | 2 | 270 | TSGCLQGSCCVTGPPGAVGRASRSR PSTRPPSRARPLGSPGCSARAQDAA DLPLPPPPPPCCSPSAGCRCSLGCF RRCPLRSSRRSRF |
| 4697 | 10194 | A | 4996 | 1 | 428 | NPCLSERQGCCEKLPLERSSTPQDS AGHPVT/HAHCSLSPVDLCPLLLAT HRISCWHCQDEVQGGTD/SADTGD LEALSLLAGHGD TDGHIILDVPDGA PYPQRTKAGIDHLHQKILKHEQITIE HEARDDNAPDYPKLANN |
| 4698 | 10195 | A | 4997 | 131 | 412 | RKWLKLLPCSFFSSKNIYAETFSPCV CIRVCIHVCVYTCVYTCVCIHVCSC PC/VGQASALKSVSLCQLHCILVLTP MLTLRFDKKFFTQDSHFI |
| 4699 | 10196 | A | 4998 | 2 | 175 | KFTWKHKGPRIARNILKRKIKVEGF TLPNFKTYKAAVTETVWYWHKD SGLDHFVLL |
| 4700 | 10197 | A | 4999 | 2 | 175 | KFTWNHKGPR IARNNLEKENKVEG FTLPNFKSYKAAVTETVWYWHK DSGLDHFVLL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4701 | 10198 | A | 5000 | 1 | 909 | MVLEVSVSDDRAVWRLWRAPIGES QQRSLGFWWSKVLPYSADNYFPFER QLLACYWALLETDRLTVGHQVTLQ PELPIMNWVLSDPSSHKVGHVHQH SIIKWKWYIRDQTRAGPEGTTTPVIT Q/WDAHEQSGLSGRDGGKQRFVLT GVDTYSGYWFAYPAHNASAKTSIY GFTECLIHCHGIPHSIASDQGTLFTA KEVWQWAHAHGIHWSYHIPHPHPIA AGLIEWWNGLLKSQQLQCQLGDNTL QGWGKDLQKAMYSLNQRLIYSTVS PISRIHGSRNQRVEVEVAPLTITLSD PLAKFFFLLP |
| 4702 | 10199 | A | 5001 | 1 | 1014 | |
| 4703 | 10200 | A | 5002 | 349 | 718 | AGPEGTTTAACP/I/CQQQRPILSLRY GTISWG/DQSATWWQVDYIRTLIS WKWQSASAKTTIHGLTKLIHHDIP HSIASD*GTCFMAKEVWQWYCFSH SQDSRVQESRGGIGSCTTHHPCSF PN |
| 4704 | 10201 | A | 5003 | 1 | 558 | |
| 4705 | 10202 | A | 5004 | 1 | 2205 | MGAVFEALWQYSPPELPAKASVMVQ EASKAIGQCQSSAAKLRRSGKESVT EPWARVLGALEMAARLYKVTS GH CHGIHTPSWRCLCFSTGGKERHAH DLPHVTAQSQGHQGGQKISRTALK EPTVHKVTASLSPVATSPQPMLP SDFPPLSEEINPMLPEATVIASPKAIA RQDNVDSPQEPPTPQFSSRPITRLK SQWAPRGPECVIGIDILSSWQNP HIG SLTGRVRAIMVGKAKWKPLELPLP RKIVNQKQYHILGGTVEISATIKDLK DTEAVTPTTSPFNSPIWPVQKTDGS WRMTVDYCKLNQVVTPIAAAVPD V/VSLLEQINTSPGTWFEWSPKKAL QQVQAAVQAALPFGPYDPADPMVL EVSVADRDALWLSLWNAAGESQRR PLGFWKALLSSADNYSPPFERQLLA SYWALVETERLTVGHQVTLRPELPI MNWVLSDPSSHKVSGAQQRSIIKLK WYIHDWVRAGPEGTTTSVITQWAH EQSGHGGRDGGHAWAQHGLPLT KADLATATARIHRSRNQGVKVEVA PLTITPSDPLAKFLLISATSTSLEVT VPEGEMLPPRDTTKIATFGTQTGFL ALQLADGLLWDLVIIPGKGKPSRDL VESPSYSTYEGIDGWDEPAPTAT KPPVMPAPALPPDTRSGSKAPTVP PYPQMEHHQVQLASNNNSNTEALGH LSPQSSWVQTPGQNSGAIPNHLGK DMISPPQMAPAGVKWESQKY |
| 4706 | 10203 | A | 5005 | 155 | 531 | GNLWSVDLRPGTPLRQNFRTIRQQ HSRFTKNHCSQTPLLIPRTGSGVD LSKLQQTCS*GSCLVCTIDLANAFFS IPVHKA/HQKQFAFSWQYTFVLP LTWLQPC*VPNLPAETNTEPSNGT |
| 4707 | 10204 | A | 5006 | 1 | 518 | MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VHKAQQKQFAFSWQQQYTFVLP QWYINSPALCHNLIRRDLCFSLPL DITLVHYIDDIMLIGSTIKWVVHSS/ DSIIKWKWYVHDWARAGPEGTTN GLAG*SGTCKKHEWKTGDKGIRGR G |
| 4708 | 10205 | A | 5007 | 1 | 2592 | MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAQLVLGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEKAQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLS DPSR HKVGHAQQHSIIKLKWIYICDQARA VPEGTC*LNKEVAQMP/MGTTRKW TAAALQSLSGISLKDSGEGKSSQWT ELQAVHLVVHFAWKEKWPGTWKK HDWKTGDNEIWGRGIWMDCSEWS KTVKIFVSHAHEPSGHGGRDGGYA WAQEHLSFTKADLATGIVECPICQ QQRPTLSPRYGTIPQGTFLTGIN YSIYGFAYPAHNASAKITIRGLTECL IH HHGIPHS/IVSD*GTHFTAKDVET RIHRPRNQGEVEVAPLTITRSDTL AKFLLPVPTTFRSANLEVLLLEGGT LPPGDPTTIPLNWKRLRPRGHFGLPL PLSQQAKKGVSVLAGVTDLDYQDE FSLLLHNRVTAAPFSLHSSFAILD NMIEKANKCHVEGVHDVSDPAQRR ECDRHTGSSCHLLRGPPQLQSQLVS GPRSPKSDSGESCLAWDPTFKA EVS PLAQGSPRNSVQEPSRGTGSPKSLG ALIALWPSWYLSSDPDPQGSNSRNL EISACQKYLSPAFGNSDYSTAEDFN SDYTLKSPENSIGYARLEKHRRLYG GDGGDGGGDDVRGGKRGDDASR KGVTERV |
| 4709 | 10206 | A | 5008 | 1 | 942 | MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAAVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFVLPQDYINSLA L*HNLIWRDLDFLLQDITLVHYI DDIMLIGSNDHKVGGAAQQHSIIKWK LYIHDQAQTGPEGTTTSVIAQWAHE QSGPGSRDGGYAWAQHGLPLTK ADLATTTAECPCVQQQRPTLSPRYG TIPSLPLTKALTLQLKKCSSGPMLM EFTGLAMFPIILKQLD |
| 4710 | 10207 | A | 5009 | 1 | 1795 | MRKCGKPQFKLGQTNKANSRIQEE LIHKSLSIEQEGEKPQVQSAFHRMW QPADSQCDIIDSADIWADPLVRHREI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ITGSGGINRRRTRGGRGRGGEEAAGG AENCGSREERERAGVGTAVTQLQN LNTIGIIGSRGGRGQVAANHQRQG GHSYCKGQKQNSNQNSVTHVEL WHWLNHSVPRSEIDRKPTTFLNL YKQKTSRDLWPFTRVTLHRGKRND QTFQGLLDTGSEMLIPEDTKHHCG PPVKVEAYGGQVINGVLAQIQLTV GPVSGSHTPVVIYPVPECIIGILSS WQNPHIGSLTSRKTDGSRMTVHY HKLNQMVTPIAAAIPDVVSLEQVN TSPGSWYAAIDLANAFFPIPVHKAH QKQFAFSWQGQYTFVLPQGETL VNFSLPQDITLFHYIDIMQIGSSDQ EVANTDLLPRKSTTPSG/LYGFWR QHIS/HLGLLTPIY*VTQKAA/SFEW GLEQEALQQVQATVQASLPLGVY DPADPMVIEM/SLDPSSHKVGCAQ QHSIIKWCRYVCDQA*ASPEGTS*L YCTSFIMEKEEVC/LSLEQTLTDMG LPILHAMLLWIHLWIHGLPYPSSWY STQQCL |
| 4711 | 10208 | A | 5010 | 3 | 169 | DFQPFTRVTVHWGKGNQDQTFRGLL DTGSELTLPIDPKHHYGPVKVG/ AYGAQLL |
| 4712 | 10209 | A | 5011 | 1 | 562 | |
| 4713 | 10210 | A | 5012 | 3 | 591 | DPADPMVLEVSEADRDA\VPISSEQ QRPLGFWSKALPSSANNYSFFKRQL LACYWVLVEIEHLMGHQVTMRPE LPIINCVLSDPCSHKVGHAQQHSIIK WRWYIHDWAEGTSKLHEEVAQIPM VSTPSLPQAPMASWEVPYDQLTEE EKTRAWFTDGSARHAGATQKWT VALQPLSGTSLQDSSEEKSSQWTEI |
| 4714 | 10211 | A | 5013 | 2 | 586 | |
| 4715 | 10212 | A | 5014 | 3 | 514 | |
| 4716 | 10213 | A | 5015 | 1 | 994 | MVRKAKWKPLQLPLPRKIVNQKQH RIPGGTVEISAITKDLKDAGVVIPTT SPFNSPIWSVQKTDGCWRMTVDYC KLTQVMTPIAAVVPDVVSLKQINT YPGTCK\FLGVQWCGACRDI/PSKV KDKLLHLAPPTTKKEAHLVGLFG FWREHIPHLGVLLQPMYQVTRKAA SFEWGLEQEALQQVQAAVQAALP FGPYDSADPTVLEMSVADRVAVWS LWQAPIGESQWRPLGLWSKALPFS ADNYSPFERRLLACYWALMETEGL TMGHQVTMQPELPIMNWVLSDP SRHKVGHAAQQHSIIKLKWIYICDQARA VPEGTC*LNKEVAQMPPM |
| 4717 | 10214 | A | 5016 | 1 | 643 | MVGKAKWKPLELPLPRKIVNQKQH HIPEGIAEIAATIKDLKDAGVVIPTTS PFNSPIWPVQKTDGSRMTVDYCK LNQVVTPIAAVVPDVVSFLEEINTSL GTWYAAIDLANAFFSIPVHKVHQKP FAFSWQG/QQYTFVLPQDYINSLA L*HNLIWRDLDYFALLQDITLVHYI DDIMLIGSNDHKVGGAAQQHSIIKWK |

| SEQ ID NO: of nucleo- tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | LYIHDQAQTGPEGT |
| 4718 | 10215 | A | 5017 | 3 | 1074 | VTASLSPVVATSPPPQMLPSDFPPLS EENPMLPEATVIASPKFIARQDNVD SPQEPPPTPQFSSRPITRLKSQWAPR GPECVIGIDILSSWQNP HIGSLTGRV RAIMVGKAKWKPLELPLPRKIVNQ KQYHILGGTVEISATIKDLKDTEAV TPTTSPFNSPIWPVQKTDGSWRMTV DYCKLNQVVTPIAAAVPDV/VSLLE QINTSPGTWFEWSPKKALQVQAA VQAALPFGPYDPADPMVLEVSAD RDAIWSLWNAAGESQRRPLGFWS KALLSSADNYSFPERQLLASWAL VETERLTVGHQVTLRPELPIMNWV LSDPSSHKVSGAQQRSIIKLKWYIH DWVRAGPEGT |
| 4719 | 10216 | A | 5018 | 1 | 1482 | MAPNSRVQELVLGQVAVICQGLLS LQPRTEGYTVGFLTFEVLDLTGSSA CRWPIVGLHSVILLDKVTKEKDEL RDSNSWLQKQILSLKFSKTALSES LI SCRQRAEIVENQTQGLIMRPLAFHR GNCIGERGMTILFRGYWTEPTLIPED PKHHCSPPVKVRA YEDGSWKMTV DYHKL NQVMIPVTA A VPDVVSLL E KINTSPALFHNLVQRNLDCFSLPQDI TLVHYVDDIMLIGSSEQEVANTLDL LVRRLCAKGWEINLT KIQGPSSLVK FLGVQWCGASQDIPSKVKNKLLHL ALPTTKKEAQCLVGLFGFWKQLIPH LATPIIPQRAHEQSGHGGRNGGYTW AQQHGLPLTKADLATATAECPICQQ QRENGA/PRYGTIPRGDQPATWWQ VDYVGPLPSWKGQQFVLTRIDTYS AYGFAYPTCNASAKTTIHSLTACLI HRHGIPHSIASDQGSHTAKEVQQW AHAHGIHWSYHVPYYPEATGLIEW |
| 4720 | 10217 | A | 5019 | 1 | 1494 | |
| 4721 | 10218 | A | 5020 | 101 | 304 | |
| 4722 | 10219 | A | 5021 | 1 | 1912 | MTVDYCKLNQVVIPIAAAVSDVVS LLEQINTSPGTWYAAIDLANAFFSIP VHKAQQKQFAFSWQQGQYTFVLP QWYINSPALCHNLIRRLDCFSPLPL DITLVHYIDDIMLIGPRQLLACY/W ALVETEHLTISHQVTMRPELPIMNW VLFDPSHKVGCAQQHSIIKWVWY VHDWARAGPEGTTTPVISQWPHEQ CGHGGRDGGYAWAQQCRLPLTKA DLNTATAKRPICQQQRPTLSPQYGT IPQGDQPATWWWVDYMGSLPSWK GQRFVLTGIDTYSYGFAYPACNAS AKTAICGLTECLIHHDIPHSIASDQ GTHFMAKEVRQWAHDHGIHWSYH VSHHPEAAGLIEWWNGLLKSQ LQC QLGDNTWQGWGKVLQKV VYALN QHPIYGTVSPIAKIHRSRNQGLEVAP LTITPRDPLAKFLLPFATLQSAGLE VLVPEEGTLPPGDTMIPLNWKLRLP PRHFGLLLPLNQQA KGVTVLAGV |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | TDLDYKDEITLLLHNGGKEEYAWN TGDPLGLLLILPCPMIKVNGKLQQL KPEALVPKGVVFPDGTMLSLSW KLRLPSGHVGLLMPLSQVQKGV VLAGVIDPGHTSAASLVLRSCVWS GSDTIVSPGSQDFRLGINDTTGFPVF PD |
| 4723 | 10220 | A | 5022 | 3 | 835 | DLWPFTRVTVH/WGKANDQTFQGL LDTGSELTLPGYPKRHCCPPVKVR VYGGQTDGSRMTVGYHKLNQVV TPIAAAVPDVVSLEQINTPSTWY GQVAAPPTTKKEAQRLVGLFDF GGNTLLIWVYSGPLSSDLKGCQFE WDPEQERLCKAFSAHSQWFGCQGL GRSVDWKIDDKKLGRMRMDLSE LGKNREEYWYPVQQAKKGVKVLA VVIDQTIKMKSVYYFTMEKTCQRQ ATTAELEPEKNVIGVDETVEGQSYH SSKQKDIPFQGEK |
| 4724 | 10221 | A | 5023 | 2 | 1300 | DLWPFTRVTLHRGKRNDQTFQGLL DTGSELMIPEDTKHHCGPPVKVEA YGGQVINGVLAQIQLTVGPVSGT HPVVIYPVPECIIGILSSWQNPFIG SLTSRKTDGSRMTVHYHKLNQVM VTPIAAAIIPDVVSLEQVNTSPGSW YAAIDLANAFFIPVHKAHQKQFAF SWQQQQYTFTVLHQGYNSPALYH NLIWRDLDRFSLPDITLIHYIDDMT LIGSSEQDVANTLDLL/SDLRGGF* *SSG*DDPFCGHHSASFSPHPCNRP MGP*TK*PWGQGWRLRMGSATCTP THQG*PGYGHC*VPNLPAETNTKP SIWHHSSG*SASYQAAG*LYWTSFI MERA EVRP/TWSTCLLIWVCLSCT QCFCQDYHLWTHGMPYPLSRYSAQ HCL*PRHSLYS*RSVAVGSCSWNSL VLPCSPSS*SSWI |
| 4725 | 10222 | A | 5024 | 2 | 790 | PRGRNRRRKTFQERRMTL NESPEKI GKWIECYGHPPASKLVEIYIHTVFV EDKLSICIRSFNKKADGSRMTVD YCKLNQVVTAIAAAIPDVVSLEQI NTSPDTWYAAIDLANALFSIPVHKG YINSLALCHNVIWRELD CFS LPRDT TLVHYIDIMLIGSSVQEVENKLDL LVKDKLLHLAPPTTKEEVQHMVGL FGFWRQH IPHLGVLHQPIYRVIRKA A/SFEWGPEQE KALQQVQAAVGGK QSENNLGHQ RSPGLWFS |
| 4726 | 10223 | A | 5025 | 281 | 1461 | VRVLS PVEKELKLWKNTHKLLSYP TVGAAVTQLQNL TAMGVIGSHGAR GOVVALNRQRQGDLPFTRVTVH WGKG/NMQIFGGLD TGSELTLP DPKHHCGPPVKV GAYGGQVINGVL AQVQITVGPQTHPVVISPVPECIIGID ILSSWQNP HIGSLTGIMVGKAKWK QLELPLPRKIVNQKPYCIPGGTVEIS ATIKDLKDAGVVIFTTSLFNSPIWPV QKTDGSRMTVGYRRLNQVVTPIA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | AAVPDVVSLEQINTSPGTWYAAID MANAFFSIPVHKAHQKQFAFTWQG QQYAFTVLPQGYINSPALCHNLIWR DPDCFLLLQNITLLVHYVDDIMLIGS SEQEVANALDLLVFSDLAIKWVM HSSIASSSGSGICVIRLKKVLKAQ |
| 4727 | 10224 | A | 5026 | 1 | 3179 | MAEDKEEQVPSYTDGSRQRENEED TRVKTPDKTIRSHETYSLPREQYGG NYAHDSIISHQVPPTTCGNYGSTIQD EIWVGDSHSGYVRPVPVPRSLNSDIS YFGVGGKQAVFFVGQSARMISKPA DSQDVHELVLKEDFEKKEKNKEAI YSGYIRNRKDDYDNHTGIDLVTGII ATIKGSNEEDTDTPFIGKVRTLEFP FVNGSAEIMLMPSNQQHKTEKGR ANLGVFSVFAPRGEHTLQVKAIYN KSIIEGPIIKLMILPDPEKPVRLNVKY DKDASFLAGGLFTAPPLPAQLMSSL SCAWIIESVLNSWRKGCNKLNRQR ALHKKQDRGKLPEDRELQHTKKQT NWAGLLIPAMNNVDMTARKLQR DLQPFTSVTVHCRKGNDQTFGGPL DAGSELTLPKDPKHHCPPVKVGA YGGQVINGVLAHPLIWLTVQKTDGS /WRMTVDYCKLNQVVIPIAAVSD VVSLEQINTSPGTWYAAIDLANAF FSIPVHKAQQKQFAFSWQQGQYTF TVLPQWYINSPALCHNLIIRDLDLDCF SLPLDITLVHYIDIMLIGSSEQEVA NTLDLFVRHLRARGWEINPTKIQGP STSVKFLGFQWCGACQAIPSKMRD KLLHLVPPTTKKEAQCL\QLLACY/ WALVETEHLTISHQVTMRPELPMN WVLFDPSSHKVGCAQQHSIWKW YVHDWARAGPEGTT/HPCHFPMAP *TMWPWWQGWRLCMGSAM*TST H*G*PEYSHR*APNLPTAETNTEPSI WHHSSG*STSYLVVG*LYGISSIMER AEVCPHWNRYLLWIWVCLSCMQC FCQDCHLWTHGMPYPPS*YPTQHC L*PRHSLYG*RSAAVGS*SWNSLV PCFPSS*SSWIDRMVEWPFEVTITVS TR*QYLAGLGQSSPEGRVCSESASNI WYCFSHSQDSQVQESRARS GTTHH HP*GSTSKIFASFSCNITVCWPRGLS SRGRNAATTRHNDIKLEVKIATQT LWAPPTFKSTG*EGSYSVGWGD*PG L*R*NHSPTP*WR*GRVCMERYRSI RASLNITMPYD*GQWETTAAQARSS |
| 4728 | 10225 | A | 5027 | 2 | 1284 | CHCGPP/VKVEAYGSQVLKGVLQAQ VQLTVGPVGPRTHPVVFVPECIIGI DMLSSRQNPHTGSLTGRVWTIMVR KAKWKPLELPLRKIVNQKQYHIPE GIVEISATIKDLKDAGVVIPTTSPFNS PIWPVQKTDGSRMTVGYCKLNQ VVTPIAAAVPDVVSLEQINTPPGT WYAAIDLANDFFPIPVHKAHQKQF AFRWQGRQYTFTVLPQGRWEINMT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KIQGPSTSVKFLGVQWCGACQDIPS KVVDKLLHLVPPTIKKEAQCLVGLF GFWRQHPLHGMPLQPIYRVQTMA ASFEWGS\EQEKALQQAG\QAAVQA ALPLGP/HKDPADPLVLEVS\SDRD AVWRLWQASI/GHKVGHAAQQHSIIK WKWYIRDWARADPEGTTKGQGGQR RWWQLAERQDSRDREAAIGERQET AVGKTARDGEAVCD |
| 4729 | 10226 | A | 5028 | 422 | 1252 | TTLFSVQIFQWRQLENLYFREKKFS VEVHDPRRASVTRRTFGHSGIAVHT WYACPALIKSIWAMAIHQFYLD RKQSKSKIHAARSLSEIANDLTRTRT LENSKLANMGSKGKIISGSSGSLSS GSGARRHCILLPGSQESDSSQSACK DMLAALKSRQEALEETLRQRLEEL KKLCLREAELTGKLPVEYPLDPGEE PPIVRRRIGP\AFKLDEQKILPKGEEA ELERLEREFAIQSQITEADRLASDP NVSKKLKKQRKTKYINAVKKLQVY |
| 4730 | 10227 | A | 5029 | 1 | 400 | RHEERTTGILTSEGLASDTSLICVIED FFDTALIISRSSEGGKIQMLDSFLLSL GFLVTEKTVNHLLQQEERPCMDTL DCG/LQVAISEALCRLTIKKSRDELV HKWFDDEVIAEAFKEIKDREFETDS RRFLN |
| 4731 | 10228 | A | 5030 | 1 | 612 | |
| 4732 | 10229 | A | 5031 | 64 | 323 | LFPTLWLLDLLGTVEEILPSLSENIS VWGMKDSVPQGVISLKEKL\STSPD EPVPRSHHVVSLLKSTCLYIFTSGT TGMIOFFWKA |
| 4733 | 10230 | A | 5032 | 287 | 508 | YYSIFLIYYYYYFLRWSFALVAQAV VQWCDLGSQPLSPGFKRFS\PSALS SWDYRHEQPRPANFIFLVETGFL |
| 4734 | 10231 | A | 5033 | 1 | 3627 | |
| 4735 | 10232 | A | 5034 | 3 | 3613 | |
| 4736 | 10233 | A | 5035 | 353 | 406 | MLHLQGIILMIVLYSCCRELIHSFLK DSKSMPCNWGESDGPVTGARHPSW EEEEGGVWNTTGSQGSASSHNSA SWGQGGKKQMK/CSLKKE |
| 4737 | 10234 | A | 5036 | 1 | 514 | ECKDCGKSFTVSSSLTEHARIHTGE KPYECKQCGKAFTGRSGLTKHMRT HTGEKPYECKDCGKAYNRVYLLNE HVKTHTEEKPFTCTVCRKSFRNSSC LNKHI\HIHTGIKPYECKDCGKTFTV SSSLTEHIRTHTGEKPYECKVCGKA FTTSSHLIVHIRTHTGEKPYICK |
| 4738 | 10235 | A | 5037 | 1 | 3222 | |
| 4739 | 10236 | A | 5038 | 1 | 4267 | MGPWAWKLRWTVALLAAAGTA VGDR CERNEFQCQDGK CISYKWVC DGSAECQDGSDESQETCLSVTCKSG DFSCGGRVNR CIPQFWRC DGQVDC DNGSDEQGC PPKTCSQDEF RCHDG KCISRQFVCDS DRDCLDGSDEASCP VLTCGPASFQCNSSTCIPQLWACDN DPDCEDGSDEWPQRCRGLYVFQGD SSPCSAFEHCLSGECIHSSWRC DG |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | GPDCKDKSDEENCAVATCRPDEFQ CSDGNCIHGSRQCDREYDCKDMSD EVGCVNVTLCEGPNKFKCHSGECIT LDKVCNMARDCRDWSDEPIKECGT NECLDNNGGCSHVCNDLKIGYECL CPDGFQLVAQRRCEDIDECQDPDTC SQLCVNLEGGYKCQCCEGFQLDPH TKACKAVGSIAYLFFTNRHEVRKM TLDREYTSILIPNLNRNVVALDTEVA SNRIYWSDLSQRMICSTQLDRAHGV SSYDTVISRDIQAPDGLAVDWIHSNI YWTDVSLGTVSVADTKGVKRTLF RENGSKPRAIVVDPVHGFMYWTD WGTPAKIKKGGNGVDIYSLVTENI QWPNGITLDLLSGRLYWVDSKLHSI SSIDVNGGNRKTILEDEKRLAHPFSL AVFEDKVFWTDIINEAIFSANRLTGS DVNLLAENLLSPEDMVL FHNLTQP RGVNWCERTTLSNGGCQYLCLPAP QINPHSPKFTCACPDGMLLARDMRS CLTEAEAAVATQETSTVRLKVVPD KTVRWCAVSEHEATKCQSFRDHM KSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLDAGLVYDAYLAPN NLKPVVAEFYGSKEDPQTFYYAVA VVKKDSGFQMNQLRGKKSCHTGL GRSAGWNIPIGLLYCDLPEPRKPLE KAVANFFSGSCAPCADGTDFFPQLC QLCPGCGCSTLNQYFGYSGAFKCL KDGAGDVAFVKHSTIFENLANKAD RDQYELLCLDNTRKPVDEYKDCHL AQVPSHTVVARSMSGKEDLIWELL NQAQEHFGKDKSKEFQLFSSPHGK DLLFKDSAHGFLKVPQRMDAKMY LGYEYVTAIRNLREGTCPEAPTDEC KPVKWCALSHHERLKCDEWSVNS VGKIECVSAETTEDCIAKIMNGEAD AMSLDGGFVYIAGKCGLVPVLAEN YNKSDNCEDTPEAGYFAVAVVKK SASDLTWDNLKGKKSCHTAVGRTA GWNIPMGLLYNKINHCRFDEFFSEG CAPGSKKDSSLCKLCMGSGNLNCE PNNKRGDTTGYTGAFRCLVEKGD VAFCKHQTVP TGT LGGEKNPD PW AKDLNEKDYELLCLGWVPGKPV EEYAN\CHLARAPNHRCGSHGKDK EACVHK\LRSTASHLFGASNVTDCS GNFWLVRS\ETKDLLFRDDTVCLW AKLHDRNTYEKYLGEYVKA VGN LRCSTSSLLEACTFRP |
| 4740 | 10237 | A | 5039 | 2 | 342 | LSRVVL SAAATAAPSLRNAA/FLGP GVLQATRTFHTGQPHLVPVPLPEY GGVRYGLIPEEFFQFLYPKTGVTG PYVLGTGLILYALSKEIYVISAETFT ALSCSAFELFRDHF |
| 4741 | 10238 | A | 5040 | 53 | 940 | DCYLDVSLTMLS RVVLSAAATAPT IIMKNAAFLGPGVLQATRTFHTGQP HLCPMYPIIPEY GGVRYGLIPEE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FFQFLY/PLKTGVNTDPNVPETWG LNLVTVLFQRKYMVEFRRRGPSLA LIKY*GGKWVYGNLKKYGSPLVAG LWLD*TPMEQKLGPT*EE/ARQGGF PSQHIQNAIDYGRSLYQALVQKRH YLFADVQRNNIAMALEVTYRERLYR VYK\EVKNRLDYHISVQNHDAVRN GTTNSLLNWVEKHVRAKLFPPQA RKEDILPKWHCRPIKLLAKEGSKAQ AQLW |
| 4742 | 10239 | A | 5041 | 2 | 205 | APVTSW/IQPKDGSCPFSESTKTISLY ISSEQQFHLRPSSEDDFIEDTADML\ VSFSGYSSAPKNQEQ |
| 4743 | 10240 | A | 5042 | 1 | 360 | SPCLSERQFCCEKLPLQRSSRPQDSA GQPVT/HAHCSLASTVDLCPPLLAT HRISCWHCQDEVHGGRD\SVDKGD LEALSLPAGHGDTDGPISLDVPDGA PDPQRTKAAIDHLHHKILKSTE |
| 4744 | 10241 | A | 5043 | 106 | 396 | |
| 4745 | 10242 | A | 5044 | 77 | 4026 | |
| 4746 | 10243 | A | 5045 | 1 | 344 | LDFIQTMLQVVGVSVAVPV/IPWI AIPLVPLGIIFILRRYFLETSRDVKR LESTTRSPVFSHLSSSLQGLWTIRAY KAEERCQELFDAHQDLHSGLSISGN GFKGQDLLFLA |
| 4747 | 10244 | A | 5047 | 3 | 378 | ERDGALTPLTPGLSPPPPLPP/HTSS QAHYRLSAFGQQFLFNLTANAGFIA PLFTVTLLGTPGVNQTKFYSEEEAE LKHCFYKGYVNTNSEHTAVISLCSG MLGTFRSHDGDYFIEPLQSMDEQE |
| 4748 | 10245 | A | 5049 | 2 | 278 | FVNHGCSQTLHFVFKVGNRFQTAR FYRDVLGMKVQAGADRGWRARLE PAPEPALAEGGENGCVVNLSRRVS DLRPCAVFSFRSVASCRWGS |
| 4749 | 10246 | A | 5050 | 1 | 1539 | MRLTPFSLSTGNSFRYSRRLKKNIFG TAPALRVSEMSLRPSSRIFFCFSRNG LDFTIVITLAQPPVPGISFIVAKPRLF PGAGSAGCGLLERLFLSLLGTGLR WCLRGCFPGARFCSTTSPEGHTTFT GLRRSARTQRLAQGPKPGPPAATV ARQTSRVSPAPPCSLRPLRHESAPS GIGDVTARGALRGLGCTVRVTAAC GGNHGCSQ/LCLHFVFKVGNRLQT AAFHIGTSMGMKVQQHEEFEEG\CK AA\CNGPIYDG\KWSKTMVG/YLGP EDDHFAELTYNYG\VG DYKLGND FMG\ITLA\SSQAVSNARK\LEWPLT EVAEGVF\ET\EAPGGYKFYLQNRSL PQSDPVLKVTLAVSDLQK\SLNYWC NLLGMKIYEKDEEKQRALLGYAGL TSVSLELQGVKGGVDHAAAF\GRI\ AFSCPQKE\LPDL\EDLMKRENQKIL TPLVSLDTPGKATVQVVILADPDGH EICFVGDEAFRELSKMDPEGSKLLD DAMAADKSDEWFAKHNPKASG |
| 4750 | 10247 | A | 5051 | 21 | 223 | HPGSRGCSEPRSGHCTPAWGTKVK T/SRLNKNKTKQKKEVKDCMSSTPL |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | AHPPGVWCEWRGLIPSSSP |
| 4751 | 10248 | B | 5052 | 64 | 543 | RGWKRDRDKRDDQDDVSSVRSEG GNIRGSFRGRGRGRGRGRGRGN PRLNFDYSYGYQEHGERTDQPFQTE LNTSMYYYYDDGTGVQVYPVEEA LLKEYIKRQIEYYFSVENLERDFFLR GKMDEQGFPLISLIAGFQRVQALTT NLNLILPPLKDSTE* |
| 4752 | 10249 | A | 5053 | 1 | 567 | AAATSAGA/PGRAVAGAGAGTQRA PGGCPREAPGAAPGVHKARGPGGPF GGEPPPPPP/LVAVAAVAAGSAGR GRPGR\VAAGPAEKRPPLPPKGN PWTKKPPQHLSPDTTGPPPPPLETLE AEFGSLKIIKAGKLKTKKSNKASDF SDMENWPTPSELVNTGFQSVLSQG NKKPPNRKEKEEKGEREEQ |
| 4753 | 10250 | A | 5054 | 3 | 763 | SGRPHPVIRESSPSSSLALGGQLGRG RPSGRAAPGRANPSAPAGGPAREGP EFGSLKIIKAGKLKTKKSNKASDFS DMENWPTPSELVNTWISERPQPRK\ KKPQNRKEKEEKVEKRSNSDSKEN RETKLNGPGENRQ/STDEAQSSNQR KRANKHKWVPLHLDVVRSESQERP GSRNSSRCQPEANKPTHNNRRNDT RSW/ESEIEKKE/HDQDDVSSVRSEG GN\SRGSFRGRGRGRGRGRGRGRG NPRLNFDYSSC |
| 4754 | 10251 | A | 5055 | 1 | 372 | RHEQGISFLETESTFMTDQLVDALT TWQNKTGVGLLSA\AHIRFKPTLS QQKSPEQHETVLDGNLIIRYDVDR AISGGSIQTREALIKILDDLIPRDQFN LIVFSTEATQWRPSLPASAEN |
| 4755 | 10252 | A | 5056 | 1 | 1021 | AQAQYSAAVAKGKSAGLVKATGR NMEQFQVSVSVAPNAKITFELVYEE LLKRRLLGVYELLKVRPQQLVKHL QMDIHIFEPQGISFLETESTFMTNQL VDALTTWQNKTKAHIRFKPTLSQQ QKSPEQQETVLDGNLIIRYDVDR AISGGSIQENGYFVHYFAPEGLTTPK NVVFVIDKSGMSGRIQQTREALI KILDDLSPRDQFNLIVFSTEATQWR PSLPASAENVNKARSFAAGIQALG GTNINDAMLMAVQLLDSSNQEERL PEGSV\SLIILLTDGDPTVGETNPRSI QNNVREAVSGRYSFLCLGFGFDVS YAFLEKLALDNGGLGRG |
| 4756 | 10253 | A | 5057 | 570 | 831 | HGNYRNVICILLGLFYPHFVGEKKIH IGFFLFFPAIDLKSGSGKVYQGPAGK AADTTIILSDEYFMEVVLGKLDLPQK AFFSGRLKAEG |
| 4757 | 10254 | A | 5058 | 1 | 2229 | MGSPLRFDGRVVLVTGAGAGLGRA YALAFARGALVVVNDLGGDFKG VGKGSAAADKVVEEIRRRGGKAVA NYDSVEEGEKVVKTALDAFGRIDV VVNNAGILRDRSFARISDEDWDIIH RVHLRGSFQVTRAAWEHMKKQKY GRIIMTSSASGIYGNFGQANYSAK LGLLGLANSLAIEGRKSNIHCNTIAP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NAGSRMTQTVMPEDLVEALKPEYV APLVLWLCHESCEENGGLFEVAG WIGKLRWERTLGAIVRQKNHPMT EAVKANWKKICDFENASKPQSIQES TGSIIEVLSKIDSEGGV SANHTSRAT STATSGFAGAIGQKLPPFSYAYTELE AIMYALGVGASIKDPKDLKFIYEGS SDFSCLPFTFGVIIGQKSMGGGLAEI PGLSINFAKVLHGEQYLELYKPLPR AGKLCCEAVVADVLDKSGSVVIIM DVYSYSEKELICHNQFSLFLVGSGG FGGKRTSDKVKVAVAI PNRPDAV LTDTTSLNQAALYRLSGDWNPLHID PNFASLAGFDKPIHLGLCTFGFSARR VLQQFADNDVSRFKAIKARFAKPV YPGQTLQTEMWKEGNRIHFQTKV QETGDIVISNAYVDLAPTSGTQAKT PSEGGK\LQITFVFEE\GPRLKDIGP VVVK\KVNAVFEWHITKGGNIGAK WTIDLKSGSGKVYQGPAAKGAADT TIH\ILSDEDF/LWEVVLGQA*PSRKA FFSGRLEGQEGNIMLS\QKLQMLAK DYAKL |
| 4758 | 10255 | A | 5059 | 1 | 7449 | |
| 4759 | 10256 | A | 5060 | 1 | 7458 | MTDSKPITKSKSEANLIPSQEPFPAS DNSGETPQRNGEGHTL/HQDTQPGR ASLPQRPQR\SGRRRNSLPPSHQKPP RNPLSSSDAAPSPELQANGTGTQGL EATDTNGLSSSARPQGQAGSPSKE DKKQANIKRQLMTNFILGSFDDYSS DEDSVAGSSRESTRKGSRASLGALS LEAYLTTELLALDFGIFIRGSLVFA GYPLTLLHTYRQGSNTSSLVFTGLG SGFIELLGCPRLPQQKAAVQRPSMS GLHLVKRGREHKKLDLHRDFTVAS PAEFVTRFGGDRVIEKVLIANNIA AVKCMRSIRRAYEMFRNERAIRF VVMVTPEDLKANA EYIKMADHYV PVPGGPNNNNYANVELIVDIKRIP VQAVWAGWGHASENPKLPPELLCK NGVAF LGPPSEAMWALGDKIASTV VAQTLQVPTLPWSGSGLTVEWTE DLQQGKRISVPEDVYDKGCVKDVD EGLEAAERIGFPLMIKASEGGGGKG IRKAESAEDFPILFRQVQSEIPGSPIF LMKLAQHARHLEVQILADQYGNA VSLFGRDCSIQRRHQKIVEEAPATIA PLAIFEFMEQCAIRLAKTVGYVSAG TVEYLYSQDGSFHFLELNPRLQVEH PCTEMIADVNLPAALQGFKPSSGT VQELNFRSSKNVWGYFSVAATGGL HEFADSQFGHCFSWG ENREEAISN MVVALKELSIRGDFRTTVEYLINLL ETESFQNNIDITGWLDYLIAEKVQA EKPDI MLGVVCGALNVADAMFR TC MTDFLHSLERGQVLPADSLNLVD VELIYGGVKYILKVARQSLTMFVLI MNGCHIEIDAHRLNDGGLLSYNG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NSYTTYMKEEVDSYRITIGNKTCVF EKENDPTVLRSPSAGKLQYTVEDG GHVEAGSSYAEMEVMKMIMTLNV QERGRVKYIKRPGAVLEAGCVVAR LELDDPSKVHPAEPFTGELPAQQT PILGEKLHQVFHSVLENLTNVMMSGF CLPEPVFSIKLKEWVQKLMMLLRH PSLPLELQEIMTSVAGRIPAPVEKS VRRVMAQYASNITSVLCQFPSQQA TILDCHAATLQRKADREVFINTQSI VQLVQSLGTEQDLVFYEKEKRNQSI LGFEPVNSRHVSHVPETHRYKESHY DKCVINLREQFKPDMSQVLDClFSH AQVAKKNQLVIMLIDELCGPDPSLS DELISILNELTQLSKSEHCKVALRAR QILIASHLPSYELRHNQVESIFLSAID MYGHQFCPENLKKLILSETTIFDVLP TFFYHANKVVCMALEVVRRGYI AYELNSLQHRQLPDGTCVVEFQFM LPSSHPNRMTVPISITNPDLLRHSTE LFMDSGFSPLCQRMGAMVAFRRFE DFTRNFDEVISCFANVPKDTPLFSEA RTSLYSEDDCKSLREEPIHILNVSIG CADHLEDEALVPILRTFVQSKKNIL VDYGLRRITFLIAQEFAEDRIYRHLE PALAFQLELNRMNRNFDLTAVPCAN HKMHLYLGAACKVKEGVEVTDHRF FIRAIIRHSDLITKEASFEYLQNEGER LLEAMDELEVAFNNTSVRTDCNHI FLNFVPTVIMDPFKIEESVRYMVMR YGSRLWKLRLVLAQEVKINIRQTTTG SAVPIRLFITNESGYLDISLYKEVT DSRSGNIMFHSFGNKQGPQHGMILN TPYVTKDLLQAKRFQAQTLGTTYIY DFPEMFRQASPAAQTRVHVHNVQA LFLKWGSPDKYPKDILTYTELVLDS QGQLVEMNRLPGGNEVGMVAFKM RFKTQEYPEGRDVIVIGNDITFRIGS FGPGEDLLYLASEMARAEIGPKIY VAANS GARIGMAEEIKHMFHVAW VDPEDPHKKKKTVAFSAGNWIRSL TKVFFKGFKYLYLTPQDYTRISLNL SVHCKHIEEGGESRYMITDIIGKDD GLGVENLRGSGMIAGESSLAYEEIV TISLVTCAIGIGAYLVRLGQRVIQV ENSHIILTGASALNKVVEPCTVQDIA NHVVSKQVLGREVYTSNNQLGGV QIMHYNGVSHITVPDDFEGVYTILE WLSYMPKDNHSPVPIITPTDPIDREI EFLPSRAPYDPRWMLAGRPHPTLK GTWQSGFFDHGSFKEIMAPWAQTV VTGRARLGGIPVGVIAVETRTVEVA VPADPANLDSEAKIIQQAGQVWFPD SAYKTAQAVKDFNREKLPLMIFAN WRGFSGGMKDMYDQVLKFGAYIV DGLRQYKQPILYIPPYAELRGGSW VVIDATINPLCIEMYADKESRGGVL EPEGTVEIKFRKKDLIKSMRRIDPAY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KKLMEQLGEPDLSKDRKDLEGR KAREDLLLPIYHQVAVQFADFHDTP GRMLEKGVISDILEWKTARTFLYW RLRRLLEDQVKQEILQASGELSHV HIQSMRLRRWFVETEGAVKAYLWD NNQVVVQWLEQHWQAGDGPRSTI RENITYLKHDSVLKTIRGLVEENPE VAVDCVIYLSQHISPAERAQVVHLL STMDSPAST |
| 4760 | 10257 | A | 5061 | 6 | 906 | EQPALLPRYRSGIRGYMKTIVLDDL RRYL RVEITIFSKARDADANTSGMV GGVRSLSFTSVWVLSPPAHYDKCV INLREQFKPDMSQVLDICFISHAQVA KKNQLVIMLIDELCGPDPSLDELISI LNELTQLSKSEHCKVALRARQILIAS HLPSYELRHNQVESIFLSAIDMYGH QFCPENLKKLILSETTIFDVLPTFFY HANKVVCMA SLEVYVRRGYIAYEL NSLQHRQLPDGTCVVEFQFMLPSSH PNRMTVPISITNPDLLRHSTELFMD GFSPLCQRMGAMVAFRRFEDFT |
| 4761 | 10258 | A | 5062 | 2 | 560 | APRLDVFSFSQIHRDIKPENILVSQSG ITKLCDFGFARTLAAPGDIYTDYVA TR*PVDI WALGCMIIEMATGNPYLP SSSDLDLLHKIVLKVGNLSPHLQNI SKSPIFAGVVL PQVQHPKNARKKYP KLNGLLADIVHAWLQIDPADRISS DLLHHEYFTRDGF I*KFMP ELKA*L LQEAKSQF |
| 4762 | 10259 | A | 5063 | 1 | 573 | |
| 4763 | 10260 | A | 5064 | 2 | 791 | NLVN LIEVFRQKKKIHLVF EFIDHTV LDELQHYCHGLESKR LRKYLFQILR AIDYLHSNNTVDI WALGCMIIEMA TGNPYLPSSSDLDLLHKIVLKVGNL SPHLQNI FSKSPIFAGVVL PQVQHPK NARKKYPKLNGLLADIVHEIEKEKK PKEIKVRVIKVKGGRGDISEPKKKE YEGGLGQDANENVHPTSPDTKL TIEPPNPINPSTNCNGLKENPHCGGS VTMP PINLTNSNLMAANLSSNLFSP QCEVSCNREEP |
| 4764 | 10261 | A | 5065 | 3 | 524 | TYGPASRGICRVSLGRPRWENAAT WKLAAMASIRLQGLHKPVYHALSD CGDHVVIMNTRHIAFSGNKWEQKV YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLQ/NNLHRRMTME RLHLFPDEYIPEDILKNLVEELPQPR KIPKRLDEYTQEEIDAFPRLWTPPED YRL |
| 4765 | 10262 | A | 5066 | 1 | 250 | YSSHTGYPGGFRQVTAAQLHLRDP VAIVKLAIYGMLPKNLHRRMTMER LHLFPDET*RLSAIRE*ELQKITVK*L KLSSDEFL |
| 4766 | 10263 | A | 5067 | 129 | 796 | MGKCSHLANFAAIASIRLQGLHKPV YHAFE*L/CGDHVVIMNTRHICIF/H GNKWGTSILFRILAYPGWSLDKVT SLAPAFTLRRSQW/CNL*NLAIYGIP AKKTFTRRTIDWKGLHLFPDELYS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RKIFLKKFS*EELPSTTEKYLNVLDE YTTRNRRLFKIVDSTLKIIGYKRIRI AENNSEVIETFLMSFSNLQDGVKQ LLQFEHLFLCAESLWGKVRKV |
| 4767 | 10264 | A | 5068 | 15 | 350 | GPGSAITVGPQPL/RAQRNHRLPVPS PGLSIVMGLRPVPSPGPTGLPGHRQ SSEMRPREAGSLRSSGEKGLPAPVP RPQQSDMTKRTLPRDTPDTPRCPPQ HCPWSRVRGQPQ |
| 4768 | 10265 | A | 5069 | 1 | 2175 | |
| 4769 | 10266 | A | 5070 | 3 | 86 | KNYRG TMS/KTKNGITCQKWSSTSP RRPR |
| 4770 | 10267 | A | 5071 | 2 | 583 | LLLLFLKSGHGEPLDYYVYAQGA SLFSVTNHLGAGSTEECASQCVED KEFTCGAFQYHSKEQQCAIMAENK KSSIIIRMRDVVLF EK*MYLSECQTG NGKNYRG TMSKTKNGITCSKMGPV LFPHRPRFSPATHPSEGLARNPDNDA QGPWCYT TD\PEQRYDYCDIPECEG QEWALGKCFHFCSSPVKINLL |
| 4771 | 10268 | A | 5072 | 844 | 4515 | TVKAPGYSHSHPGALLDLEVGDPN GTNAQLIKCFLPLCPSFPLCPEECM HCSGENYDGKISKTMSGLECQAWD SQSPHAHGYIPSKFPNKNLKKNYCR NPDRELRPWCFTTDPNKRWELCDIP RCTTPPPSSGPTYQCLKGTGENYRG NVA VTVSGHTCQHWSAQTPH THN RTPENFPCKNL DENYCRNPDGKRA PWCHTTNSQVRWEYCKIPSCDSSPV STEQLAPTAPPELTPVVQDCYHGDG QSYRGTSSTTTTGKKCQSWSSMTP HRHQKTPENYPNAGLTMNYCRNPD ADKGPWCFTTDP SVRWEYCNLKKC SGTEASV VAPPV VLLPDVETPSEE DCMFGNGKGYRGKRATTVTGTPC QDWAAQEPHRHSIFTPETNPRAGLE KNATECGGASTELCSTSLCAFTML MDYEGQGEPLDDYVNTQGASLFSV TKKQLGAGSIEECAAKCEEGEEFTC RAFQYHSKEQQCVIMAENRKSSIII RMRDVVLF EKKVYLSECKTGNGK NYRG TMSKTKNGITCQKWSSTSPH RPRFSPATHPSEGLEENYCRNPDND PQGPWCYT TDPEKRYDYCDIL\EC *RRECMFAVGGKLLTGKIFPR TMS WDWECQAWGLFRSPHGHGYIPSK FPNKNLKKNYCRNPDRELRPWCFT TDPNKRWELCDIPRCTTPPPSSGPTY QCLKGTGENYRG NVA VTVSGHTCQ HWSAQTPH THNRTPENFPCKNLDE NYCRNPDGKRAPWCHTTNSQVRW EYCKIPSCDSSPVSTEQLAPTAPPEL TPVVQDCYHGDGQSYRGTSSTTTT GKKCQSWSSMTPHRHQKTPENYPN AGLTMNYCRNPDADKGPWCFTTDP SVRWEYCNLKKCSGTEASV VAPP VLLPDVETPSEEDCMFGNGKGYR GKRATTVTGTPCQDWAAQEPHRHS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | IFTPETNPRAGLEKNYCRNPDGDVG GPWCYTTNPRKLYDYCDVPQCAAP SFDCGKPQVEPKKCPGRVVGCV HPHSWPWQVSLRTRFGMHFCGTL ISPEWVLTAHCKLEKSPRPSYKVL GAHQEVNLEPHVQEIEVSRLFLEPT RKDIALLLKSSPAVITDKVIPACLP PNYVVADRTECFVTGWGETQGTFG AGLLKEAQLPVIENTKVCNRYEFLNG RVQSTELCAGHLAGGTDSCQGDG GPLVCFEKDKYILQGVTSWGLGCA RPNKPGVYVRVSRFVTWIEGVMRN N |
| 4772 | 10269 | A | 5073 | 9 | 141 | FYRLSLGFKCDWFTMEKRVKLEER YRDMAEENLKKDISISLKL |
| 4773 | 10270 | A | 5074 | 3 | 360 | QTKPKESRKRIIMFRTEFNETENRI ESSSSSSSSSFSSSSSYKCLARLT/ RKK/EKIQIIVRSEKIEITNYRIKRIT KGYEELLYANQLYHLMKCPKFLER HKLLKLTQEETKSGV |
| 4774 | 10271 | A | 5076 | 1 | 245 | AAAYYYTAAARRRQKGERRKKRK EEER/KEEKKRKKKKEKKRRRRG GRTTKKEEKEKEKKRRTKKEKKK KKKKKKKVSM |
| 4775 | 10272 | A | 5077 | 68 | 246 | SMAFLTIEDTALKFIQNHKRPQIA/ KPILSKNRAESITLFNSKIHYPMTVI KPLRVTST |
| 4776 | 10273 | A | 5078 | 3 | 364 | TSIVAAQMFMVITVMQVRISPQHMT SMWPIMVCELSQFTQLEEDVKDK VESLRSTNKVNRTKVSVDANGPS VGYIPQSELIMYLSACKFLDAALSIP HYKIPLFKIYRWAFIPEVDTE |
| 4777 | 10274 | A | 5079 | 2 | 1315 | GKDAKILCSNPNTGEVLVELPTNTQ RCFDIQWCPNPAVLAAASFAGRIS VYSIMGGSTDGLRQKQVDKLSSFG NLDPFGTGQPLPPLQIPQQAQHSIV LPLKKPPKWIRRPVGASFSGGKLV TFENVRMPSHQGAEQQQQHHVFI SQVVTEKEFLSRDQLQAVQSQGF INRQKKIDASQTELEKNVWPFLPV TFEDDSRGKYLELLGYRKEDLGK/K DCFGL/GTKWMEPMWLLKTLTKYH ITNHEPAG*PPVTNAAATASSSSTA KPVFIPTDTSSRWALPWRTATSW NRHAPIFFTAQY*RCPRGSYWKYLP ACAVFGNKKNYQETYSR*APHSKD HI*GSYSALPFFSNRPSNQEEAR*CQ QTFGVSV**T*GTDTFTNNHQWFTQ HCKEH*NSKLLRRIDHAYPHS*HQQ LQ*DLCFHASSQSCL |
| 4778 | 10275 | A | 5080 | 18 | 3600 | |
| 4779 | 10276 | A | 5081 | 238 | 480 | SIQFYFFSFQDSKGKHSLSVIGPQN GWNDPPALNRVPKKKKMPENFMPP VPITSPIMNPLGDPQSQMLQQQPSA/ PVPLS |
| 4780 | 10277 | A | 5082 | 352 | 4060 | DYSRRYILRMKLKEVDRTAMQAW SPAQNHPIYLATGTSAQQLDATFST |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NASLEIFELDLS DPSLDMKSCATFSS SHRYHKLIWGPYKMDSKGDVSGVL IAGGENGNILYDPSKIIAGDKEVVI AQNDKHTGPVRALDVNIFQTNLVA SGANESEIYIWDLNNFATPMTPGAK TQPPEDISCIAWNRQVQHILASASPS GRATVWDLRKNEPIIKVSDHSNRM HCSGLAWHPDVA TQMVLASEDDR LPVIQMWDLRFASSPLRVLENHAR GILAIAWSMADPELLLSGCKDAKIL CSNPNTGEVLYELPTNTQWCFDIQ WCPRNPAVLSAASFDRISVYSIMG GSTDGLRQKQVDKLS SSGNLDPFNG TGQPLPPLQIPQQT AQHSIVLPLKKP PKWIRRPVGASFSGGKLVTFENVR MPSHQGAEEQQQQHHVFISQVVTE KEFLSRSDQLQQA VQSQGFNYCQK KIDASQTEFEKNVWSFLKVNFEDDS RGKYLELLGYRKEDLGKKIALALN KVDGANVALKDS DQVAQSDGEESP AAEEQLLGEHIKEEKEESEFLPSSGG TFNISVSGDIDGLITQALLTGNFESA VDLCLHDNRMADAILAIAGGQELL ARTQKKYFAKSQSKITRLITAVVMK NWKEIVESCDLKNWREALAAVLTY AKPDEFSALCDLLGTRLENEGDSSL QTQACLCYICAGNVEKLVACWTKA QDGSHPLSLQDLIEKVILRKAVQL TQAMDTSTVGVLLAAKMSQYANL LAAQGSIAAALAFDPDNTNQPNIMQ LRDRLCRAQGE PVAGHESPKIPYEK QQLPKGRPGPVAGHHQMPRVQTQ QYYPHGENPPPPGFIMHGNVNPNA AGQLPTSPGHMHTQVPPYPQPQPY QPAQPYPFGTGGSAMYRPQQPVAP PTSNAYPNTPYISSASSYTGQSQLYA AQHQASSPTSSPATSFPPPPSSGASF QHGGPGAPPSSSAYALPPGTTGTL AASELPASQRTGPQNG\WNDPPALD KVPPKKKKMPENFMPPVPITSPIMN RLGDPQSQMLQQQPSAPVPLSSQSS FPQPHLPGG\QFPWGYSKPFGFKQ GMATIFFQSPNIEGAPGAPIG\NTFQ HVQSLPTKKITKKIPD\EHLILKTT FEDLIQRCLSSATDPQTKRKLDDAS KRLEFLYDKLR\DRTFSPITISGLHNI ARSIETRNYSEGLTMHTHIVSTSNFS ETSAFMPVLKVVL TQANKLGV |
| 4781 | 10278 | A | 5084 | 121 | 419 | DLCFTTPKAGRRQEITKIRAE LNKV EVQETIQKISEKRSWLFNIINKIARLL TRLIQKKD\QINTVRNDKGDITTYPT EIQKTLRDY YEHLYACRVENLQ |
| 4782 | 10279 | A | 5085 | 1 | 279 | TMDSNNTV\DQLDLTDIYRTLHLTS AA YTFSSAHLRLCSR\DLRLSHKTS LNKFKKIVIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL |
| 4783 | 10280 | A | 5086 | 1 | 279 | TMDSNNTV\DQLDLTDIYRTLHLTS AA YTFSSAHLRLCSR\DLRLSHKTS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LNKFKKIVIIPGIFCDQNGIQPEINSG RKMRRVSNVWKLNNIL |
| 4784 | 10281 | A | 5087 | 1 | 1915 | MAILPLLLCLLPLAPASSPPQSATPS PCPRRCRCQTQSLPLSVLCFGAGLL FVPPSLDRRAAELRLADNFIASVRR RDLANMTGLLHLSLSRNTIRHVAA GAFADLRALRALHLDGNRLTSLGE GQLRGLVNLRLHLSNNQLAALAA GALDDCAETLEDLDLSYNNLEQLP WEALGRLG\NVNTLGLDHNLLASV PAGAFSP\LHKLARLDMTSNRLTTIP PDPLFSRLPLLARPRGSPASALVLA GGNPLHCNCELVWLRLAREDDLE ACASPPALGGRYFWAVGEEEFVCE PPVVTHRSPPLAVPAGRPAALRCRA VGDPEPRVRWVSPQGRLLGNSSRA RAFPNGTLELLVTEPGDGGIFTCIAA NAAGEATAAVELTVGPPPPQLANS TSCDPP/PGRGLPDALTPSAASASA KVADTGPPTDRGVQV\TEHGATAA LVQWPDQRPIPGIRMYQIQYNSSA DDILVYRMIPAESRSFLLTDLASGRT YDLCVLAVYEDSATGLTATRPVGC ARFSTEP\SLRPCGAPHAPFLGGTMII ALGGVIVASVLVFIFVLLMRYKVHG GQPPGKAKIPAPVSSVCSQTN\GAL GPTPTPAPPAPPAALRAHTVVQLD CRALGARPRTCGLARRPPL |
| 4785 | 10282 | A | 5088 | 1387 | 1567 | GKNLLPLFFFFFFFETVSQSVAQAG VQWRHLGSPKPLPP\GSSDSPASVSQ AAETTGTCHH |
| 4786 | 10283 | A | 5089 | 96 | 408 | SPRKRKTRHSTNPPLECHVGWVMD SRDHGPGTSSVSTSNASPSGAPLA GRYGCTPHSFPKFQNPSELLKEN GFTQQVYHKYRRRCLSERKRLGIG QSQEMNT |
| 4787 | 10284 | A | 5090 | 390 | 665 | PLNIHYCFLGGKYL VFGFSVAANKT SGAP\GNSPVSAIRAFGDAHPDLVT PGTFIPYCSMAHAQLCFHGHRDAV KFFVAVPGQVISPOSSSS |
| 4788 | 10285 | A | 5091 | 185 | 386 | WEASKKKPRGAQISNAITTYKYLPK VGV\KNYQTEALYKPIQTGKIGHPV FFQKPPLLGDGQNYDTPP |
| 4789 | 10286 | A | 5093 | 3 | 330 | GTGLKARKSASSLPETFPTRTRHGE AALPLSPTWKMTGPGVGNPMIPRQR SMSLLTAVSGQPHFQDSALSQASSS PDLL/LHLSPR\SCPGRVQETLKATD RPPRCPAGCG |
| 4790 | 10287 | A | 5094 | 2 | 349 | PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLKKGENPPNSFYGAIP RIPNPNMDLPSSSPT/RPVSGRNMEA KIFTKFLAGHFKQSFGREIHHDQREF IPGIQGGFNIGN |
| 4791 | 10288 | A | 5095 | 2 | 353 | PRVRKSPGPNGFTANFYQTFKELISI LLKLFSSSSSLASSSSSSSSSSSSSS SSPPNMDLPSSSPT/RPVSGRNIEAKI FTKFLPGHFQQSFGRVTHLDQRELI LGNQGGSTICKS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4792 | 10289 | A | 5096 | 1 | 262 | RGRAGGEPLPATTGAAPPPGRRLLH/ RQLPDRRGLASMPREEKASLNEPG GPGRGRRRGSVQLHGEGGPRGCEE GTGREEWNEKAEFTL |
| 4793 | 10290 | A | 5097 | 116 | 177 | LGEHGVYSGVGTGGRLLS*KKGKP WFK*KKLKGGPIPI*RDPRGFSRFSV |
| 4794 | 10291 | C | 5098 | 231 | 347 | MGLGPHLKFFYLKHGLPFFKELNPL KVKIWPRNPWIKKI* |
| 4795 | 10292 | A | 5099 | 518 | 931 | ATRHSMLSCHITYTYIYIKHTHTHVFI YIYTYTYIHTHIYTYTYICHTHIHIYI YIYIHTHFFFFFFFETESRSVTQAGV QWHDLGSLQAASWGHADSPASTS QAAGTTGAHHHAQ/LIFFFVFLVET GPHRASQDS |
| 4796 | 10293 | A | 5100 | 2 | 1109 | DAEMLVMAPRTVLLLLSAALALTE TWAGSHSMRYFDTAMSRPGRGEPR FISVGYVDDTQFVRFDSDAASPREE PRAPWIEQEGPEYWDRNTQIFKTNT QTDRESLRNLRGYYNQSEAGSHTL QSMYGCDVGPDRLLRGHNQYAY DGKDIALNEDLRSWTAADTAAQI TQRKWEAARVAEQDRAYLEGTCV EWLRRYLENGKDTLERADPPKTHV THHPISDHEATLRCWALGFYPAEIT LTWQRDGEDQTQDTELVEPTRAGD RTFQKWA AVV VPSGEEQRYTCHVQ HEGLPKPLTLRWEPSQSTVPIVGIV AGLAVLVVTAVVAVVAVMCRR KSSGKGGSYSQAASSDSAQGS DV SLTA*KA |
| 4797 | 10294 | A | 5101 | 3 | 1145 | SDSPQTPMRVMAPRTLILLLSGAL ALTETWACSHSMRYFYTAVSRPGR GEPRFIAVGYVDDTQFVRFDSDAAS PRGEPRAPWVEQEGPEYWDRETQ KYKRQAQTDRVSLRNLRGYYNQSE AGSHTLQWMYGCDLGPDRLLRG YDQSA YDGKDIALNEHLRSCTAA DTAAQITQRKWEAARAAEQQRAYL EGTCVEWLRRYLENGKETLQRAEH PKTHVTHHLVSDHEATLRCWALGF YPAEITLTWQRDGEDQTQDTELVE TPAGDGTQFQKWA AVV VPSGEEQRY TCHVQHEGLPEPLTLRWEPSQSTIP IVGIVSGPAVLAVLAVLAVLAVLGA VVA AVIHRKSSGKGGSQAAS SNSAQGSDES LIACKA |
| 4798 | 10295 | A | 5102 | 3 | 242 | GFWAPRVCKDIDKWHLSEPEALWF GEGGSPGGCRWGGWLCQGNRA AGGVGAEGACLGLLSATGLLWMT GLQEPREPQV |
| 4799 | 10296 | A | 5103 | 1 | 138 | FPLIPKPGKDPFN/ENFRPIFLMAKN AKILKKILANLIFQPLKKIL |
| 4800 | 10297 | A | 5104 | 59 | 337 | IPYPALPFTSVEAPNSHVKA VMKTS VLLSWEIPENYN SAMPFKILYDDGK MVEEVDGRATQKLIVILNPEKSYSF ELTYRGNCAGGLELMVT |
| 4801 | 10298 | A | 5105 | 54 | 226 | TKAETENLNRPVTEIKSVI/NSLPTK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KSPGLDGFIAKFFQTYKREIIPDLLK LLQKLKW |
| 4802 | 10299 | A | 5106 | 2 | 265 | ETVKLLEENI/GQKLFDIGLGSDFLDI TPKAQETKINKWDFIKLSFCTVKE TIKMKRQSVWEKILVSHVSDKWFI SKIQGIYITQYQ |
| 4803 | 10300 | A | 5107 | 1 | 296 | GREKEEGESGEDWGRV\GREKEGG EGREEEGEGGEGGEGGRKEEGE GGREEEGEGGEGGEGGEGGEGE/ GREEEGEGGRQEEGEGGRREGRG GRS |
| 4804 | 10301 | A | 5108 | 1 | 253 | |
| 4805 | 10302 | A | 5109 | 190 | 472 | |
| 4806 | 10303 | A | 5110 | 1 | 314 | HNVPVPHVFMQLQKEITKKNSTFRVHI KAVFYN/HDIYCMPLLNRYKTFDV IVIDPPWQSKSVKRSNRYSLPLQI KQIPIPKLAAPNCLLVTLTNTQKH LRFIK |
| 4807 | 10304 | A | 5111 | 3 | 362 | FFFFFETESLSVPQAGVQ*HDLSSLQ PP/PPGFTPFSCSLSPSSWDYRCPPPR PA/NIFFVFLVETGFHHVSQDGLDLL T/S/GDPPASASQSAGITGVSHRARPP PPQFFIQLPLYNHITLEGR |
| 4808 | 10305 | A | 5112 | 3 | 385 | FFFETESRSVAQAGGQWHDLSLQ APTPGFTPFSCSLSPSSWDYRCPPPC PANFFVFLVETGFHHVSRDGLDFT SDPPTSASQSVGITGVSHCARARPF FKKKKKKKTSILSSSSLSFSHKQRSFG F |
| 4809 | 10306 | A | 5113 | 1 | 390 | SKAVKV/YRLITRNSYEREMFDKAS LKLGLDKAVLQSMGRDGNITGIQ QFSKKEIEDVLRKGAYAAIMEEDDE GSKFCEEDIDQILLRRTTITIESEGK GSTFAKASFVASGNRTDISLDDPNF WQKWA |
| 4810 | 10307 | A | 5114 | 2 | 214 | GRVDIERAILVQTGQQALEPA\VRL RRAPYPCHTSDLFLNNVGFFFLIM MLTWMVSVASMRPLVSQGE |
| 4811 | 10308 | A | 5115 | 30 | 379 | KRSVNSPGRALSELVSTELGFLRC VSVVCSLSQEYFLFTLLYFGL/LPF ACLLSSSPVFFVFRCSVPLFFCFLFC VSLCLPFLGFFHVLFFHRLPLIVFSF MEGFYWA WCLVFFCL |
| 4812 | 10309 | A | 5116 | 1 | 304 | GTRETVGLGDTNLAHQCSRLTMVN NDNHSEAYNNLAVLEMRKGHVQQ ARALLQTASALSPHMYETDFNFATI CDMTGYLHRSYVDAQKSEAALSEH VDTQH |
| 4813 | 10310 | A | 5117 | 119 | 264 | |
| 4814 | 10311 | A | 5118 | 720 | 2798 | VYWPHSFLGCPSNYPLYLGAETRQ GGRARPPFLPLSFPPFRPNPSPFQ VLETQRISYSFLLADTSNTRATSGH AQQPAPILPLREVAGAEDIHVHVPF SLSDLSQIAKRLGSFSSDPDTYIKEF KYLTQSYELTWHDLIILSSTLLPEK KERVWLAAQAHANDLHRQDPTKPI GAAAVPLEPPWKYQPTDPGRASR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NHMITCLIAGLNKAAHKAVNFEKL KEISQRADENPAEFLSRFTEALQKY TRVDPTSREETIVLNNHFISQSAPNI QHKLKKAEDGPQTPQQDLLNLT VFNNREEQIKLDAQRDCAKYQLL AVAIHQPSHSTQGHKKPNGSNPPGP CFKCSKEVTVLGVQLSPGAQAMTP AQATLINSPLPSSKNEILSFLRLEGF FRIWIPNFALLAQPLYEAAKGPLNE PLSPIHNILPSFCKLQTALITAPALS PDLSQPFVLYTTKNQGIALGVLGQQ KGNPPSFDPAVYLCKQLDNTVKGQ PTCLKASSAVAVLPLESKKLTFGQS TTIHSPHNLQDLLSSWALSSSPSQI QSLYALFIKNPEFSLAKSAPLNLASL LPISPPPTHSCDILDHLQPQFPNISS KPLTNPDDQLFIDDSSSRAPGSPKIV GYAVVTLNHVIEAKPLPETSSQKA ELVALTRALTSKDKQHWLISEPVQ RPPSSVHST |
| 4815 | 10312 | A | 5119 | 2 | 697 | HGRLLLLLLLLLPCCEKTTEGEAM KEITAGLPVKVVVDVLRQASKACV VKREFKKAELIKHAVYLARDHFG SKHPKYSDDLGYGYLLNVDNICQ SVAIYQAALDIRQSVFGGKNIHVAT AHEDLAYSSYVHQYSSGKFDNALF HAERAIGIITHILPEDHLLLASSKRV KALILEEIAIDCHNKETEQRLLQEAH VDVHLLSLHLASKSYGDLAVVVLVH MSLLKSY |
| 4816 | 10313 | A | 5120 | 3 | 277 | EEEEAPPPGRERARGKGGDRPRGG NPEHQCGGTPRAEGSSTA/A/PPTCT SSSRTPASTVGPEPCGAGSAATAPG PELSGQNQMGRGPPVEDTE |
| 4817 | 10314 | A | 5121 | 1 | 337 | GTSSCVREVQAMGKKKVLVKVH LKDKFVIDVDKNISISDVTSSLVVL RNDSTYTLHKILPNKVHSLVSLMMV NTVPY/STNETIVSLDGPMVTILFSD KLSFTAPQLYIFTG |
| 4818 | 10315 | A | 5122 | 2 | 302 | ARGLPFFTRNDFSVWTIA/RNKCVG LELSKITMPIAFIQPLIFLHRITEYME HVYLIHRAFCQPQPLERMQVGLKG ARQEFVMKVMPLACLATQSWGPR HL |
| 4819 | 10316 | A | 5123 | 3 | 346 | HENWKLLPCSSKAGLSVLLKADR LFHTSYHSQAVHIRPVCARNARCT SISWELRQTLVVFDFAFITGQKKDWS LF/RMFSRTLTEPCPLASESRVYVDI TTYNQDNETLEVHPPP |
| 4820 | 10317 | A | 5124 | 213 | 425 | QNSQGKLFSSGCLPFCGSNTKGILK YIQNH/KKPQIAKATLSKKNKAGSIT LPDFKIYYKALKPKITWYWH |
| 4821 | 10318 | A | 5125 | 1 | 356 | GTSTRIIFYRDGVSEGQRQQLHHE MLAIREACIKLQKDYQPGITFIVVH NIHHTRLLCSDKNHPLGKRGNSPTG SNCGTKITHPTFEFDYLRRHAGIQG TSRPSYYHVLWD\DNRRFS |
| 4822 | 10319 | A | 5126 | 1 | 238 | HMHSHHMHSTPHA/HHTHHMHS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | HHMHSHTHHMHSHHMHSAPHAL TPHACTHTHHMHSHHMHSHHMHA LTPHACTHTPH |
| 4823 | 10320 | A | 5127 | 180 | 405 | IWGEQDTFHSMKWIHLNVNHKT VKLLDDNIG/IKRGDLG/VDNEFLGT TPKAQSMEETIDKLDFIKMKNFCSV KDG |
| 4824 | 10321 | A | 5128 | 61 | 85 | PS*NYPP*KGITFGPLNKK |
| 4825 | 10322 | A | 5129 | 3 | 2004 | RRRRRPASPPAGLALAPRSPASPEP REGETLSPSMQREEGFNTKMADGP DEYDTEAGCVPLLHPPEIKPQSHYN HGYGEPLGRKTHIDDYSTWDIVKA TQYGIYERCRELVEAGYDVRQPDK ENVTLHLHWAANNRIDLKYYISKG AIVDQLGGDLNSTPLHWATRQGH SMVVQLMKYGADPSLIDGEGCSCI HLAAQFGHTSIVAYLIAKGQDVDM MDQNGMTPLMWAAAYRTHSVDPTR LLLTFNVSVNLGDKYHKNTALHWA VLGNTTVISLLEAGANVDAQNI KGESAPDLAKQRKIVWIINHLQEAR PAKGYDNPSLPRKLKADKEFRQKV MLGTPFLVIWLVGFIADLNIDSWLI KGLMYGGVWATVQFLSKSFFDHS MHSALPLGIYLATKFWMYVTWFF WFWNDLNLFIHLPFLANSVALFYN FGKSWKSDPGIHKATEEQKKKTIVE LAETGSLDLSIFCSTCLIRKPVRSKH CGVCNRCIAKFDHHCWPVWGNCVG AGNHRYFMGYLFFLLFMICWMIYG CISYWGLHCETTYTKDGFWTYITQI ATCSPWMFWMFLNSVFHFMWVAV LLMCQMYQISCLGITTNERMNARR YKHFKVTTTSIESPFNHGCVRNIDF FEFRCCGLFRPVIVDWTRQYTIEYD QISGSGYQLV |
| 4826 | 10323 | A | 5130 | 3 | 144 | HEKYHKNTALHWAVLAGNTTVIS LLEAGANVDAQNIKAILRCHMAL |
| 4827 | 10324 | A | 5131 | 148 | 325 | RQGECKIHCKKKLSPGIRSYPVEN/ F/VDTMYDYLQPAYYKLNDLTNAD PCAVRYLLFDQN |
| 4828 | 10325 | A | 5132 | 175 | 405 | NILNSQFSTFLNDYVEFFVVFKIFNFI IIIF*DRVSICCPGWSIMVQSWLTAA LTFGR*SSNLSLPSSWDYRRVP |
| 4829 | 10326 | A | 5133 | 14 | 26 | YSPHEVGWKGRNREKMFCSEINVV FPDSVCQEMGFHHVAPAGLELMSS SDSPASASQSAGITSVSHSCLYTSK GVE*FTGIIFSS |
| 4830 | 10327 | A | 5134 | 177 | 454 | PLLERAKIGPRPEKPMETROGWGPF SPKVPGQKKFWG*LAPISPGMHPN PILGPMV*EGGP*PPGILGPP*PYGKP LF*RKRGSNNGGPYLQ |
| 4831 | 10328 | A | 5135 | 3 | 92 | NAWRTATEEWWTWDWNEDCSEP* HFTYVI |
| 4832 | 10329 | A | 5136 | 1 | 442 | PLIMNSIKSFSDDHAQCGRFEFDRQED DIHLVTLCVTELNDREENENHFPVI YGIAVNIKTAEIYRASQDRGPPEEQL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RAARTLAGGPMISIDYDAETEQLRNG PYSWTPFPFHVDFWLHQDDKQIFEN LSTSPLAEPFHFVEHIRSYLD |
| 4833 | 10330 | A | 5137 | 177 | 566 | EPFWSLSYLSLRGGRNVRLCRLSA LVFCQFKAMLLTLTAGNNKTAEIY RASFQDRGPPEQLRAARTLAGGPMI SIYDAKTEQLRIGPYSWTPFPFHVDF WLHQNDKQILKGRVYRLGKS*ISAP WFPHL |
| 4834 | 10331 | A | 5138 | 1 | 981 | PLLVEGR*VRLPQSAGDLVRAHPPL EERARLLRGQSVQVGPQGLLYVQ QRELA VTSPKDGSIILGSDDATTCH IVVLRHTGNGATCLTHCDGTDTKA EVPLIMNSIKSFSDDHAQCGRLEVHL VGGFSD\DRQLSQKST\HHFLIEFDR QEDDIHLVTL CVTELNDREENEN\H FPVIYGI\AVILLSLTAVNIKTAEIYR\ ASFQRSGVREEQA/LRAARKL*AGG PMIS\IYDAETETTS**DPYFLGHFPF HVGF\WL\HQD\DKQILDES FHRPL AE\PPHF\VEHIRSTLMVF*KNTPSA VNTLFPGNKALLYKKNEDGLWEKIS SPGS |
| 4835 | 10332 | A | 5139 | 1 | 405 | AYVTVCNQCGRESKLLSKFYELEL NIQGHKQLTDCISEFLKEEKL*GDN RYFCENCQSKQNA TRKIRLLSLPCT LNLQLMRFVFDROTGH TKKLNTYI GFSEILDMEPYVEHKVW*PTSLNSM LSLKLGGMCMLT |
| 4836 | 10333 | A | 5142 | 2 | 204 | ETGFCHVVQAGLKLGGSSDLPASAP QSAGITGMCHCAQPTKVS VASKVF KGSHKD*ILT*GYANKGA |
| 4837 | 10334 | A | 5143 | 1 | 360 | QQLTVLVAHLGVTLMDQRGYHWL LKSLMTQYQGLLYENP*ITLEIVNTL NPGTLLPNESVPGSALHCRVDVVHE MLSIQRDLTDHTLRDSIEYFIDRS FILGGDPLSGVCSSDFGLST |
| 4838 | 10335 | A | 5144 | 36 | 380 | FVALMGHKMSHNKFKIEIIRSMFSN HNRSQ*SK*IKEIYKCGN*HTSK**M H*GKKSLAKLENNEMNENESTT*Q NLWDAAKTALNEQFML*MPILKKG *MSQINKPTFHLKTIK |
| 4839 | 10336 | A | 5145 | 1 | 362 | ELNLPAPELPRKR TENLFLQLAEYV AHS LNVT S*YVCEGTTMGD*WPWE TQELEPTDPVPDIIPVQKAQTSNFW VLKTSINGQYCIPRKGKDF TIPVGR L N*LGQKLYKSITGTQGQSPG |
| 4840 | 10337 | A | 5146 | 2 | 428 | MFLLVVINLHILFVF*FKLFSWS*AIF L*FLF*FMSESENIYYAEIGHITIVT LKSLIATYCINPSSH CYKVYL VLSY LYCIIVNFDIYFLLLCVPFCYFSLIISL SPLFLLIYMIFLYIHFILLFVIFYTFIP FSFY |
| 4841 | 10338 | A | 5147 | 3 | 361 | TLFQL*DLRKQRLEDLSTLIPRIYPG WKCRT HFLLMKKSQIV IAGWYRRY AQHKRNQPTKSTVLVLQSYIRGRK ARKILRELKHQKRCTEAVTTIAAY |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | WHGTHALTETERLKEEARRKH |
| 4842 | 10339 | A | 5148 | 1 | 424 | VHLTADDKVIIAGLWSIVNAQDAV GETLGRLLQGVYPWIQRFSGFNLS SASAI VVNPKVTAHGKNVLTSLVD AITHLV DLMGTFAQLRELH*DKLYE DPENLHTLGHVLT VLVVIHFGT*FT AEVQASWLMMDTERANAL |
| 4843 | 10340 | A | 5149 | 24 | 452 | APSPDAMG/HSLWGKVNVEDAGGE TLGRLLVVYPWTQRFFDSFGNLSA SAIMGNPVKVKAHGKKVLTSLGDAI KHLDDLKGTFAQLSELHCDKLHVD PENFKLLGNVLT VLVLAHFGKEFTP EVQASWQKMVTGVASALSSRYH |
| 4844 | 10341 | A | 5150 | 38 | 501 | APSPDA\MGHFTTEEDKAT\TSLWGK \VNVE\ DAGGETLGRLLVVYPWTQR FFD\ SFGNLSASAI\ MGNPKVKAH GKKVLT\SLGDAIKHLD\DLKG\TFA QA*SELH\CDK\LVHDPENFKAPGG NVAGDPFLAIPFSAKEFHPLKVARL SWAERWVTW |
| 4845 | 10342 | A | 5151 | 2 | 198 | KVRPPPLKKTFFDSVDYRVLSEVD ERFAELPEFRPEDDLSSFS*PFLSPP CMSTALAHGDFSL |
| 4846 | 10343 | A | 5152 | 1 | 119 | DIMTGPHEVA AKNIQLTNEIQTLE TE*HEATKEFQVLS |
| 4847 | 10344 | A | 5153 | 3 | 83 | RMVLR LMP LSTDEALCFHAMFQPF LDMIHEAQQAMDIHFHSPDFQHPPT EFIREGDDDRTVLREMHHI*TG*LR VKWRCEEWR*I |
| 4848 | 10345 | A | 5154 | 2 | 370 | GAARLDERTKEGSDDDEDSG*GARA ELEGNKEGESEGQYKAKGERSAWS KLRTEIRQKAEESIDGIKVDDPS*IS MKATYTTMKIS*RQIRKIROREKKN TAKGEGQERQKNL SHKRHDISC |
| 4849 | 10346 | A | 5155 | 106 | 344 | RPCQQMQINVIHPINRMDKKHVIIPI DTSDKI*HPFMIQTLNTLCI**MYLSI IKAIYDPYTADIILTG*TFNAFFSTI |
| 4850 | 10347 | A | 5156 | 198 | 474 | |
| 4851 | 10348 | A | 5157 | 1 | 131 | PQEV PQSFGPPGDKAGC*GAGKMS PRERGGFLKCAEGGHPAPA |
| 4852 | 10349 | A | 5158 | 104 | 440 | FSKIYHFLCCCFVLSKNCPILLHFL KIYLLALGNINISYFYSHSKTLATG LKLTDSDSQHISHGTSGSRFKCLLS KAVLMSSLPVYS*LLKLLDVREVS NMVHDTLGIL |
| 4853 | 10350 | A | 5159 | 2 | 393 | EVWPRGLMGYVTVTEPSAVLVVRG VRDRLVITYPHEHHALTSSRLYLLM LFVGDP SGSGSNGSPDS*GLLLFRN DQAHIDLFVCFVLS CFFLFLSLCEL LWNAKQAMDQRQEQRRLQEMTK MARRPF |
| 4854 | 10351 | A | 5160 | 2 | 154 | FRDGVSLHCSGWS*TPGLK*SSCLS LPKCWDYRHEPPLLFPLWRAIGNIY |
| 4855 | 10352 | A | 5161 | 142 | 399 | HLLTYSEMFLGGVRYFLQSTLPADL SKHAYLYAP*LRLFA*RYTSAFTEW THSANKTVCLMPKLYELTYVGIDTL ATPVIKRYYS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4856 | 10353 | A | 5162 | 3 | 410 | HEG*PTFSSILHPPGAWAQLQ*PSQ ATTALFTLISVA*QQAGCSPQPGAG NTPPPPPNSGTLTPSPACAHWAQC* ANKDEFSVPGPQCLWPR*GPSYTAS LPQALRARPSQMTRVPQAPPPTGPG PVVSPCANTN |
| 4857 | 10354 | A | 5163 | 168 | 435 | IIAQ*N*FLKNNFQ*TI*K*NKTILFTT RSK**I*QKQQKNLYLEKYKTLLKEI KDLNKWKNISCSWIGTLSIDKLVTL SKLNRYRVNVI |
| 4858 | 10355 | A | 5164 | 2 | 427 | QIFRYLIMEKEQEHTYRGFKTVNR WTDAYDYAQHYSEASVASKDVS W*FHDYLGMSRHPDVLQA*QETLQ RHGAGSGGSRNLSGTRNCHVELEH ELADLHLKDSSLIFSFCFIANDCTLF TLAKILPGREIHS DACQHA FM |
| 4859 | 10356 | A | 5165 | 11 | 1232 | MAGAATGSRTPGRSELVEGCGWRC PEHGDRVAELFCRRRCRCVCALCP VLGAHRGHPVGLALEAAVHVQKLS QECLKQLAIKKQQHIDNITQIEDATE KLKANAESSKTWLKGFTELRLLL DEEEALAKKFIDKNTQTLQVYREQ ADSCREQLDIMNDLSNRVWSISQEP DPVQRLQAYTATEQEMQQQMSLG ELCHPVPLSFEPVKSFFKGLVEAVES TLQTPLDIRLKESINCQLSDPSSTKP GTLLKTSPSPERSLLLKYARTPTLDP DTMHARLR\MSADRLTVRCGLLGS\ LGPVPVLRFDALWQVLARDCFATG RHY\WEVDVQEAGAGWWVGAAY ASLRRRGASAAARLGCNRQSWCLK RYDLEYWAFHDGQRSACGPATTST GSASSWTTRPASSPSTT |
| 4860 | 10357 | A | 5166 | 115 | 447 | MSSWARLCESPVVWYF*HVLVCL HKLRLISQQFLTGINCQLSDPSSTK PGTLLKTSPSPERSLLLCKTPGSGD RVETVEMVGCWVEEDHGNGGPSFF LIRIYLFYLF |
| 4861 | 10358 | A | 5167 | 1 | 423 | ADMKAHLLHSGGMGFSCECSTGF VKHS*LIEHIRTHTGEKPFQCPKCDK SFRLKAQLLSHHGLLTGDRPFHCPE CDKNLRERGHMLRHQRIHRPERPF ACGYCGKGFYKSKLAEHIRVHTKS CPAANELDIKKMLHPLV |
| 4862 | 10359 | A | 5168 | 481 | 908 | EGSQWEAQKALAIQVPCGAVRVP WTTSSPASIPKQSVGKGCDCLR*L GDFAPARGEACECHTEPFRNSRGV GGAWARPGYLVLSLLSLQCPDSAC NQDLLAYLQRIALYCHQLNICKSVK AEVQNLGGELVVSGVSIS |
| 4863 | 10360 | A | 5169 | 2 | 2799 | EMTAVHAGNINFKWDPKSLEIRTLA VERLLEPLVTQVTTLVNTNSKGPSN KKRGRSKKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVVAVEDV RKQGDLMKAAAGEFADDCSSVKR GNMVRAAPALLSAVTRLLILADMA DVYKLLVQLKVVEDGILKL RNAGN EQDLGNQYKALKPEVDKLNIMAAK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RQQELKDVGHRDQMAAARGILQSN VPILYTASQACLPDVAAYKANR DLIYKQLQQA VTGISNAAQATASD DASQHQGGGGGELAYALNNFDKQI IVDPLSFSEERFRPSLEERLESIIISGA ALMADSSCTRDDRRERIVAECNAV RQACRTCSEYMGNA GRKERSDAL NSAIDKMTKKTRDLRRQLRKAVMD HVSDFSLETNVPLLVLIEAAKNGNE KEVKEYAQVFREHANKLIEVANLA CSISNNEEGVKLV RMSASQLEAGCP QVINAATWALAPKPQSKLAQENMD LFKEQWEKQVRVLTDAVDDITSIDD FLAVSENHILEDVNKCVIALQEKDV DGLDRTAGAIRGRAARVIHVVTSE MDNYEPGVYTEKVLEATKLLSNTV MPRFTEQVEAAVEALSSDPAQPM ENEFIDASRLVYDGIRDIRKAVLMIR TPEELDDSDFETEDFDVRSETSVQT EDDQLIAGQSARAIMAQLPQEQKA KIREQVASFQEEKSKLDAEVSKWD DSGNDIIVLAKQMCMIMMEMTDF RGKGPLKNTSDVISAACKIAEAGSR MDKLGRTIADHCPDSACKQGLVA YLQGIALLYCHQLNICKSKVKA EVQNL GGELVVSGNCDTCGALQGLKGWPP PLCLATHWVDSAMSLIQA AKNL MN AVVQTVKASYVASTKYQKSQGMA SLNLPVSMKMKAPKPLVKREK QDETQTKIKRASQKKHVNVPVQALS EFKAMDSI |
| 4864 | 10361 | A | 5170 | 25 | 458 | |
| 4865 | 10362 | A | 5171 | 3 | 764 | GPLCIALALQEFGTRRRWACRSLSS SGRRSLFRRMGSVKAVKNKAYFKR YQVKFRRRRKRGKTDYYAR*RLVIQ DKNKYNTPRYRMIVRV TNRDIICQI AYARIEGDMIVCATYAH*LPKYGV KVGLTNYAAAYCTGLLLARLLNR FGMDKIYEGQVEVTGDEYNVESID GQPGAFTCYLDAGLARTTTGNKVF GALKGAVDGGLSIPRSTKRFPGYDS ESKEFNAEVHRKHIMGQNVADYM RYLMQEDEDAS |
| 4866 | 10363 | A | 5172 | 8 | 400 | PLASFDTGDVECALCMRLFYEPDTT PCGHTLCLRCL*RCLYHNAKCP LCK DGLSQ**ASIKYSYNVIVEELIAKFL PEELKEREKLYE*EMEELYNLNNNV PILMCTMAYANVTCP LHMFEPCYR LMIRIW |
| 4867 | 10364 | A | 5173 | 2 | 400 | SLPLASFNTCNVECALCMRLFYEPV TTPCGHTFCLKCLERCLDHNAKCP L CKDGLSQCLASRKYIKNVIMEELIA KFLPE*LNERMKLYEYEMEELS NLN NNVPIFVCTMAYPTDPCPLHIFPCY RLMIRIC |
| 4868 | 10365 | A | 5174 | 1 | 216 | AGRTGRPEERAPESKSGSGSESEPS RGGSLRRGGEACGTSDGGPSPF*GS SVVSFTLLSYLGYYSYLLSTV |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4869 | 10366 | A | 5175 | 301 | 446 | SYFSYIILIIRGNESEGGFFEN*YFCL LINGGSWSGEPPrRNSHTFNC |
| 4870 | 10367 | A | 5176 | 155 | 404 | AAVPSRILKQYSHPNIVRLIGVCTQK QPIYIVMELVQGERGALSSR*GAQP GQVAALPQEAQQGSSPPAGGDFLTF LRTEGAR |
| 4871 | 10368 | A | 5177 | 172 | 443 | TGMIRGPWTKVGPGAIEKPPVGDGK VPNGCPKSLGNRQPCF*VLEVNEPY VPKKFKAEPFFHANICPLSEKERQF RKQTALVDL*KPKPR |
| 4872 | 10369 | A | 5178 | 3 | 428 | PDQTLCCCAEMGSHCVAQAGLEL LGLSDLPLASQSAITGVGHACAP VLGS*RPSQMLCPFPWWLLSATFY LAVPHLLPCLLFQPHSLRCSRSSSSA NLPVVFSFGAGCLSLSCMECSFP AKVLVIPFSPSERPPCS |
| 4873 | 10370 | A | 5179 | 2 | 432 | NIVSQNNDLPQTVIWMGDCIISLETR IQMQCDWNTSDFCVTPHS*NETEH HWEIKCHLVGREENLTLDIVKVKE QVFEASQAHLTLLPGTDIFSEAANG LSAINSLKWIKTTGNSTLVNFVLIIC LFLAAAFSPEAASASVD |
| 4874 | 10371 | A | 5180 | 163 | 585 | VEVRAHPKKRQRKKKEKKKSDRYS SSSSSSSDSSSSSDSEDEKDKKENR RKKKKNRSHKSSSESSMSETESDSKD SLKKKKKSKDGTEKEKDIKGLSKK RKMYSEDKPLSSESLSESEYIEEVQA KKKKSSEEREKATEK |
| 4875 | 10372 | A | 5181 | 18 | 566 | AEQSGEAAARGPVAGPLRPSLWPGFP RRATVCSVQHHGEAGQSGWPYMN PNSNGEIKGSQSQSSGPTIQDYLNRP RPTWEEVKEQLEKKKKGSKALAEF EEKNE*ELEERTGKTQGEIVKWK*E LIQKKDRERKKRRNLVGSSSDSED EDKKQGKRRKKKKNRSHKSSSESSM SETESDSKDSL |
| 4876 | 10373 | A | 5182 | 27 | 382 | SVILSFFFFFFYIAWATVRLCLKQTN ENNDKRDLTSLKVVRK*TLNLHPSI KAMIIRLYFEQLYDNRLANLDEMDI FLATQKLPKLAQEEVKNFSCRVTM DYVNNQNL*TNKGPEPDD |
| 4877 | 10374 | A | 5183 | 2 | 342 | GRSCDPKSVGQTLCVALLSVPLPGD PGQRKLPSQNSEEL*SQKCGPNPM CCSFPVPLAGGPGHSRRSTQSRTR*L KPQLPGWRTEKGAPEEIGKMMLQV IDERPGSALSCRC |
| 4878 | 10375 | A | 5184 | 2 | 147 | AETGFHHASQDGLDLLTS*STRLGL PKCWDYRREPQRPADTWFLKSTT |
| 4879 | 10376 | A | 5185 | 8780 | 9035 | LALQVHTMTPSKFFFIFLVETGFHH VSQDGLDLLTF*STRLGLPKCWDYR SEPPRPAYFYIFLRRSLSPRAGVA VSRDHATAL |
| 4880 | 10377 | A | 5186 | 75 | 355 | SNKNPSISCPRTWGECVCQATSRST WFLYPMPYAPIKPTPGDVPGTAPS GRPDSTPS**HRLQGTLPKPAPPLLG VFPKPLLAPLFPEGPGP |
| 4881 | 10378 | A | 5187 | 262 | 354 | VWSPPLTWCLVCQCRY*PGLLM |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MCFILPT |
| 4882 | 10379 | A | 5188 | 1 | 104 | ESETLPGGVAHACNPITLGG*GGRIT RSGV*DQP |
| 4883 | 10380 | A | 5189 | 1 | 144 | RDKVFALSHRLECSGAIHAHYNLQL LG*NNHRVSDSPVAGMAGVCHHT |
| 4884 | 10381 | A | 5190 | 99 | 241 | CFPGA W V R L Q L T Q A S D G P W Q C S S S Q R L H H A P H V V T L Y L C C A F S P C S P V K L R D F E S A V N N F E K A L E R A K L V H N N E A Q Q A I I S A L D D A N K G I I R E L R K T N Y V E N L K E K S E G E A S L Y E D R I I T R E K D M R R V R D E P E K V V K Q W D H S E D E K E T D E D D E A F G E A L Q S P A S G K Q S V E A G K A R S D L G A V A K G L S G E L G T R S G E T G R K L L E A G R R E S R E I Y R R P S G E L E Q R L S G E F S R Q E P E E L K K L S E V G R R E P E E L G K T Q F G E I G E T K K T G N E M E K E Y E * S H R * R * G S S V L V L D G D I A Q E H G G K D G A E Q L S D A S L G P G S D Y S S H K L L M G P G S A R V A R G S I M H H T L S H S T C V V P S P L A L Q |
| 4885 | 10382 | A | 5191 | 303 | 427 | I V L F E K K I F F F F F E T G S C S V P K A G V Q W C G H S S L Q P * P T G L M |
| 4886 | 10383 | A | 5192 | 82 | 352 | R V P E R V L P R P I P P A S C P V S P P A S R P L * G T P R A A P E T R R R P R T A R D P R G L R W Q T Q P A A P L L A S P G P G V A P V A S G A P I S R N D F Q L C K A R M L L |
| 4887 | 10384 | A | 5193 | 1 | 248 | Q K L K K L A R H G G A C A C G H K L L G W L R W * D H M S L R G Q G C S E S * S C R C T P A W T T E * D P V Y Q H K I L S L * D F L I * K A S S N R S S V I Y E L |
| 4888 | 10385 | A | 5194 | 3 | 370 | A Q W R V D S D G A P K R I A D S A T S P K L L Y V D R V V Q E I L E T E R T Y V Q D L K S I V * D Y L D C I R D Q T K L P L G T E E R S A L F G N I Q D I Y H F N S E L L Q D L E N C E N D P V A I A E C F V S K S E E F H I Y T Q Y C T N Y P R |
| 4889 | 10386 | A | 5195 | 28 | 183 | Y D R K R P V G K E K I G K L D C M K T * N F C A S K N T I K E M K R Q R T V W E K I F A H Y I S E R K |
| 4890 | 10387 | A | 5196 | 1 | 681 | M H P I G I A L S K V P V E S K E G D I M S H T G G S V P Y L D N L N K A S V C R G Q S C R V F Q V K E M V T Q V E S E N N Q E E Q K Q V R L P E S R L T P W E V W F I G K E K E E R D R L Q L K A L E F K E D W K L L K R R V T K K S G S V S V S I S S Q G \ N L T V C D C C E S F L L T K P V S C K H L I K S H S C P A L A V A S / C Q R P E G Y W S D C G T R S H S D Y A D E E D S F V S D S S D Q V S S R R T V T H S Y A P P Q S Q P H R H T Q T G T T A T Y L |
| 4891 | 10388 | A | 5197 | 1 | 2862 | M P G P L G L L C F L A L G L L G S A G P S G A A P P L C A A P C S C D G D R R V D C S G K G L T A V P E G L S A F T Q A L D I S M N N I T Q L P E D A F K N F P F L E E L Q L A G N D L S F I H P K A L S G L K E L K V L T L Q N N Q L K T V P S E A I R G L S A L Q S L R L D A N H I T S V P E D S F E G L V Q L R H L W L D D N S L T E V P V H P L S N L P T L Q A L T L A L N K I S S I P D F A F T N L S S L V V L H L H N N K I R S L S Q H C F D G L D |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | NLETLDLNYNNLGEFPQAIKALPSL KELGFHSNSISVIPDGAFDGNPLLR IHLVDNPLSFVGNSAFHNLSDLHSL VIRGASMVQQFPNLTGTVHLESLTL TGTKISSIPNNLCQEQKMLRTL YNNIRDLPSPFNGCHALEEISLQRN YQIKEGTFQGLISLRILDVSRNLI HSRAFATLGPITNLDVSNELTSFPT EGLNGLNQLKLVGNFKLKEALAAK DFVNLRLSVPYAYQCCAFWGCDS YANLNTENNSLQDHSVAQEKGTAD AANVTSTLENEEHSQIIHCTPSTGA FKPCEYLLGWSMIRLTVWFIFLVAL FFNLLVILTTFASCTSLPSSKFLIGLIS VSNLFMGIYTGILTFLDVSWGRFA EFGIWWETGSGCKVAGFLAVFSSES AIFLLMLATVERSLSAKDIMKNGKS NHLKQFRVAALLAFLGATVAGCFP LFHRGEYSASPLCLPFTGETPSLGF TVTLVLLNSLAFLMAVIYTKLYC NLEKEDLENSQSSMIKHVAWLIFT NCIFFCPVAFFSFAPLITAISISPEIMK SVTLIFFPLPACLPVLYVFFNPKFK EDWKLLKRRVTKKSGSVSVSISSQG GCLEQDFYYDCGMYSHLQGNLTVC DCCES\FLLTKPVSCKHLIKSHSCPA LAVASCQRPEGYWSDCGTQSAHSD YADEEDSFVSDSSDQVQACGRAC FYQ\SRGFPLVRYAYNLPRVKD |
| 4892 | 10389 | A | 5198 | 2 | 413 | VDFFFFLRRSLATVAQAGVQWRDL GSLQAPPPGFTPFCSLPSWDYRR PPRPANFFVFFFF**RWGFTVLAR MISIS*PRDPPTSASQSAGITGVSDRT RLDFKKKKKYCGKKDIMYRKVYTS LIQLTKKSLIH |
| 4893 | 10390 | A | 5199 | 1 | 142 | RKMFGNGRARGVIVLPCGKGYQS **GGQAVGSGSASCLPLSLCTFP |
| 4894 | 10391 | A | 5200 | 1 | 375 | GEATMNPSEAEVVCVPTWWPP VSTR*MGGRE*RKERAEGKRGKGG MEKEGAGERRGKEKNGDSRERGRE GKSVDNST*GAAAGLPQSPCPIQA RGVQSPRPQAMSRGEPEYSGIGGW GSGEA |
| 4895 | 10392 | A | 5201 | 109 | 331 | PLYCSPGASYMTLTALGPTQTQVPE QRLFVTCILCQEEQEVKVESRAMVL AAFVQRSSVLSKNRCKFI*DPGKS |
| 4896 | 10393 | A | 5203 | 2 | 168 | FFLDSTLKA*AIKAKINKWNDVKLK SFFKTKETINKM*QPMVWENIFANH LSDKG |
| 4897 | 10394 | A | 5204 | 107 | 357 | DLRWYSSFLWMCCIPGAKWHYPING SSCVMGMGIKYDFTGHWIVKHIGL AADLDSFYEYLLKSYILFGE*DDL* MFNAAAYQSIQ |
| 4898 | 10395 | A | 5205 | 3 | 376 | CQSQVPTDHGGQPPGSHPGWKPGP DLPPRFDPPEPSRPGN*GLLGPALCP SDLYAFGPQGISVNQGLPQWRPGW GHPWRLPEPDS*APAIQPLAEPVL WGWGGQRPRVPQQLPTAERCCSDF |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | S |
| 4899 | 10396 | A | 5206 | 1 | 262 | QNIFLHLFFCSFTAQKYPMVHLLQK SDNSFNQELLKSMVKSIMNDVYG PMSQILETLNKCPhFKRQR*VLLLD EYIVLLGRFILFA |
| 4900 | 10397 | A | 5207 | 2 | 296 | NGTHASYGAFYLEYSLLAEFTLVV KHKLPGVYVQPSYRSALMWVGVL SMWEGG*RQGLVRSTVGLGGAVLS SEDRSWGVGSLLSRASAPRLPLAHL RC |
| 4901 | 10398 | A | 5208 | 30 | 280 | FYYAFKEEIPVLYSLFQKIETGGILL NSALLLIPKST*YRRPYKKGKLNRYR PKSFVNINVKILNRI LANQIQKCIKRI TYYS |
| 4902 | 10399 | A | 5209 | 1 | 277 | NFSSLLIHGRMHTGEKPYECKNCGK AFTSAKSLQNHGRTHTG*KPCECKQ CGKAFICSSSCQRHEETHSVNMHSV ILIPKHKRVRVGKGPLR |
| 4903 | 10400 | A | 5210 | 220 | 585 | EILVRSRQDPLRSRRGKRHTGRRW DGSGWRATGARE*RRESRGWEME AREAGRRKPASERRKSGRRAGDF LEPATRSRSEKEVRTLARNGRP*AS PGSHRSSQ*LQPRVACGGRAATKSS |
| 4904 | 10401 | A | 5211 | 1 | 291 | SFLETLLPRLGCSDAIMAHCSLELLG YMRSCHLSLPS*DYRPTPSRLANSFF LIHGGFFTL SWADLQLLGLKQSF RK SWGLTG VSHHAQPPFPYYLY |
| 4905 | 10402 | A | 5212 | 228 | 379 | |
| 4906 | 10403 | A | 5213 | 317 | 534 | ATKEN*INWDLIK*NKQKPFASKDT TKQAKRQHIEWEKKVVNPIYDKAP VSRIKNLLKLNNKNTNNLIVKKK |
| 4907 | 10404 | A | 5214 | 3 | 366 | IGY/NPDTVACV/PILGWNGDNMLE QSANMPWFKGWKVTRKDGNASGT TLLEALDCILPPTRPTDKPLRLPLQD VYKIGGIGTVPVGRVETGVLPKGM VVTFA PVNVTTEVKS VEMHHEAQK AK |
| 4908 | 10405 | A | 5215 | 1 | 1254 | |
| 4909 | 10406 | A | 5216 | 33 | 1472 | KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD(CAVLIVAA GFVEFEVAGI\SKNGQTRHALLAYT LGVKQLIVGVNKMDS\TEPPYS\QKR YEEIVKEGSTYIKKIGYYPDTLAFEP ISGWNGDDMLEPSANMPWFKGWK VTRKDGNASG\TTLEALDCILPPTR PTDKALRLPLQDVYKIGGIGTVPVG RVETGVLPKGMGVTFAPVNVYN GK*KSVEMHHE/AL*SEALSWGNTN GLQLSRNVSVKDVRRGNFAGDSK\ NDPPMEA\AGFTAQVILNHP\SQKN ARHMPLELDCHTAHIACKFAELKE KIDRRSGKKLEDGPKFLKSGDAAIV DIVSG\KPMCVESFSDYPPLGRFAVR DMRQTVAVGVKAVDKKAAGAGK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | VTKSAQKAQKAK |
| 4910 | 10407 | A | 5217 | 178 | 566 | KGGATCPESPQDRKRRGNLDMKEL YSENEGMA SNHGKMENE*QPQDQR KPQVTLYSGRQEVKRGKDRKQGG NRR*GNV*RIKGKPESEGEAKEGKS ERESEMEGGSEREGKPEIEGKPE SEGEPL |
| 4911 | 10408 | A | 5218 | 27 | 336 | TNPVQQTLPVIWTSTRLPDTHEDKA FSAPQIEDRGTPGLGSRGALGPSPT PDCAG*VVAAGPGPAESHPRAPKPT AGMSPGVARLSSPGSGSQGSWQNP ERP |
| 4912 | 10409 | A | 5219 | 2 | 454 | HFNM RDPLTDCPYNKVYKNLKEFS QNGENFCKQVTSVLQQRANLEISY AKGLQKLASKLSKALQNTRKSCVS SAWAWASEGMKSTADLHQKLGA IELEAIKPTYQVLNVQEKKRKSLDN EVEKTANLVISNWNQIKAKKKLM VSTQET*STADLHQKLGAIELEAIK PTYQVLNVQEKKRKSLDNEVEKTA NLVISNWNQIKAKKKLMVSTQET |
| 4913 | 10410 | A | 5220 | 26 | 130 | TTWKYQYKNLERNQKEITELKSTIA EENITRGI*R*FEQTKE*INELEDKI MEIFKDKR*KKGEKSLRGLWPPSRD KEACMPWKLQTEKKKGAERLSEE IMAESFSNLLADMNINS*ELKSTIAEI ENITRGI |
| 4914 | 10411 | A | 5221 | 48 | 394 | SPSMCGSLDPPTLPQTLQVPSMLT HPCPPPPHPCPLAHPSSLLPSTHIY H**HLSPYPNPGTQEGHSGVRLRA TDVASPSVLGQFPSYSISVPREGHA ATVAAKGPLECRA |
| 4915 | 10412 | A | 5222 | 3 | 726 | EQEVDYDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKHPEA KRMPCAEDYLS\VVNLQLCVLH/EK TPVSDRVTKCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD EMPADLPSLAADFVESKDVCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKHPEA KRMPCAEDYLSRGPEPVMCVA |
| 4916 | 10413 | A | 5223 | 4274 | 5256 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLQHKDDNPNLPR LVRPEVDVMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KFYTAKNMIKDILKFIETGYNLSQK FKIDKFFNVFRRYVYMVVIDFVLV SNILPKFNHLCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LLESLEF GGSGENVNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELLFF AKRYKAAFECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV |
| 4917 | 10414 | A | 5224 | 1 | 332 | RMPCAEDYLSVVLTQLCVLHDKTP VSDIVAKCCSESLVNSQACLSL*V KDAYVPKEFNTETFTFHADICALSE TERRIMKQTGLDEFVKHKP*ASDER LSAVMDDFAAF |
| 4918 | 10415 | A | 5225 | 7 | 564 | TTRAAGREALSPGQGAGGGEGGA PRHTATGHAAGREGRGGRGADQG* GWPRGARALHDQAEGRGGLPAGLP VQAERPQREPCSGQVGSEPPCHP/A TAGGRKVRPAWPAAAGEAGGHSG TGRAGAAGGAAVGTGGGAAGPGG LPMSGGAGPGGSGAAAPHAAS*VQ PAAGAASAATRNIRMPKTT |
| 4919 | 10416 | A | 5226 | 132 | 917 | PGLFYLGEEQPGPQAGGPAAGQG ATAGAEAAAGCPGGAAAPAVLAG GRAGGRSAGWCAGAPGA*PGLFYL GEEQPGPQAGGPAAGQGATAGAE EAAGCPGGAAAPAVLAGGRAGGRS AGWCAGAPGA*AQP*TTGAAGREA LSPGQGAGGGEGGAEPHTATGHA AGREGRGGRGADQG*SLSQATDLW TSGPSHKWTDLSLWPYPCCSGCSW GQCL*LRAEGRGGLPAGLPVQAERP QREPCSGQVGSEPPCHPVSHTPKGP VPHCLGASPGLLWLATAGGRKVRP AGPAAAGEAGGHSGTGRAGAAGG AAVGTGGCQQRWIR |
| 4920 | 10417 | A | 5227 | 3 | 1245 | AWEFVWHPGGFDRSCPGPQGGEGS EGGEGT*EGSGSLALRPRPLSCPRA GPGPGPRLA*ASVYPWNQKRVGGL WRPQRTPARLCDPHAPEHAWAL*G KPGPAGHPAEAA*RQRE*AAGPRGT AAPAGQDRQHHAGPRGRPARGA AAAERQRAPEKGEEQPGPQAGGP AAGQGAAGAAEAAAGCPGGAAAP AVLAGGRAGGRSAGWCAGAPGA* AQP*TTGAAGREALSPGQGAGGGE GGAEPHTATGHAAGREGRGGRG ADQG*SLSQTTDLWTSGPSHKWTD LSLWPYPCCSGCSWGQCL*LRAEG RGGLPAGLPVQAERPQREPCSGQV GSEPPCHPVSHTPKGPVPHCLGASP GLLWLATAGGRKVRPAGPAAAGE AGGHSGTGRAGAAGGAAGVGTGGG AAGPGGLPM |
| 4921 | 10418 | A | 5228 | 612 | 795 | PGFISAIGGLVGLSSYDFYKEYED KPTSPPIAEMNPGYNI*HDLIKSFKM LAFICISS |
| 4922 | 10419 | A | 5229 | 1 | 345 | SSWSFTLVLTQAGVQWHDLSLQPL |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PSEFKRFSCSLPSSWDCRRLPPRPA NFLYF**RWGFTILTSLVLSY*PCVS PTSASQSAGITGVSDHARLIVGDFN TPLLITERSSTQKI |
| 4923 | 10420 | A | 5230 | 1 | 1212 | MPKKRQALVEFEDVLGACNAVNY AADNQIYIAGHPAFVNYSTSQKISRP GSDSDSRSVNSVLLFTILNPIYSITTP TRLNVFKNDQDTWDYTNPNLGQGG DPSNPNKRQRQPPLLDGHPAEYG GPHGGYHSHYHDEGYGPPPPHYEG RRMGPPVGEYGPADSPVIMVYGL DQSKMNCDRVFNVFCLYGNVEKV KISLKKQSPGGRPMGEEWLDGYAV DRAITHLNNNFMFGQKLN/CVGA QAREGSRGTGERKGGEWGPAEEHS EAEVLTHTEMGCGSVSKQPAIMPG QSYGLEDGSCSYKDFSESRRNRFST PEQAAKNRIQHPSNVLHFFNAPLEV TEENFFEICDELGVKRPSSVKVFSGK SERSSSGLLEWESKSDALETGLFLN HYQMKNPSINLVT |
| 4924 | 10421 | A | 5231 | 1 | 421 | FDPPGCFFTPIGNPFGPFQGNFHRK NGVQAMVEFDSVQSRQAASLN GADIYSGCCTLKIEYAKPTRLNVFK NDQDTWDYTNPNLGQGGDPSNPN KRQRGTVISQD*PSLLKNYCTCDF FSCSYICAAHVLCGTFQ |
| 4925 | 10422 | A | 5232 | 2 | 1883 | DEQRRRSGAMVKMAAAGGGGGG GRYYGGGSEGGRAPKRLKTDNAG DQHGGGGGGGGGAGAAGGGGGG ENYDDPHKTPASPVVHIRGLIDGVV EADLVEALQEFGPISYVVVMPKKR QALVEFEDVLGACNAVNYAADNQI YIAGHPAFVNYSTSQKISRIE*ND YR\SVNSVLLFTIVNTINWITTDVLY TMCNPGCPVQRIVIFRKNQVQAMV VFDSVQSAQRAKASLNGGDIYSGC CTLKIGYAKPTRLNVFKNDQDTWD YTNP\NLGQGGDPSNPNKRQRQP LLGDHPAEYGGPHGGYHSHYHDEG YGPPPPHYEGRRMGPPVGGHRQCP SRYGPQYGHPPPPPPPEYGPHADSP VLMVYGLDQSKMNGDRVFNVFCL YG\NVE\KVFMKSKPGAAMVEMA DGYAVDRAITHLNNNFMFGQKLN CVSKQPAIMPGQSYGLEDGSCSYK DFSESRRNRFSTPEQAAKNRIQHPS NVLHFFNAPLEVTEENFFEICDELG VKRPSSVKVFSGKSERSSSGLLEWE SKSDALETGLFLNHYQMKNP\NGPY PYTLKLCFSPAQHAFLIRCLGRVPFE QENISLSFMPFFGFCFCYLQKILGSP FFFFFFFFLKVVEEGFPP |
| 4926 | 10423 | A | 5233 | 2 | 337 | DMILAERGGVCVMMKTQCCTFIPN TSTTDGSITRALQGLTALSNEANN SGVNDPFTGWLEK*FSKWKGIIASIL TSLAAVMGVLILVRCCVIPCLQRLM ORLIKMAALTQTS |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 4927 | 10424 | A | 5234 | 62 | 343 | RQLNRNDPNRNKGKKVGIKQCLRF WNNFILTCLIGVSEIEEKKNAGAE*IF EEIMSKNFPKLIKYPNQIEA**TPS KINTEKTTFRH*IIGKR |
| 4928 | 10425 | A | 5235 | 1 | 359 | TDDDLNWLHDHSRTFREQGVDETET CLLRKFSYSQDQNVDSRDPVQLNLL YVQARDDILNGSHPVSEKACEFGG FQAQIQFGPHVEHKKHKGPFLE*MTF CFSFFSFLSSFSFSLFSL |
| 4929 | 10426 | A | 5236 | 2 | 264 | SYYPGEISVPPFNICHFFLSCFYNLS RFFCKKSPASPLCFSIKKSPFVKIHL VFSLVTSFLK*FFFYL*FFPESVISF GSFSNSD |
| 4930 | 10427 | A | 5237 | 3 | 246 | LIPRGQGSTVVLPPYNPATSIFGNDLN EIKMYGHAKTCIWMFMTSSFIIDRT RKRQ*CSSVREWINKQ*CIQTMELV FGRN |
| 4931 | 10428 | A | 5238 | 78 | 411 | VLNSPICNCLYPILCSFLFIHYFVVC FYTFIPVFYLVYHQEIVI*SLTLVFFV CVVKINTRLMVHIFILYICL*LSICNS VYLLHVHIYLEHFL*HILMVVFFKR SDQSS |
| 4932 | 10429 | A | 5239 | 2 | 175 | TKLDFIGIKGFSSVKDNVKGMRQA TDWEKIFAKETSDKGLLSKIY*KPF KLSKQPN |
| 4933 | 10430 | A | 5240 | 1 | 335 | VTIRGAGIPDESRNVNYSLASFLKR WLTLMDRGFIFNLINDYISGFSPKDP KVLAEYKFEFLQTCNHEHYIPLNLP MAFAKPKLQRV*DSDLEYSLSDEY CKHHFLGGLL |
| 4934 | 10431 | A | 5241 | 139 | 354 | SPCLPYCCLLCYRYGDGRIMIGFSC GH*VVISTHTGELGQEIFQARNHKD NLTSIAVSQTHIKVATCENNL |
| 4935 | 10432 | A | 5242 | 2 | 332 | ILAGAI*DNEIKLM*IEKEVVKLFLF TDDMILCVENSKEHTHSHTQLGLI NEFSRASG*KINVQKLFLYTNVQS KNEIKEPSLCTKASKRIGYLGHLTK EV*DLYSERTKPH*KKNRILRNTFN KRSVRLVQ |
| 4936 | 10433 | A | 5243 | 137 | 290 | GSSDINQTKHVR*VNRQICSRTTQ QSPEDCDFKKDGLVKRCMGTQTRQ SL |
| 4937 | 10434 | A | 5244 | 1 | 363 | LTCSGDKEQIKDKSHVLKKGKGNFE RETS*KKK*SLPPFDDNVEPNLDLYV EENICKSDSERPRSSSSSSSSFT PSQTRQQGPLKSMNDLHSDDYEE ESDEMEDNGPDFEMGKPVNIR |
| 4938 | 10435 | A | 5245 | 2 | 376 | VHLGWCMLPLRTHTEYVKALSYA* DKQLGA*AGLDRQIFLWDANTLSA LTASNNTVTSSLSGNTDSIYRLAM NQLVTIIVSGSNDKALRVWDPLTCA TLVNLKGHTDNGKALVFNRDGTQC LSR |
| 4939 | 10436 | A | 5246 | 60 | 185 | |
| 4940 | 10437 | A | 5247 | 1 | 146 | RWRDLGSPQAGFR*FCCLSLSSW DYRHAPLF*QFYLFILLFCKKYF |
| 4941 | 10438 | A | 5248 | 2 | 298 | TFFTFPFVAKPNPRGPKTPAPYFSPQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | GPQKIYPPKFLGPPFNFPPLLGKVF RAPNPRV*LPPGARPSSSSSLLPGF* KIPKPLFY*KKIFTPQKTKK |
| 4942 | 10439 | A | 5249 | 77 | 370 | EYS*SVVFLDLMRRQEELRRMEELH NQE |
| 4943 | 10440 | A | 5250 | 83 | 467 | YSEKSAGLWLNMLEKSLPGHRDTA TQIQHVSPMCQVEPPAKKAATLAE GDKDNDI*PCFVQRQLREGROGRA ARLWEKWLRWYVEKKAKKTALV VKSSIPLDIKPWDNETNIAQLEACM RFIQLDGLV |
| 4944 | 10441 | A | 5251 | 1 | 359 | KYTLSRLATVPPTLNPAEYNISPDTR RAQVEQLAIRAGLK*EYLLQYNNP NRRGLIEDPALIRWTYARSANVYPN FRPTPKNSLLGALCAFGPLFFWYCV FKTDMDRNQKLIREGKLDQ |
| 4945 | 10442 | A | 5252 | 3 | 349 | SSLATVPANLNPAEYSISPDNRRAQ VEQLAIRAGLK**YLLQYNNPTRIGI IKDPALIRWTYARSANVYPNFRPIPK NSLLGDLCAYGPLFFWYCVFKPDM DRKETLIPEGKLDQ |
| 4946 | 10443 | A | 5254 | 1 | 415 | NAVIQVAHPLVQKQ*VDYIHNGFL VPVMGPALHKTSVEEMIASTAYLEL FLRSISEPALLRTLRLFLLLHRHDT TILDTLVARIGSNSRLCMVSLSLFKT LLNLSCEDVLLQLGLRYLVPCNHV MLSQKPAVRDVL |
| 4947 | 10444 | A | 5255 | 34 | 394 | YRHYTICCIIGFLNTITMMTVSFHKY GEYFPGT*DLRDIDAGKC*YYAVNF PMRDGIDDESIGHIFKPIISKVMEM YQPIAVVLQCDAYSLYGDSLDCFNL TIIRHSTRLYLI*SYHFTS |
| 4948 | 10445 | A | 5256 | 178 | 417 | ILVPPAGGKGNLI*WNP GPPGARG FPGLTPPRGGKKGRAQPPENLVF* EKTGFPIVQRGGLKPPP GPPKGGE*R GGPP |
| 4949 | 10446 | A | 5257 | 749 | 1049 | DGSSLLGPRPGGKGNQTKGNPRPP G*RESPPHPPRRGKKRMAQPPQLI WDFSSSSGFPL*QGGGINPHDPPKG GKKRGEPPEPTTGPSKRGGKQGGF |
| 4950 | 10447 | A | 5258 | 1 | 359 | LFPKVNLSPVTPAKDTGLTAAPQEP KAPKASPVQHALPSSLSVPHTAILV TGAQLCGPAVNLSQIKDTACKSLLG LEEKKHAEAPAAENPHGGPGDSSA PY**GDAPKGHAIRAVEVPD |
| 4951 | 10448 | A | 5259 | 1 | 441 | FFFLNRVLTITQAGVQWCDHGSLQ PRSLGLK*PSHFSLPSS*DYRCAPPH LANFYIFYKDRWGFTMLPRLVWEL LGSSDLSILDSQSAGITGVRHHTWA NFFNFLCVSGIN*RNFYNKFTSWGS HPNSQYYSGISWGQSTNILLGY |
| 4952 | 10449 | A | 5260 | 1 | 553 | FYFYFFFFPLFFFFKPQDDFLVPGDQ NQRPGGSMPLGTAFILFQMKTLVL RRGINQDN*HWRQEDPLIPISPGFPS RIPPLKSEMSLPLSTDGSETRTQSP FDEIYMAHDASGLRLPDSPPPAAP GRDPAPSGQRAPGKLRGQCQLKSE |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RESRKEERQRSKPGEAAALGGVAC TFHLKSRS |
| 4953 | 10450 | A | 5261 | 1486 | 1695 | GKSCRPNVIYFILFSSFLRRSFALVA QAGVQWCDLGLSQPPPGFK*FSCL SLPSSWDYRYPPLCPANFC |
| 4954 | 10451 | A | 5262 | 1 | 334 | RRFVSQETGNLYIAKVE*SDVGNYT CVVTNTVTNHKVLGPPTPLILRNDG VMGEYEPKIEVQFPETVPTAKGATV KLECFALGNPVTIWRADGKPIA RKARRHEGCEM |
| 4955 | 10452 | A | 5263 | 78 | 313 | KVTYIQKNVYSKCTAGWVFTQRAR VGSREPFPAAPSPGPHGGDPPSPQ G*PLSPLPQPAPVRLPSPVMMSERIL PF |
| 4956 | 10453 | A | 5264 | 3 | 320 | IFSQENL*YSDGSDILGLLALQAEEN LGMVMIFTLVTAVQEKLEIVDQIK TSSSSSSSSSSSAEEAEKQLFHGTP VTIENVLNWESQGWRRQTFLGKILE KEKG |
| 4957 | 10454 | A | 5265 | 3 | 941 | APPRCLGDLWARARATMTDYGEE QRNELEALESIYPDSFTVDCTLIQPS *QLVFQNINGLS*YHILLQ*CFT*QG PC*VLSENPP\SFITVTSEAGENDES IHIKLLSCVLAVQTTLKFTYSEKYPD EAPLYEIFLPGKILEDNDVSDILKLL \ALQAEENLGMVMIFTLVTAVHERI NVLVDHITRCEVEMKL*DKEAEE AVKQLFHGTPVTIENFLNWKA/RSF DAELLEIKKKRMKEEEHAGLDKKIS GKQLFETDHNLDTSIQFLEDAGNN VEVDESLEFQEMDDLEDEDDDPD YNPADPESDSAD |
| 4958 | 10455 | A | 5266 | 1 | 332 | LKKHKSTRVP*NVKSGK*NFSPPFKI RPWAQKRAKKKGAREKKAD*EKG EFGKLSSSSRFRPGKKV*G*PKGFOR NFEKKPVKSQGPVNMGVIPAFEKKP RIPPAKIPI |
| 4959 | 10456 | A | 5267 | 3 | 375 | SASPQTLQQSLPRSIAPKPLTVRLPM NQIVTSVTIAANMPSNIGAPLISSMG TTMDGSAPSTQVSPSVQTQQHQMQ LSSSSSSSSSQMQMQQQQLQQHQ MHQQIQQQMQQQHFQHHMQ*HLQ Q |
| 4960 | 10457 | A | 5268 | 1 | 360 | KGAPKHGQAPLGDPPRAVGGQEH* GPARGRGPGPREPGSGQTSSPWVH VRPGGGKNDSGKARP*ILDPKSVSC IPAPSSHRPLSSPTNPFP*SSYEGSP RSPQPWTLQPQGPWPPSRQA |
| 4961 | 10458 | A | 5269 | 1 | 181 | KKKPQTWEKLV*GLF*KKRNPWG QRVPPVTPPLWGVKKRGGVFFRGL KPPLKPRENPF |
| 4962 | 10459 | A | 5270 | 10 | 108 | SHINVPMNQ*VVS LGPGQVTKGW DQGLLMCE |
| 4963 | 10460 | A | 5271 | 1 | 336 | EFLGAVGFCRLWIPNFAVLAKPLYG VTK*GDTELFKWGSQQQ*AFHELK EKLMSAPALGLPDLTKPFTLYVSER EKMAIGVLIQMVGPWPRPVAYLSK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | ELDGVSKARSEGCE |
| 4964 | 10461 | A | 5272 | 1 | 118 | TEVRH GKLDSSKWIPIRGN*NIYNP HCLSYKLEHGS DQEIPSDWYPFATV QFSVPDLC |
| 4965 | 10462 | A | 5274 | 2 | 327 | SCLVLVLLCVEYLF PYLHFQSI CVFT GEVSFLQAAYS WVMGFFVFLFI LH SYFL*LLWGLFISLHLWLSLT CEDLF LLFFSRCLYIICFVLLFMSFLILWR LLVF |
| 4966 | 10463 | A | 5275 | 171 | 331 | LKTSFRTKTCT*MLTASLFVIAKTW KQPRCPSVGE*LSNL*YVQTM ECYS VLK |
| 4967 | 10464 | B | 5276 | 83 | 332 | MGKRDNRVAYMNP IAMARSRGPIQ SSGPTIQDYLNRPRTWEEVKEQLE KKKKGSKALAEFE EKMNENWKKE LEKHREKLLSGX* |
| 4968 | 10465 | A | 5277 | 76 | 138 | |
| 4969 | 10466 | A | 5278 | 1 | 1050 | |
| 4970 | 10467 | C | 5279 | 146 | 433 | MKKKSNERWDQVYKILKGKSLRPG FPRCATVRAIQHHGEAGQSGGLYEP NSNGEIKGSNPVFRANNTGLSESTK AYLGRSKRATRKEKERLQGF G* |
| 4971 | 10468 | A | 5280 | 27 | 264 | NPNHQSLLCRAFCGVLILPVLALL TRLSFGELTYNNHFYIFKAFFKFI* VFKWTGDNMFFIKGDMDSLAFGGG G |
| 4972 | 10469 | A | 5281 | 135 | 358 | VHSPVL*LISTIPTSRLKFLKETGHGT PMEEIPEEELSEDVEQIDHADRELRR GQNLRCGIHRLP THIQVGQN |
| 4973 | 10470 | A | 5282 | 15 | 196 | KGKIVKLDIFI*NFSSAKDPVNY*K DNYRLRKMTANHISDKEFVSKTYK ECLKNLKKF |
| 4974 | 10471 | A | 5283 | 307 | 383 | YF*VSLATLCVYFLLDEGNILTATK VFTSMSLFNILRIPLFELPTVISAVVQ TKISLGR |
| 4975 | 10472 | A | 5284 | 3 | 267 | TIVRPYLLKKKTGTIVEERVNAPGW NEDDDVSVSDESELPSTTLKAFEK STMEQLVEKACFRDYHRLGL*TL SG SCCRS*P*SRRVQ |
| 4976 | 10473 | A | 5285 | 1 | 260 | TAVPSAASMTSTRAASASSVHVPVS ALGAGSAATAASEEMQTIPQATAA KYPRTIHPESSTSASRSLGT/ TISSHP VSHKCSFHKSG |
| 4977 | 10474 | A | 5286 | 60 | 292 | VTNFLIFHMRJISKYISIFLTVFFV SQ IVLLFKHSYFSYLELWKMQRDSK NAT*KRAL*RFHEKS FHEGCMCIKS |
| 4978 | 10475 | A | 5287 | 738 | 1152 | KGRVWSWC SRKRTFC SFGSFS SSSDA LTSYITTAIPTAVGGASATAVPS AASMTSTRAASASSVHVPVSALGA GSAATAASEEMSDKELITCTRQLKR DGCFGQYTNQPGTGNMGKKQPRIT LCPLNKRKVVA VKPN |
| 4979 | 10476 | A | 5288 | 3 | 555 | RKRTFC SFGSFS SSSDALTSYITHCCQ SPPAAV*LASATAVPSAASMTSTRA ASASSVHVPVSALGAGSAATAASEE MYVPRVVTSAQQKAGRTITARITGR CDFASKNRISSSLAIMGVSPHELSC |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | CGKTSSQSTVQTHSLKQLPAKYPRTHSIPESSTLSLPRSLGTQISSHPVSHKCSFP |
| 4980 | 10477 | A | 5289 | 94 | 323 | VIGYRNIRCTILTSTITSSLSIL*LNH*PETRLSE*AGV*DKGLVVAQMMWLMDHIFKYTNFGIVSLVHGDFIRQ |
| 4981 | 10478 | A | 5290 | 2 | 319 | MVLVTLDCKYAVAALWGKVKVDEVDGEALGRLMVVYPWTQRFWES*GDLSPPDADMGNPKVKVHGKVLGAVSNGQAHVDNLKGTFFATVSEMHCCKLHVAQEPEVL |
| 4982 | 10479 | A | 5291 | 1 | 159 | RDLQHFPSSVAM*DQTQNDIASTSNHESILQGIKGQSQL*EEVQLME*APVDC |
| 4983 | 10480 | A | 5292 | 187 | 282 | LRSY*CLLLMISFTRNANLFR LHGTHTDTFKCLEYEKCFNCNSDLIVHHRINMDHNPHTSA*DSGLLLGMHF |
| 4984 | 10481 | A | 5293 | 1 | 156 | SGGVDEQMMREKEELMLWLQDYEKIKKAEREL*EQIKREMKKNQKRKREKK |
| 4985 | 10482 | A | 5294 | 179 | 322 | NKVGGLTLPNCKTYYKATIIKTVWYWRKKRQIGQ*NRIESPIDPHKY |
| 4986 | 10483 | A | 5295 | 2 | 395 | RDRESDRDGQRRERERRTRKWSRSRSHYRSPSRCRTKSKSSSFGRIDRDSYSPR*KGRWANDGWRCPRGNDRYRKNDPEKQENARKEKNDIHLADDPNSADKHRNDCPNWITEPINC GPDPRTRNPEKL |
| 4987 | 10484 | A | 5296 | 3 | 228 | HELPHPGGLGLKRGCVWLEVAEHVVLGKALLILLPYRFKRNILAMDDKTGMTRNPHFSHNNWIPTFFSTQYFWIIFKVRWPRLKDTTDLRILAPNCLADRLSRHRCNIWQFMQGIRPLVLNFGSCT*PSFQPQQLYTNLFQHPVFLDHL |
| 4988 | 10485 | A | 5297 | 61 | 360 | YVNSKCSNHRK*SLSSSSSERESSFVPQVELHGRDLG*LQLWLPFGFKFPGLTPLRNGDDGPRPQPANLGLLVKTGFSPVAHLGVNLGTLGDCPALP |
| 4989 | 10486 | A | 5298 | 124 | 351 | EREFRFVPQVELHDRDLGSLHPGTPGLRKFSGLTLPRSGDNGPGPPPVNLGFLEETGFSHVAHFGLNFGT*GDCP |
| 4990 | 10487 | A | 5300 | 3 | 388 | HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQRQLHLNGTFPNTSDADMEPCVDGWVHDIISFSSTIVTE*DLVCDSQSLTSVAKCAFMTG*TADGFLGAHLSHRVRASSNVCMSGGSIVC |
| 4991 | 10488 | C | 5301 | 47 | 269 | MPPLIQSGMSSRTKTRTSSPCWNVHPAPEQYEAPDKDFMIVALDCSAAWPRAWVVTWSSWCPQQHHDIAVPVHA* |
| 4992 | 10489 | A | 5302 | 1 | 253 | MYTQ/HPEQYEAPDKDFMIVAL/DLSGLAEGLGGHVEQL/VARSNIMTL LFQCM/QAEFMPILGTNLNPEF/ISVCNNATWAIGEICMQW |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 4993 | 10490 | A | 5304 | 229 | 2984 | PCPCQNFLRCSTSFNFSLPCAMDWQ PDEQGLQQVLQLLKDSQSPNTATH RIVRDKLKQLNQFPDFNNYLIFVLT RLKSEDEPTRSLSGILKNNVKAHY QSFPPPVADFIKQECLNNIGDASSLI RATIGILITTIAASKGELQMWPELLPQ LCNLLNSEDYNTCEGAFGALQKICE DSSELLDSDALNRPLNIMIPKFLQFF KHCSPKIRSHAIGCVNQFIMDRAQA LMDNIDTFIEHLFALAVDDDPEVRK NVCRALVMLLEVRIDRLIPHMHSHIQ YMLQRTQDHDENVALEACEFWLTL AEQPICKEVLASHLVQLIPILVNGM KYSEIDIILLKGDVEEDEAVPDSEQD IKPRFHKSRVTLPHEAERPDGSED AEDDDDDDALSDWNLRKCSAAAL DVLANVFEELLPHLLPLLKGLLFH PEWVVKESGILVLGAIAEGCMQGM VPYLPHELPHLIQCLSDKKALVRSIA CWTLSTRYAHWVVSQPPDMHLKPL MTELLKRILDGNKKVQEAACIAFAT LEEKACTELVPYLSYILDTLVFAFG KYQHKNLLILYDAIGTLADSVGHHL NQPEYIQKLMPLLIQKWNEKDED KDLFPLLECLSSVATALQSGFLPYC EPVYQCCVTLVQKITLAQAMMYTQ HPEQYEAPDKDFMIVALDLFSGLA GLGGHVEQLVARSNIMTLLFQCMQ DSMPEVRQSSFAFLGDFTKACSSHV KPCIAEFMPILGTNLNPEFISVCNNA TWAIGEICMQMGAEMQPYVQMVL NNLVEIINRPNTPKTLLENTGRILTSP SAIPAITIGRLGYVCPQEVAPMLQQF IRPWCTSLRNIQDNEEKDSAFRGIC MMIGVNPGGVVQDFILFCDAVASW VSPKDDLDRDMFYKILHGFKDQVGE DNWQQFSEQFPPLKERLAAFYGV |
| 4994 | 10491 | A | 5305 | 47 | 411 | |
| 4995 | 10492 | A | 5306 | 20 | 1020 | LSLTSRMEEAELVKGRQLQAITDKRK IQEEISQKRIRKLGEDKPKA/QPLKT KALREKWLPWNPASGKEQEEM KKQNQQDPAPRSQVPRTKYPSGLR KRSQDLEKAELQISTKEEAILKKLKS IERTTEDIIRSVKVEREERAEESEDI YANIPDLPKSYIPSRLRKEINEEKED DEQNRKALYAMEIKVEKDLKTGES TVLSSIPLPSDYFNVTGIKVYDEGQK SVYAVSSNHSAAYNGTDGLAPVEV EELLRQALERNSSKSPTEYHEPVYAN PFYRPTTPQRETVPGPNFQERITIK TNGLGIGVNESIHNMGNGLSEERGN NFNHISPI |
| 4996 | 10493 | A | 5307 | 1 | 95 | GTRTFLRITYLSEIARRHPEFYAPELL *FAKR |
| 4997 | 10494 | A | 5308 | 1 | 338 | GTSLSA*GLNIDGQLGLGHTEDIPIY YTPCRSLFG*PIQQVACGWHVITIML TEHGQALLCGCNSIVQLAGPHGHL RRVGT*TIELRRENAVHIGAALMPH |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VALTTSRSIFQCR |
| 4998 | 10495 | A | 5309 | 3 | 472 | VTEFAKTCVADESAENCCKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLQHKDDNPNLRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGRAF KA\VARLSQRFP |
| 4999 | 10496 | A | 5310 | 12835 | 13995 | TIPIESDIFPSIFYLYLSSLAYADTYE ALSRFY*KKKLINLLLSLN*ATHFPK IMPVVQVELKAKFN*LFR\KCFLPST NPLLCRWR*YDEWNIATS*LIPAKC SLFYLLC*TVSCLAENT*LLFFRLLV RYTKKVPQVSTPTLVEVSRNLGKVS SKCCKHPEAKRMPCAEDYVSL*KHI IN***KNFPFRYC*CYLS*AEGSNVC VCMFCACVCACTCVYV*YWQSRPR G**FFFF*DGVSLLCCPGWSAVVPSR LTATSASQVQAILLPQPPK*LGLQV HATMPG*FFVFLVENFQLHLF*ISAL LPVL*LSVVLNQLCVLHEKTPVSDR VTKCCTESLVNRRPCFSALEVDETY VPKEFNAETTFHADICTLSEKERQI KKQT |
| 5000 | 10497 | A | 5311 | 1 | 349 | GTSKKLANKVVYNVGLCICLFDITK LEDAYVFPDGDGASHTKVHFRVCEC HPFLHEILTGKIKGCSPEGAHPLR* HPDFPLFSRPPAFLSPSQYILSPREIL VHPSILKFRTRRPY |
| 5001 | 10498 | A | 5312 | 1 | 410 | IEHGIVTNWDDMEKIWHHTFYNEL RVAPEEHPVLLTEAPLNPKANREK MT/QGSVPLPAFPP*SLQIMFETFNT AMYVAIQAVLSLYASGRITGIVMD SGDGVTHTVPIYEGYALPHAILRMD LAGRDLTDYLMKIL |
| 5002 | 10499 | A | 5313 | 216 | 390 | GSADARAPPVLSPVIFCPS*FLTGRP LQGVVMVGMGQKDSYVGDEAQSQR GILTLKYPIEHGIVTNWDDMEKIWH HTFYNELRVAPEEHPVLLTEAPLN KANREKMTQVRLGRRPCSSRPFP FLPILISDGSSPAGRHHGGHGPGLLR GRRGPEQAWHPDPEVPH |
| 5003 | 10500 | A | 5314 | 4 | 1254 | HAHAKLGTRAASSRTLFFRQLRRR VSLPVAMEEEIAALVIDNGSGMCK AGFAGGDA\PRA\VFPSIVGRPRHQG VMVG\MGQK\DSYVGDEAQSQRGI LTLKYPIEHGIVTNWDDMEKIWHH TFYNELRV\APEE\HPVL\TEAPLEP QGQTREKMTQ\IMFETFNT\PAMYR GPSRAVLSL*ASGR\TTGHCHGTLG DGVTHTVPIYGGLPHCSTPFLRLGP GLARDLTDYLMKILT*SEGYSFTTH GPSGKFVRDIKEKLCYVALDFEQE MATAASSSSLEKSYELPDGQVITIG NERFRCPEALFQPSFLGMESCGIHET TFNSIMKCDVDIRKDLYANTVLSGG TTMYPGIADRMQKEITALAPSTMKI KIIAPPERKYSVWIGGSILASLSTFQ |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QMWISKQEYDESGPSIVHRKCF |
| 5004 | 10501 | A | 5315 | 279 | 418 | VEHSISNKENFLGQGTGCHACNLNT LGGRGGRITWRSGV*DQLDQH |
| 5005 | 10502 | C | 5316 | 274 | 530 | MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE XQIXKQTALV* |
| 5006 | 10503 | A | 5317 | 2 | 736 | RLAKTYETTLEKCCAAADPHECYA KVFDEFKPLVEEPQNLIKQNCSELF QLGEYKFQNALLVRYTKKVP/SVVL LLRLAKTYETTLEKCCAAAHPEC YAKVFDEFKPLVEEPQNLIKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLGKVGSKCKHPEA KRMPCAEDYLSVVLNQLCVLHEKT PVSDRVTKCCTESLVNRRPCFSALE VDETYVPKEFNAETFTFHADICTLS |
| 5007 | 10504 | B | 5318 | 120 | 1070 | MPADLPSLAADFVESKDVCKNYAE AKDVFLGMFLYEYARRHPDYSVVL LLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNFHT ECCHGDLLECADDRADLAKYICEN QDSISSKLKECCEKPLLEKSHCIAEV ENDEMPADLPSLAADFVESKDVCK NYAEAKDVFLGMFLYEYARRHPDY SVVLLLRLAKTYETTLEKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQNC ELFEQLGEYKFQNALLVRYTKKV PQVSTPTLVEVSRKPRKSGQQML* |
| 5008 | 10505 | A | 5319 | 2 | 668 | |
| 5009 | 10506 | C | 5320 | 246 | 365 | MDDFAAFXXXCCXXDXKGDLLXR RKVKNNLLQVQLPLGF* |
| 5010 | 10507 | C | 5321 | 261 | 656 | MPCAEDYLSVVLNQLCVLHEKTPV SDRVTKCCTESLVNRRPCFSALEVD ETYVPKEFNAETFTFHADICTLSEKE RQIKKQTALVELVKHKPKATKEQL KAVXDDFXAFVEKCKGDXXKGELL XRRXVXNLL* |
| 5011 | 10508 | C | 5322 | 158 | 607 | MLCQSVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKTPVSDRVTK CCTESLVNRRPCFSALEVDETYVPK EFNAETFTFHADICTLSEKERQIKKQ TALVELVKHKPKATKEQLKAVXDD FXAFVEKCKGDXXKGELLXRRXVX NLL* |
| 5012 | 10509 | C | 5323 | 158 | 532 | MLCQSVPCAEDYLSVVLNQLCVLH EKTVPVSDRVTKCCTESLVNRRPCFS ALEVDETYVPKEFNAETFTFHADIC TLSEKERQIKKQTALVELVKHKPKA TKEQLKAVMDDFAAFVEKCKKAD XKG* |
| 5013 | 10510 | A | 5324 | 2 | 740 | PADLPSLAADFVESKDVCKNYAEA KDVFLGMFLYEYARRHPDYSVLL LRLAKTYETTLEKCCAAADPHECY AKVFDEFKPLVEEPQNLIKQNCSELF EQLGEYKFQNALLVRYTKKVPQVS TPTLVEVSRNLGK/VCCTESLVNRR |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | PCFSALEVDETYVPKEFNAETFTFH ADICTLSEKERQIKKQTALVELVKH KPKATKEQLKAVMDDFAAFVEKCC KADDKETCFAEEG*KLGAASQAAL GLY |
| 5014 | 10511 | A | 5325 | 1 | 588 | |
| 5015 | 10512 | A | 5326 | 364 | 1356 | TGDHAFQLWKSMMKHTFQVSTPTLV EVSRLGKVGSKCKHPEAKRMPC AEDYLSVVLNQLCVLHEKTPVSDR VTKCTESLVNRRPCFSALEVDETY VPKEFNAETFTFHADICTLSEKERQI KKQTALVELVKHKPKATKEQLKAV MDDFAAFVEKCKKADDEMPADLPS LAADFVESKDVCKNYAEAKDVFLG MFLYEYARRHPDYSVVLRLAKT YETTLKCCAAADPHECYAKVFDE FKPLVEEPQNLIKQNCLEFQGEY KFQNALLVRYTKKVPQVSTPTLVE VSRNLGKVGSKCKHPEAKRMPCA EDYLSVVLNQLCVLHEKTPVSDRV TKCTESLVNRRPCFSALEVDETYV PSVNSNSCRGLKKPRKSGQQL*TS *SKKNALSEDYLSVVLNQLCVLHE KTPVSDRVTKCTESLVKGDHAFQ LWKSMMKHTFPKSL/YAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCELFEQGEYKFQNALLVRYTKK VPQVSTPTLVE/VLKKPRKSGQQL* TS*SKKNALCRRLSIPWS*TSYVCC MRKRQ*VTESPISRNLGKVGSKCK HPEAKRMPCAEDYLSVVLNQLCVL HEKTPVSDRVTKCTESLVNRRPCF SALEVDETYVPKEFNAETFTFHADI CTLSEKERQIKKQTALVELVKHKPK ATKEQLKAVMDDFAAFVEKCKKA DDEMPADLPSLAADFVESKDVCKN YAEAKDVFLGMFLYEYARRHPDYS VVLRLAKTYETTLKCCAAADP HECYAKVFDEFKPLVEEPQNLIKQ NCELFEQGEYKFQNALLVRYTKK VPQVSTPTLVEVSRNLGKVGSKCK HPEAKRMPCAEDYLSRGPEPVMCV A |
| 5016 | 10513 | A | 5327 | 1468 | 1946 | LHISWEGEPIDYSVVLRLAKTYE TTLEKCCAAADPHECYAKVFDEFK PLVEEPQNLIKQNCLEFQGEYKF QNALLVRYTKKVPQVSTPTLVEVS RNLKVGSKCKHPEAKRMPCAED YLSVVLNQLCVLHEKQ*VTESPA AQNPW*TGDHAFQLWKSMMKHTFP KSLMLKHSPSMQIYENQDSISSKLK ECCEKPLLEKSHCIAEVNDEMPAD LPSLAADFVESKDVCKNYAEAKDV |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | FLGMFLYEYARRHPDYSVVLRLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRN/LRKSGQLR*I*TSCGRASEFNQTKL*AF*AAWRVQIPECAISSLHQESTPSVNSNSCRGLKKPRKSGQHTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLGGTGRPCFSSSGKSMETYP/KGFNAETFTFPGSFCT/LSWEGEPIDYSVLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPVC |
| 5017 | 10514 | A | 5328 | 1 | 2063 | MKKVKERDSFIMEDLGAELKSSAYSRGVFRRDAHKSEVAHRFKDLGEENFKALVLIAFAQYLQCPFEDHVKLVNEVTEFAKTCVADESAENCCKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLOHKDDNPRLRVRPEVDVMCTAFHDNEETFLKLYLYEIAARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELDEGKASSAKQRLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRA DLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLIKQNCLEFEQLGKYKFQNA AISSVTPKKVPQVSTQLLTPTLVEVSK/NTLGKVGSKCKHPESKKCPVAENYLSVVLNQLCVLLHEKTPVSDRVTKIAAQEPLVNRRP/CFSALEVR*NIPFPKEVNA/ETFTFHADICTLS/EKERQIRKQTALVELVETQAPRQKEQLKA/VLWDDFAAFVKIAAKA/DDKETCFAEETISGNAGAKKAIFLVNDEFILMSLTLIQNHRITYSSLPPCLYDSKLLLFHYLASIYPFVPPQDACKGVSE L |
| 5018 | 10515 | A | 5329 | 1 | 339 | RRRRKKNEKRKRQRKIKDEKSRKNSLRVEMRETWRQREKQKEEDREKRGQQEKERRKREIEEKEST*CEQMEIGKTKKVNIHCRWQTQLKLKFHLFS LFSIKMSLSFSTRA |
| 5019 | 10516 | A | 5330 | 2 | 189 | ARGGDAGDAFDGFGFGDDPSD*LSCHIDVHRYLFSALCDCYTFFVHIRVFLLSMRLADTA |
| 5020 | 10517 | A | 5331 | 3 | 346 | HELETFP*CHNMPLLFYRDRLSASDMLQVRKVMMDHVYESIITLNNESQSTSSNNNEHPGGQERSLARA |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5021 | 10518 | A | 5332 | 2 | 442 | VFMDADTLVLANIDDLFDREELSA APDPGWPD CFNSGVFVYQPSVETY NQLLHLASEQGGDQGILNTFFSSWA TTDIRKHLPIFYNLSSISIYSYLP AI*S EDVSGAISHLVPLGGDSQAMAQAV LVFLGKEPGRGTEWGNKGPR A |
| 5022 | 10519 | A | 5333 | 1 | 292 | VLANIDDLTREEMSAAQTQGWPD C/FNSGVFVYQPSVET/YNQLLHLAS EQGSFDGGDQGILNTFFSSWATTDI RKHLPIFYNLSSISIYSYLPVLPE |
| 5023 | 10520 | A | 5334 | 81 | 1163 | VTNLR LPRPPAHFVITMTDQAFVTL TTNDAYAKGALVLGSSLKQHRTR RLVVLATPQVSDSMRKVLETVFDE VIMVDVLDSGDS AHL TLMKRPELG VTLTKLHCWSLTQYSKCVFMDAD TL\VLANIDDLFDRE\ELSAAPDPG G\PD CFNSGVFVYQPSVETYNQLL HLAS\EQGSFDGG\ DQGILNTFF*QL GQQQDIRKHLAFIYNLSNISIYSYLP AFKVFGASAKVVHFLGRVKPWN Y TY\DPKTKSVK\SEAHDPNMTHPEFL ILWVGTSFTTNVLP LL\QQFGPWSK DT\CSYVN\VGRC LQGAISHLSLGEI PA\MAQPF\VSSEERKERWEQQQAD YMGADSF DN IKRKLD TYLQ |
| 5024 | 10521 | A | 5335 | 1 | 241 | GTSNSEHALDDRSTAQCRVQM QVV QQ*LQLAKDKERLQAMMTHLHV KSTEPKAAPQPLNLVSSVTLSKSAL EAYALET |
| 5025 | 10522 | A | 5336 | 13 | 229 | ACPRSPPPDRLGCCFP PP PAVC*AP AGPHPDGTTSELECTPAPHPSCPEV S VQQKPEPSALYGTGF PFGLQS |
| 5026 | 10523 | A | 5337 | 1 | 341 | GLGSGTSSSSSVKSSISPKRVARWSFS SRVCPVCPSSALSV*DSRSP*ASKSS SNASGSPFCRVKLLSCELQSKADS FSSSSAVSRDRLSSSSMLSRGQL*Q ETSKEAQMPR |
| 5027 | 10524 | A | 5338 | 3 | 168 | |
| 5028 | 10525 | B | 5339 | 978 | 1502 | MSNLTLCISTKHTPGISR AKEKKK GTSRLPTSLCQRRVGLTEEKSCSPEL QQKFRSETITEELVGLMNKFVEDT KKG VHQKEGW PSSAYGVTKIGVTV LSRIHARKLSEQRKGDKILLNACCP GWVRTDMAGPKATKSPEEGAETPV YLALLPPDAEGPHGQFVSEKRVEQ W* |
| 5029 | 10526 | A | 5340 | 3 | 239 | HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLESESMGT |
| 5030 | 10527 | A | 5341 | 3 | 322 | HEAKSSPNLVKAILQIQEATQIPRRI NKNKSTLRHRIEFLKTKDKEKSLRT PREIYYL*GNKISITVNLSETMEAR KKWHNYQMIEKNCQPTILHPAKLS FK |
| 5031 | 10528 | A | 5342 | 4 | 351 | VGRGRQSHLSHSHPTDPKGQQASP GWNPGVRMLPGLKWLPQPPAASLS *VPSSPTQQT SAGHLLSMSHEALTW |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VDRATGLAGNGEACVSGTQRHPGL SLAPPGCAPSPSSRAARA |
| 5032 | 10529 | A | 5343 | 3 | 163 | HEEQPEGLSPNLDRLFDRHCNQFS SRD*PIFLARCSHEYSGRHPRLADSI LL |
| 5033 | 10530 | A | 5344 | 112 | 362 | EREQRFTGLNDVHYLPIMYIVVGCA IFIT*V*RGWSSPTKCRSTDYCVNP STRLHAYMAPRHKLHSHCAERDPD QFTLLRHC |
| 5034 | 10531 | B | 5345 | 85 | 206 | XFSDPEVKKETRPALGSTVLLAPFL HEHEPPSAEVLPGSWRX* |
| 5035 | 10532 | A | 5346 | 142 | 653 | GFWHQRILGASDQAHLPLPHKQDG SADGARRVLACARGQGDLRLRLH LAAVPLQLPGGLRRRAVHVHGGGC QQDGGAESWS/PSPSSPRGPRTLHR VEKVPGAPVTPLPVAFSCNPDHGIE DPAFP*PAAGPR*LQEGPCGSRAS RAPPTSTRSCCTECLRNLSLILIC |
| 5036 | 10533 | A | 5347 | 261 | 538 | GSRRLLFSPRGPRTPYPAWKSTGA PVTSPPIAFSCNPDHGIEDPAFP*PAA GPR*LQEGPCGSRASRAPPTSTRS CCTKCLRNFLILIC |
| 5037 | 10534 | A | 5348 | 7 | 264 | FQKISALPQRSDYTHNTPHTDPARV SYKHAGANHTHIHTPMNTVSTTIYP PHAYLHTHTQKTPPHIYSTHAP*I*L FISTYAHTKN |
| 5038 | 10535 | A | 5349 | 208 | 713 | SVKMVRYSLDPENPTKCKSRGS\N LRVHFKNTRETAQAIGMHNRKAT\N KYLKDVTLQKQCVFRRYNGG\NGR CAQAKHWGWTQGR\WP*RVLNSL VIEHIQVNKAPKMRRRTYRAHGRIN PYMSSPCHIEMILTEKEQIVKPKEEE VAQKKKISQKKLKKQKLMARE |
| 5039 | 10536 | C | 5350 | 286 | 591 | MVRLFNLNPEKRQRKSWQIRGFQS SCFTLGLTVKLAQAIGMHIRKATE VSERWSLYRNSVYHSDGNNGGVG RRAQAKQWGLGHKVGGPKECLN FLLHML* |
| 5040 | 10537 | A | 5351 | 1 | 305 | GTSIYNVLYEVPLPPGRSLKFSGVY GPIICQRPSTNELPLDFPVKEVFELL GVDNVYQLFTWALLQKYILLYVQR *CNVTKALELSNLLLFHICDIKLV |
| 5041 | 10538 | A | 5352 | 15 | 234 | LSCPDQVHPHSLVPYPEPRRATASV PETSGPPFHPRRPYATTPALGHNP HA*LSSSFAGSRYKLGEMLHI |
| 5042 | 10539 | A | 5353 | 3 | 257 | HEVKYKNPAQ*QWHLRGPDAHVPE EFRYHKQLIQSQLFLHYHLSQTFTL QESADLQNAFLNSGQCILNKPLKFA DLHSDFMKTI |
| 5043 | 10540 | A | 5354 | 3 | 334 | IIKFIWNPKRA*IAEAILSKKNIAGGI TLPDFRLYNKAIVI*TAWYWHKNR HIDQWNRILNPEIKSHTYSQRIFDKI DKNIH*GKDTLFNKWCWERWIAIC RRIKLDLSLV |
| 5044 | 10541 | A | 5355 | 1 | 119 | QKSRW*TPPNSYMKVNVPEKSRNG ETSLRTKIAVCQYYM |
| 5045 | 10542 | A | 5356 | 3 | 349 | HEPANADFAFRFYLIASETPGKNIF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | FSPPRFPAAAYAMLSLGACSHSRSQL EGLGFNLTESESDARRRCRQ*VGT LDLTGHGLQTRGGQGPWPRARPSR GGDAAAGSARLPPR |
| 5046 | 10543 | A | 5357 | 1 | 499 | |
| 5047 | 10544 | B | 5358 | 66 | 641 | MASKINTKALQSPKRPRSPGSNSKV PEIEVTVEGPNNNNPQTSVARTPTQ TNGSNVPFKPRGREFSFEAWNAKIT DLKQKVENLNFNEKCGEALGLKQAV KVPFALFESFPEDFYVEGLPEGVPFR RPSTFGIPRLEKILRNKAKIKFIKKP EMFETAIKESTSSKSPPRKINSSPNV NTTASGVEDLNIIQ* |
| 5048 | 10545 | A | 5359 | 2 | 306 | ARGVCGGCRCLGFCGSVVGDLMY* NSFDCFKKVLRY*GFFGLYWGLIP* LIWFAPEQAIYLTDNVVFVRDKFT*R DGSDSLSAEVLAGGCALGSLVIVTN SL |
| 5049 | 10546 | A | 5360 | 3 | 120 | HEGKEPDIPLYETVQTVGPSHARTY TVASHSEGR*TIC |
| 5050 | 10547 | A | 5361 | 2 | 366 | SLPASDRPPISSPLATSGTIFSAISCF WDLPAFPLWLAPSCQPTMSSQIRQN YSTDVEAAVNSLVNLYLQASYTYL SLQDIKKPAEDEWGKTPDAMKAA MALEKKLNQALLDLHALGSART |
| 5051 | 10548 | A | 5362 | 1 | 108 | |
| 5052 | 10549 | A | 5363 | 2 | 536 | ARAARDWKNYSTDVEAAVNSLVN LYLQASYTYLSLGFYFDRDDVALE GVSHFFRELAEEKREGYERLLKMQ NQRGGRA\LFQDIKKPAEDEWGKTP DAMK\AAMALEKKLNQALLDLHAL GSARTDPH\CDFLEPHFIDEEVKLI KKMGDHLNLHRAGWPRRLGLGE YLFERLTLKHD |
| 5053 | 10550 | A | 5364 | 3 | 331 | HEQYPGSISISLTDLGCPDMPVIAR* TAAADESLVPTRLMLQLADYGPVI YSLVI*VCLTAAFTLAQQHSMKIY ADIIGSED\TTNEDYRSIALYFEREMR YLQAAKF |
| 5054 | 10551 | A | 5365 | 3 | 52 | HEQSWKAENEFTLADLKQLPELN PPVLMPRGNVGTPLRVFLELIRACR LPPRIITQLHFQIPKIGYSLRYCNVPF EYEDSDTAVQE*LT |
| 5055 | 10552 | A | 5366 | 3 | 323 | STFFFFFLRQSLALVAQAGLRTQW RNLGSLQAPPPGFTPFSCSLPSSWD YRRPPRLA\NFFFFFFFVFLAETGFH CVLARMVISIS*PRDQPASASQSAGIT GVSD |
| 5056 | 10553 | A | 5367 | 3 | 337 | HERHEDTLTLKERNRGNGILDDID DHNIIYHLPDA*SEEYEFKEQTTL LRASIPFSVGGSNQLIEAIGKMVRGR LYPWSDVKVENPQHNDFMKLITML ITHMHDLDQDV |
| 5057 | 10554 | A | 5368 | 16 | 313 | SHSVTQAGVQCWHLHAQLIFLYF LVETGFHRVSQDGLYLLTS*SARLG LPKCWDYRRDDHAWPVQFFKCS PRPQAILDFAFTSHELCLGSMRLKLS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5058 | 10555 | A | 5369 | 1665 | 1787 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5059 | 10556 | A | 5370 | 1431 | 1553 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5060 | 10557 | A | 5371 | 1740 | 1862 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5061 | 10558 | A | 5372 | 1173 | 1295 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5062 | 10559 | A | 5373 | 1027 | 1149 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5063 | 10560 | A | 5374 | 2250 | 2372 | FFVLLVETGFHRVSQDGLDLLTS*S AHLGLPKCWDYRHEPP |
| 5064 | 10561 | A | 5375 | 934 | 1092 | FFVFLVETGFHRVSQDGLDLLTS*S ARLSLPKCWDYRREPPCPRIYILTR SR |
| 5065 | 10562 | A | 5376 | 2588 | 2824 | VAGTIGACHHAQLIFVFLVETGFHH VGQDGLDLLTS*STHLGLPKCWDS RREPLRPASPVVFQRTSAPVMADLT PTVS |
| 5066 | 10563 | A | 5377 | 935 | 1138 | RRGFTMFHHVSQGGDLLTS*SARL GLPKCWDYRREPLCPAWKDY*CKL QDEVISQQGLKVSVVLHI |
| 5067 | 10564 | B | 5378 | 79 | 1551 | MSEVTKNSLEKILPQLKCHFTWNLF KEDSVSRDLEDRCVNCQIEFLNTEFK ATMYNLLAYIKHLDGNNEAALECL RQAEELIQEHADQAEIRSLVTWGN YAWVYYHLGRLSAQIYVDKVKQ TCKKFSNPYSIEYSELDCEEGWTQL KCGRNERAKVCFEKALEEKPNNE FSSGLAIAMYHLDNHPEKQFSTDVL KQAIELSPDNQYVKVLLGLKLQKM NKEAEGEQFVEEALEKSPCQTDVLR SAAKFYRRKGDLDKAIELFQRVLES TPNNGYLYHQIGCCYKAKVRQMQ NTGESEASGNKEMIEALKQYAMDY SNKALEKGLNPLNAYSDLAEFLETE CYQTPFNKEVPDAEKQQSHQRYCN LQKYNKSEDVAHQHGLEGLSISK KSTDKEEIKDQPQNVSENLLPQNA NYWYLQGLIHKQNGDLLQAACQY EKELGRLLRDAPSGIGSIFLSASEL DGSEMGQGA VSSSPRELLSNSEQL N* |
| 5068 | 10565 | A | 5379 | 925 | 1127 | FFVFLVETGFHRVSQDGLDLLTL*S THLGLPKCWDYRREPLRPATFSSYQ RNNPDLILNDTIMPNIK |
| 5069 | 10566 | A | 5380 | 438 | 815 | TRPSFSFNPLTLFFFFLRRSLALSPRL ECGSAISAHCKLRLLGSSHSPTSASR VAGTTSARHAWLMFFVFLVETG FHLVSQDSL DLLTS*SAPLGLPKCW DYRHEPPRPAHLHFLNFFLFSYT |
| 5070 | 10567 | A | 5381 | 7944 | 10115 | KQCNYGHNLTCSNFFFFWRWSLA PSPRLECNGAISAHCKLRPPGFTPFS CLSLPSSWDYRRSPRAANFFVFLV ETGFHQVSQDGLDLLTL*SARLGLP KCWDYRREPPCPESALIF |
| 5071 | 10568 | A | 5382 | 1 | 211 | LKTSEKWRNRQDKSNKGSKKAER |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RATHADRNREAARIRRKTYTNERK HYEHHRTAGKDQDERATEDSRE* RE |
| 5072 | 10569 | A | 5383 | 2 | 373 | ARECHHLCKINYMDLVKEFMTLNA SAPLRSSFSDTMIRLPALTYPLFPAL ATCAGYSDKA*SSISYVLHNSALWR ASGPTDHRDAPA*A*LESRRSTLRIC ELRTLYSLIKSTASNFDPIKLFS |
| 5073 | 10570 | A | 5384 | 112 | 913 | DFLSMPNRRGGVSLPPTPP*PPFSVT HTIFSVSFSFHWLKGSLRRQFSYCF YGMVLVPFSPHPPLSLSAPSKCLRIP PLPWGWVTAPRLRSHPSVTGRAVL ERKPSVRG*AGSLNTQARDTPPQLP ERPPEG*ALFPPFPYSMAPPSQLKPT LKITAVRS*ASGGATGLGGWSPGLL P*EQGLRPTATLTQTSIALNPRSLT PAPQLRLSCPPHFALTTRA VPGGPQ PLAWGPEPGTPPAQPRSPDSAQSH TVYRRESILFFIL |
| 5074 | 10571 | A | 5385 | 2 | 345 | SFWLLCGSSCDLRSCQVLKCTRNI PYSLVPTASCEHLHGPCIYRPSVQS VLTCTAAQATNILSAQSLLSGPTTQ* WGLTYPCLLVGAADLTPTTPPPPT PAPPHLPSTPPP |
| 5075 | 10572 | B | 5386 | 36 | 340 | MFLDEYARRHPDYSVLLRLAKT YETTLEKCCAAADPHECYAKVFDE FKPLVEEPQNLKQNCLEFEQLGEY KFQNALLVRYTKKNALCRRLSIRGP EPVI* |
| 5076 | 10573 | A | 5387 | 3 | 182 | |
| 5077 | 10574 | C | 5388 | 602 | 877 | METTLRRKCCARLQILHGMAMPKV FRWNFKPLVGRSLRNLNPNKIVEAF WSQLGRSYKFGPMRYLVSFTPKES YPKCSNFPTLCRRVFKET* |
| 5078 | 10575 | A | 5389 | 1 | 404 | GTRNDKMEPGLEQGTIPRLDSVTSS ECFASSGFHEDRSLSDVEEQEDSDG FYKEPITMEDLISYSFQVAIGMESLS SRLCIHRDLEARNFHLSGNYCDTSL EF*IENYDIYL**FNIYSPTKLKPEDT RLKET |
| 5079 | 10576 | A | 5390 | 110 | 424 | LSSLQREREGHLNGSPSFMKCSGF YRLA*GVCV*VSFVL*Y*HILIYSML TVLILCIYFFNMLISGIYTDYAYFYIC YIYYCYIF*FILLCFYTLMTIFFGLI |
| 5080 | 10577 | A | 5391 | 2 | 361 | ARETVKRIQYPIPLEGRLGLKPLIES LI*DGLLELCMSPTYTPILLVK*SDW *Y*LVEDLQAINQTVQTTHPVVPNP YTILSKIPYDHQWFTEIDLKDAFWA CPLAEDS*DIFTFEWARA |
| 5081 | 10578 | A | 5392 | 3 | 335 | QSQSWWRQKGVSRAGAGPIHPQGL LFGFS*GDLGPLGTLGEQGLIGQRG EPGLEGDSGPMGPDGLKGVRGDPG PDGEHGEKGQEGLMGEDGPPGPPG AAGVRGLHGKSGY |
| 5082 | 10579 | A | 5393 | 61 | 497 | |
| 5083 | 10580 | A | 5394 | 16 | 951 | RRPKIRDKFWGVS/KKLAHSEASPI SGASKRAKKQINVYVGKSS/QGK |

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|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MVVVWVKKLDRTVFALVNYIFFKG KWERPFVEVKDTEEDFHVDQATTV KVPMMKRLGMFNIQHCKKLSSWV LLMKYLGNATAIFFLPDEGKLQHLE NELTHD\IVTKFLE\NEDRRSASLHL PKLSITGTYDLK\TVLGQ\LGITKVFS NGAD\LSGVTEEAPLKLSKAVH*GC A*PSTEERGLKLAGGHVF*EGHYPC FIPPRGSSFNKPFVFLNGFEQN/SPSF PLFMGEKVVNPTPKITGLSLLNPSP PSLGPLPGMTLKKGLSWK |
| 5084 | 10581 | A | 5395 | 2 | 306 | GFDHVAQAGLEPLGSSDLPPSASQS AGITGMSHHTQPAYILKISFITLPFIIR SLS*VPFVFSIMYKSSFNFSPCGESVF STNLLNNEYLLIDWWLHFIY |
| 5085 | 10582 | A | 5396 | 1 | 375 | |
| 5086 | 10583 | A | 5397 | 162 | 426 | |
| 5087 | 10584 | A | 5398 | 140 | 426 | |
| 5088 | 10585 | A | 5399 | 158 | 705 | PSEKNKNNLLLGVVYVRHLPNLLD ETQIFSFSQFG\PVTRFRLSR\NKRT GN\SKGYAFLEFESEDVCQNSCLKQ WNNYLFGGKTLG/QCHFMPPEKVH K\NSFKDWDFPFKQPSYPSVKRV*S ESDTNTKA/DGMEERFKKKERLLRK KLAKKGIDYDFPSLILQKTESISKTN RQTSTKGQVFT |
| 5089 | 10586 | A | 5400 | 2 | 388 | FLFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGQAGLELLAPS DPPA |
| 5090 | 10587 | C | 5401 | 197 | 415 | MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASAF* |
| 5091 | 10588 | A | 5402 | 671 | 986 | KGVLFFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA |
| 5092 | 10589 | A | 5403 | 65 | 921 | |
| 5093 | 10590 | A | 5404 | 213 | 442 | |
| 5094 | 10591 | A | 5405 | 1 | 1506 | |
| 5095 | 10592 | A | 5406 | 1 | 286 | DRLIYIPFPDEKSLVPILKANLGKSP\ VPKDLDFLEFLDLVPWGCGRLPFRG NQGAHSLHSPAGHACYSLTLDR GFLQKSKPKAVKLPRFSFG |
| 5096 | 10593 | A | 5407 | 2 | 158 | |
| 5097 | 10594 | A | 5408 | 1 | 9064 | MLARAARGTGALLRGSLLASGRA PRRASSGLPRNTVVLFVPQQEAWV VERMGRFHRILEPGLNILIPVLDRI YVQSLKEIVINVPEQSAVTLDNVTL QIDGVLYLRIMDPYKASYGVEDPEY AVTQLAQTTMRSELGKLSLDKVFR ERESLNASIVDAINQAADCWGIRCL RYEIKDIHVPPRVKESMQMQVEAE RRKRATVLESEGTRESAINVAEGKK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | QAQILASEAEKAEQINQAAGEASAV LAKAKAKAEAIRILAAALTQHNGD AAASLTVAEQYVSFAFSKLAKDSNTI LLPSNPGDVTSMVAQAMGVYGALT KAPVPGTPDSLSSGSSRDVQGTDA LDEELDRVKMTWSPVPNFQLLNIPS NWGQPHAPGQTSTEV PADGDGATD GPLCLAHASLCCQVAGAAAAALPG AIAGGAVGWARIPRLRLSLSTGMQ KASVLLFLAWVCFLFYAGIALFTSG FLLTRLELTNHSSCQEPGPGSLPW GSQKGPGACWMASRFSRVVLVLID ALRFDAQPQSHVPREPPVSLPFL GKLSSLQRILEIQPHHARLYRSQVDP PTTTMQRLKALTGTSLPTFIDAGSN FASHAIVEDNLIKQLTSAGRRVVM GDDTWKDLFPGAFSKAFFPFSFNR DLDTVDNGILEHLYPTMDSGEWDV LIAHFLGVDHCGHKHGHHPPEMAK KLSQMDQVIQGLVERLENDTLLVV AGDHGMTTNGDHGGDSELEVSAA LFLYSPTAVFPSTPPEEPEVIPQVSLV PTLALLGLPIPGNIGEVMAELFSG GEDSQPHSSALAQASALHLNAQQV SRFLHTYSAATQDLQAKELHQLQN LFSKASADYQWLLQSPKGAEATLP TVIAELQQFLRGARAMCIESWARFS LVRMAGGTALLAASCFCILLASQW AISPGFFCPLLLTPVAWGLVGAIAY AGLLGTELKLDLVLLGAVAAVSSF LPFLWKAWAGWGSKRPLATLFP GPVLLLLLFR LAVFFSDSFVVAEAR ATPFLG SFILLV VQLHWEGQLLP PKLLTMPRLGTSATTNPPRHNGAY ALRLGIGLLLCTRLAGLFHRCPEETP VCHSSPWLSPLASMVGGRAKNLW YGACVAALVALLAAVRLWLRRYG NLKSPEPPMLFVRWGLPLMALGTA AYWALASGADEAPRLRVLVSGAS MVLPRAVAGLAASGLALLLWKPVT VLVKAGAGAPRTRTVLTPFSGPPTS QADLDYVVPQIYRHMQE EFRGRLE RTKSQGPLTVAA YQLGSVYSAAMV TALTLAFLPLLHAERISLVFLLLF LQSFLLLHLLAAGIPVTPGKYLSDD SLKDNSDSQGLRKRQQPPGNEADA RVRPEEEEEPLMEMRLRDAPQHFY AALLQLGLKYLFILGIQILACALAAS ILRRHLMVWKVFAPKFIFEAVGFIV SSVGLLLGIALVMRVDGAVLLSSAS TERHCQQTTRGRKPTLVSVLVLDSE QRKDGRLRSALVSSYRFLETSPAGA ELFRPASATMSRQTTSVGSSCLDLW REKNDRLVRQAKVAQNSGLTLRRQ QLAQDALEGLRGLLHSLQGLPAAV PVLPLELTVTCNFILRASLAQGFTE DQAQDIQRS LERVLETQEQQGPRLE QGLRELWDSVLRASCLLPELLSALH |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RLVGLQAALWLSADRLGDLALLLE TLNGSQSGASKDLLLLKTWSPPAE ELDAPLTLQDAQGLKDVLLTAFAY RQGLQELITGNPDKALSSLHEAASG LCPRPVLVQVYTALGSCHRKMGNP QRALLYLVAALKEGSAWGPPLLEA SRLYQQLGDTTAELESLELLVEALN VPCSSKAPQFLIEVELLLPPDLASP LHCQTQSQTKHILASRCLQTGRAGD AAHYLDLLALLLDSSEPRVGPCMP EVFLEAAVALIQAGRAQDALTLCEE LLSRTSSLLPKMSRLWEDARKGTKE LPYCPLWVSATHLLQGQAWVQLG AQKVAISEFSRCELELLFRATPEEKEQ GAAFNCEQGCKSDAALQQLRAAAL ISRGLEWVASGQDTKALQDFLLSV QMCPVSAKRLRPSFESSLPLPLPLPL PPRGSGASVVRPTPRCRPRPARLAP LERTSGPGQVFRPTPPGRRPGALGR QSAVRPTTRRKPLVPGESRPREPEA PAGPEEDIKVQRLGNLPKITIKQWH NWNSDPMGLTIEFLLLTLLSKGDD LSTAILKQKNRPNRLIVDEAINEDNS VVLSQPKMDELQFRGDTVLLKG KKRREAVCIVLSDDTCSDEKIRMNR VVRNNLRVRLGDVISIQPCPDVKYG KRIHVLPIDDTVEGITGNLFEVYLKP YFLEAYRPIRKGDIFLVRGGMRAVE FKVVETDPSPYCIVAPDTVHCEGEP IKREDEEESLNEVGYYDDIGGCRKQL AQIKEMVELPLRHPALFKAIGVKPP RGILLYGPPGTGKTLIARAVANETG AFFFLINGPEIMSKLAGESNLRKA FEEAEKNAPAIIFIDELDAIAPKREKT HGEVERRIVSLLTLMDGLKQRAH VIVMAATNRPN SIDPALRRFGRFDR EVDIGIPDATGRLEILOHTKNMKLA DDVDLEQVANETHGHVGADLAAL CSEAALQAIKKMDLIDLEDETIDA EVMNSLAVTMDDFRVRTTPVPQW ALSQSNPSALRETVVEVPQVTWEDI GGLEDVKRELQELVQYPVEHPDKF LKFGMTPSKGVLFYGPFGCGKTLL AKAIANECQANFISIKGPELLTMWF GESEANVREIFDKARQAAPCVLFFD ELDSIAKARGGNIGDGGGAADRVIN QILTEM DGMSTKKNVFIIGATNRPDI IDPAILRPGRLDQLIYIPLPDEKSRVA ILKANLRKSPVAKAGARSWADVVD LGVPGLKMTNGFSGS*P*QEILPACF AKLAI\RESNREVKIKAKNREEGKT NPIKPMGRYE*WIDPVPEIR\RDSSL KEAQSFCAFLFSDNDIR\K\EMFA QTLSQ/ESRGFGSFRFPNGNQQGGAGP SQGSGGGTGGSVYTEDNDDDLYG |
| 5098 | 10595 | A | 5409 | 96 | 299 | |
| 5099 | 10596 | A | 5410 | 174 | 324 | |
| 5100 | 10597 | A | 5411 | 74 | 242 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5101 | 10598 | A | 5412 | 129 | 899 | AAPGLGRGGGAAAGGGAVCPGTE RPCAMAYAYLFKYIIIIGRTTGVG*N PCPNALQFTD/KRGFQPSAMTLTIGV EFGA\RMITIDGKQIKL\QIWDTAGQ ESFRS\ITRSYYRGAAGALLVYDITR\ *DTFNH\LTW\LEDARQHSNSNMV IMLIG\NKSD\LESRREVKK/EKGEA FA\REHGLIFM\ETSAKTGFQCRKEG ILFNTAKEILLKKFPRKGVFLTFN*W RANGH\IKLGPQPAAYPIATHAGQS GGQQAGGGCC |
| 5102 | 10599 | A | 5413 | 1 | 408 | MQLKRANPGPRRAPVRETVMLLLC WGVPPGRPYKVDTESALLYQGPHN TLFGYSVVLHSHGANR\WGAPTAN WLANASVINPGAIYRCRIGKNPGQT CEQLQLGSPNGEPCGKTCLEERDNQ WLGVTLSRQPGENG |
| 5103 | 10600 | C | 5414 | 1 | 1026 | MGLGIYLDQYTRQKGQDPVAELKQ LIPLVVSLAPNLEMPLLKKKTNP TFLKSLSGGLNLFNPFVETVVEE VKVHPRNNTGGYNPEEEEDETASE NCFPWNVDGDLMEVASEVHIRRVQ KKEYVEENKIPRNPTYKGCCEGPLQE NYKPLLNKIKEDTNKWKNIPCSWIG RTDVTKMAILPKHDRVAEQRVVGA LVKQRASQCPRCGRSGPPGTAT ASPSPGRRPFGAVIAPRFP SHALSSW YAGCNAEKSEVNAPFGTQGMRFIS AASYKDWVQVLQQKDVSRNMGT K ARMMPLGSSGGCHTIRTEVTQDSE GQLAAVTTTGYTVVGLEPPKVS* |
| 5104 | 10601 | A | 5415 | 1 | 681 | |
| 5105 | 10602 | A | 5416 | 1 | 779 | MNNGRNYRCQNLVDKGVGENRGP ADNRMLVAHQCSREEKLKEPDEQV TPAVCQQDSLAMERLGRSPTAEEK VPETTTTFWAPGVEAPGDDAERRR REASGPATRHSPPTAGITAPKAGS AKVQLSILKPSKLDKCSHKTSHTKS SYHYFLHYPVSSTVQPVAAAATPSY ALIGSSLWPVNERGRQESRTCIIDQ SAWHVGRAEIRKLLPYCSTQGG LK YSDVTSGMVKDPPDVL/DRQKCLD ALAALRHAKWSSEIRF |
| 5106 | 10603 | A | 5417 | 1 | 1274 | MEMRRYEEDMYWRRMEEEQHHW DDRRRMPDGGYPHGPPLGLLGV RPGMPPQPQGPAPLRRPDSSDDRYV MTKHATIPTTEELQAVQKIVSITER ALKLVSDSLSEHEKNKNKEGDDKK EGGKDRALKGVLRVGVFAKGLLLR GDRNVNLVLLCSEKPSKTLISR IAE NLPKQLAFISPEKYDIKCAVSEAAII LNSCVEPKMQVTITLTSPHIREENMR EGDVTSGMVKDPPDVLDRQKCLDA LAALRHAKWFQARANGLQSCV IIIR ILRDLCQRVP/TWS/DFPSWAMELLV EKAISSAS\SPQSPGDALRRVFECIS SGVILK\GSPG\LLDPCEKDPFDTLG QQ*PD\QQR\EDITSSAQFA\LRLLAF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | RQIHKVLGMDPLPQMS\QRFN\IHNNH QDR\RRDSGDGVDGFEAEGKKDKKD YDNF |
| 5107 | 10604 | A | 5418 | 144 | 522 | VDLLRAAGRQWQGPLRPRPSGRR* SARRA/LGKTTYCTDPAKFISVLWT YLATMLHVELPHMNLLSTMDLIEH YGKLAFNLDYYTEVLDLS*LLDHL AS/VPFLTAYRQVTEKLVQLIEDYIL RCFIHP |
| 5108 | 10605 | A | 5419 | 1 | 2437 | MAVPGEAEEEEATVYLVVSGIPSVLR SAHLRSYFSQFREERGGGFLCFHYR HRPERAPPQAAPNSALIPTDPAEAG QLLSQTSATDVRPLSTRDSTPIQTRT CCCVISVRGLAQAQRLIRMYSGRR WLDShGTWLPGRCLIRRLRLPTEAS GLGSFPFKTRKELQSWKAENEAFTL ADLKQLPELNPPVLMPRGNVGTPL RVFLELIRACRLPPRIITQLQLQFPKT GSSRRYGNVPFEYEDSETVEQEELV YTAEGEEIPQGTYLADIPASPCGEPE EEVGKEEEEESHSEDDDDRGEEWE RHEALHEDVTGQERTTEQLFEEIE LKWEKGGSGLVFYTDAQFWQEEE GDFDEQTADDWDVDMSVYYDRDG GDKDARDSVQMRLEQRLRDGQED GSVIERQVGTFERHTKGIGRKVMER QGWAEGQGLGCRCSGVPEALDSGD QHPRCKRGLGYHGEKLQPFQGLKR PRRNLGLISTIYDEPLPQDQTESLL RRQPPTSMKFRDMAFAVIGPPGSG KTTYCLGMSEFLRALGRRVAVVNL DPANGLPYECAVDVGLVGLGDV MDALRLGPNGLLYCMEYLEANL DWLRAKLDPLRGHYFLFDCPGQVE LCTHHGALRSIFSQMAQWDLRLTA VHLVD\SHYCTDPAKFISVLCTSLAT MLHVELPHINLLSKMDLIEHYGKLA FNL\DYYTEVLDLSYLL*PPGLLTLS SATTRPASIEEA/MCKLIEDYNLVSF IPLNIQDKESIQRVLQAVDKANGYC FGAQEQRSLEAMMSAAMGADFHS STLGIQEKYLAPSNQSVEQEAMQL |
| 5109 | 10606 | A | 5420 | 2 | 78 | |
| 5110 | 10607 | A | 5421 | 94 | 253 | |
| 5111 | 10608 | A | 5422 | 2 | 318 | |
| 5112 | 10609 | A | 5423 | 460 | 672 | |
| 5113 | 10610 | A | 5424 | 357 | 795 | |
| 5114 | 10611 | A | 5425 | 310 | 478 | |
| 5115 | 10612 | A | 5426 | 1 | 399 | |
| 5116 | 10613 | A | 5427 | 2 | 390 | |
| 5117 | 10614 | A | 5428 | 3 | 392 | GGKIIVGDATEKDASKKSDSNPLTE ILKCPKVVLLRNMVGAGEVDEDL EVETKEEKEKYGVGKCV\FEIPG APDDEAVRIFLEFERVESAIKAVVD LNGRYFGGRVVKACFYNLDFRVL DLAEQV |
| 5118 | 10615 | A | 5429 | 837 | 1005 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5119 | 10616 | A | 5430 | 174 | 247 | |
| 5120 | 10617 | A | 5431 | 1 | 360 | |
| 5121 | 10618 | A | 5432 | 1 | 382 | |
| 5122 | 10619 | A | 5433 | 338 | 442 | |
| 5123 | 10620 | A | 5434 | 1 | 140 | |
| 5124 | 10621 | A | 5435 | 3 | 339 | PINFESVGPTYRGSSCLAVVPEFLG MSVAFVPDWLRGKAENVQETIQRL LE*NDQLIRCI\LEYQNKARGNECVQ YQHVLHRNLI\YLATIADAQSQPALS KAMGIIFQKQ |
| 5125 | 10622 | A | 5437 | 157 | 371 | |
| 5126 | 10623 | A | 5438 | 150 | 284 | |
| 5127 | 10624 | A | 5439 | 84 | 901 | ARKSVRMASRMTRRDPLTNKVAL VTASTDGIGFAIARRLAQDRAHVVV SSRKQQNVVDQAVATLQGEGLSVT GTVCHVGKAEDRGAAWWPPAVKL HGGIDILVSNAAVNPFFGSIMDVTE EV\WDKTLDI\NVKGPKP*MTKAVV PEMEKRGGGSVVIVSSIAAFSPSPG FSPYNVSKTALLGLAQTLPIELAPR NIRVNCLAPG\LIKTSFSRMLWMD KEKEESMKETLR\IRRLGEPEDCAGI VSFLCEDASYITGETVVVGGGTPS RL |
| 5128 | 10625 | A | 5440 | 2 | 468 | |
| 5129 | 10626 | A | 5441 | 63 | 219 | |
| 5130 | 10627 | A | 5442 | 3 | 558 | |
| 5131 | 10628 | A | 5443 | 7 | 909 | DQCEVCRNSEVRPAACPGHSGSPA QGPPRPFRMKAAVLTAVLFLTGSQ ARHFWQQDEPPQSPWDRVKDLAT VYVDVLKDSGRDYVSQFEGSALGK QLNLKLLDNWDSVTSTFSKLREQ GPVTQEFWDNLEKETEGLRQEMSK DLEEVKAKVQPYLDDFQKKWQEE MELYRQKVEPLRAELQEGARQKLH ELQEKLSPGGEEMRDRARA\HVDAL RTHLAPYSGELRQRLGAR\LGALRE NGGARMGQYHA\QATEHLSTLSEK AKPALEDLRQGLLPVLESFKVSFLS ALEEYTKKLNTQ |
| 5132 | 10629 | A | 5444 | 3 | 195 | |
| 5133 | 10630 | A | 5445 | 189 | 263 | PPGSHLGHPANAPSH*GPYPGLHS |
| 5134 | 10631 | A | 5446 | 1905 | 2052 | |
| 5135 | 10632 | A | 5447 | 1903 | 2050 | |
| 5136 | 10633 | A | 5448 | 1 | 115 | |
| 5137 | 10634 | A | 5449 | 1 | 402 | GKTSKLEFSIYLAPHSTTAAIEPYNSI LTHTTLEHYDWAFMAYNGAIYDI CRRNLDIGRTTYTNLNTLIGQIESSIT ASLRFDGALNGDLT*FQTNLVPYPR IHFPLATYAPVISAEEKAYHEQLSVA EITNAC |
| 5138 | 10635 | B | 5450 | 81 | 319 | XVVEPYNSILTHTTLEHSDCAFMV DNEAIYDICRRNLDIERPTYTNLNL IGQIVSSITASLRFDGALNVDLTFEQ TNL* |
| 5139 | 10636 | A | 5451 | 1 | 422 | GKSKLEFSIYPAPQVSTAVVEPYN SILTHTTLEHSDCAFMVDNEAIYDI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | CRRNLDIERATYTNLNRIGQIVSSIT ASLRFDGALNVDLTEFQTNLVPYPR MHLPLGTYAPVICA EK/A YHETA FV QKTTCLG*PSQQMW |
| 5140 | 10637 | A | 5452 | 771 | 1640 | ALQLHPHPHPHPWSTLIVPFMVDN EAIYDICRRNLDIERPTYTNLNRVIR A/QMGPSITASLRFDGALNVDLTEF QTNPGAPTPIHLP/LWPTYAPVHLL AGGKPYHGTAFL*AGGFTNGLVLE ARPTQMGGNVDPWHGVNYMGLL AWLYRGDVGFPKIDNGWPLPTIKN QAQHSSFVDW/CGPTGLSRFGHSTY QPSTVVPGLT WAKV\QRAV\CML\ SNTTAAIAEA*ARLDHKFDLMYAKR AFVHWYVVGEGMKEGEFSEAREDM AALEKDYEEVGVDSVEGEGEEGE EY |
| 5141 | 10638 | A | 5453 | 89 | 435 | |
| 5142 | 10639 | A | 5454 | 2 | 287 | TNEIEPEEN*HTKARNFRRFVTAINN TPRNIRED/GDHLHWHWIALADCP TAHMYEDVALIKDHTLDNSLIRELQ TLQEFNITLETALVKGIDI |
| 5143 | 10640 | B | 5455 | 218 | 3940 | MSGGGGGGGSAPSRFADYFVICGL DTETGLEPDELSALCQYIQASKARD GASPFISSTTEGENFEQTPLRRTFKS KVLARYPENVEWNPFDQDAVGML CMPKGLAFKTQADPREPQFHAFIT REDGSRTFGFALTFYEEVTSKQICSA MQTLYHMHNAEYDVLHAPPADDR DQSSMEDGEDTPVTKLQRFNSYDIS RDTLYVSKCICLITPMSFMKACRSV LQQLHQA VTSPPQPPPLPLESYIYNVL YEVPLPPPGRSLKFSGVYGPICQRP STNELPLFDFPVKEVFELLGVENVF QLFTCALLEFQILLYSQHYQRLMTV AETITALMFPFQWQHVVYPILPASL LHFLDAPVPYLMGLHSNGLDDRSK LELPQEANLCFVDIDNHFIELPEDLP QFPNKLEFVQEVSEILMAFGIPPEGN LHCSESASKLRRLRASELVSDKRNG NIAGSPLHSYELLKENETIARLQALV KRTGVSLEKLEVREDPSSNKDLKV QCDEEELRIYQLNIQIREVFANRFTQ MFADYEVFVIQPSQDKESWFTNRE QMQNFDKASFLSDQPEPYLPFLSRF LETQMFASFIDNKIMCHDDDDKDP VLRVFDSDRVDKIRLLNVRTPTLRTS MYQKCTTVDEAEKAIELRLAKIDHT AIHPHLLDMKIGQGKYEPGFFPKLQ SDVLSTGPASNKWTNRNAPAQWRR KDRQKQHTHLRLDNDQREKYIQE ARTMGSTIRQPKLSNLSPSVIAQTN WKFVEGLLKECRNKTKRMLVEKM GREAVELGHGEVNITGVEENTLIAS LCDLLERJWSHGLQVKQGSALWS HLLHYQDNQRKL TSGSLSTSGILL DSERRKSDASSLMPPLRISLIQDMR HIQNIGEIKTDVGKARAWVRLSME |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | KKLLSRHLKQLLSDHELTKKLYKR YAFRLCDDEKEQFLYHLLSFNAVD YFCFTNVFTTILIPYHILIVPSKKLGG SMFTANPWICISGELGETQIMQIPRN VLEMTFECQNLGKLTTVQIGHDNS GLYAKWLVEYVMVRNEITGHTYKF PCGRWLKGMDGSLERILVGELL TSQPEVDERPCRTPLQQSPSVIRRL VTISPNNKPKLNTGQIQESIGEA VNG IVKHFHKPEKERGSLTLLCGECGL VSALEQAFQHGFKSPRLFKNVFIWD FLEKAQTYETLEKNEVVPEENWH TRARNFCRFVTAINTPRNIGQGWO VSDAGVLGEPEITSYTTGICPAG* |
| 5144 | 10641 | A | 5456 | 238 | 406 | |
| 5145 | 10642 | A | 5457 | 2 | 204 | |
| 5146 | 10643 | A | 5458 | 1 | 431 | |
| 5147 | 10644 | A | 5459 | 1 | 225 | |
| 5148 | 10645 | A | 5460 | 3 | 321 | |
| 5149 | 10646 | A | 5461 | 1 | 1257 | MSHRKFSAPRHGSLGFLPRKRSSRH RGKVKSFPPKDDPSKPVHLTAFLGY KAGMTHIVREVDRPGSKVNKKEVV EAVTIVETPPMVVVGIVGYVETPRG LRTFKTVFAEHISDECKRRFYKNWH KSKKKAFTKYCKKWQDEDGKKQL EKDFSSMKKYCQVIRVIAHTQMRL LPLRQKKAHLMGDQVERGALWPE KADWARERLEQQVPVNQVF/GQD EMIDVIGVVTQGGKAYKGVTSRWH TQESCPRKDPTEGLRKIVACIRAWH PARVAFSVARA/GQ/KGYHHRTEIN K/KIYKIGQGYLIKGG/KLIKNNAST DYDL/SLDKSINPSGWAFVHLW*K* PNDVFVML/KG/CVVGTKKRVLTLR KSFAGCRRKRRGFGEELTLSSIDTTS KFGHGRFQTMEKKAFMG/PLKKD RIAKEEGA |
| 5150 | 10647 | A | 5462 | 114 | 456 | |
| 5151 | 10648 | A | 5463 | 3 | 76 | |
| 5152 | 10649 | A | 5464 | 2 | 951 | CWNSGEVRWPLPPPPPRFVARRKM ADLEEQLSDEEKVRIF/LKFFIHAPPG EINEGFNDVRLLLNNDNLLREGAA HAFAQYNLDQFTPLKIEGYEDQVLI TEHGRLGEMGKFLDPKNRICFKF* SL*GRRATDPKDPCAEVENAVESWR TSVETALRAYVKEHYPEWESGTVY GQKNRWDSQTHIACIESHQFQAKNF WNGRWSEWKFTITPSTTQVVGIL KIQVHYEDGNVQLVSHKDIQDSL TVSNEVQTAKEFIKIVEAAENEYQT AISENYQTMSDTTFKALRRQLPVTR TKIDWNKILSYKIGKEMQNA |
| 5153 | 10650 | A | 5465 | 3 | 553 | |
| 5154 | 10651 | B | 5466 | 26 | 384 | MHHEALSEALPGDNVGFNVKNVSV KDVRRGNAVAGDSKNDPPMEAAGF TAQVILNHPGQISAGYALYWIAIVD MVPKGPMCVESFSDYPPLGRFAVR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | DMRQTVAVGVKAVDKKAAGLAS* |
| 5155 | 10652 | A | 5467 | 1 | 1254 | |
| 5156 | 10653 | A | 5468 | 1 | 1386 | |
| 5157 | 10654 | A | 5469 | 33 | 1653 | KLPLKAKMGKEKTHINIVVIGHVDS GKSTTTGHLIYKCGGIDKRTIEKFEK EAAEMGKGSFKYAWVLDKLKAER ERGITIDISLWKFETSKYYVTIIDAPG HRDFIKNMITGTSQAD\CAVLIVAA GVGEFEAG\SKNGQTREHALLAYT LGVKQ\LIV\GVNKMMDSTEPPYSQK RYEEIVKEVSTYIKKIGYY\PDTLAF EPISGWN GDDMLEPSANMPWFKG WKVTRKDG\NAS\GTTLLEALDCVL PPTRP\DKPLR\LPLQDVYKIGGIG\ TVPVGRVETGVLPKPG\MGVTFAPS QRLQREVKICPKMHHEAFE*SSFLG DNVGFNVKNVSCQGCSVRGNV*H GDSK\NDPPMEA/SLGFTAQVI\LNH PGPNKAPG*CPWYWDCHTAH\AC KVCLSLKEKI*F/DRSW*KSLEDGP*I LGSLGDAGHWLIWVPGQAPCVFEK LLKTIPP LGRFAVRDNEDRQLCGW VSIKSSWTKKAAGSWAKVTK\SAQ KSSERLKWNIIPNTCHPTLYQVWEE RSQELFGSIGHLSLSSKRLVNDNNA S |
| 5158 | 10655 | A | 5470 | 2 | 4966 | |
| 5159 | 10656 | A | 5471 | 2 | 4821 | RWPRRARLLRRGRGGGGVESLPHF GAPVPRARLQLTARRGHAGLRARM REAAAALVPPPAFAVTPAAAMEEPP PPPPPPPPPEPETESEPECCLAARQE GTLGDSACKSPESDLEDFSDETNTE NLYGTSPSTPRQMKRMSTKHQRN NVGRPASRSNLKEKMNAPNQPPHK DTGKTVENVEEYSYKQEKKIRAAL RTTERDHKKNVQCSFMLDSVGGSL PKKSIPDV DLNKP YLSLGCSNAKLP VSVPMPIARPARQTSRTDCPADRLK FFETLRLLLKLTSVSKKKDREQRGQ ENTSGFWLNRSNELIWLELQAWHA GRTINDQDFFLYTARQAIPDIINEILT FKVDYGSFAFVRDRAGFNGTSVEG QCKATPGTKIVGYSTHHEHLQRQR VSFEQVKRIMELLEYIEALYPSLQAL QKDYEKYAAKDFQDRVQALCLWL NITKDLNQLRIMGTVLGIKNLSDI GWPVFEIPSPRPSKGNEPEYEGDDT EGELKELESSTDESEEEQISDPRVPEI RQPIDNSFDIQRDCISKLERLESE DDSLGWGAPDWSTEAGFSRHCLTSI YRPFVDKALKQMGLRKLILRLHLK MDGSLQARIALVKNDRPVEFSEFP DPMWGS DYVQLSRTPPSSEKCSA VSWEELKAMDLPSEFPAFLVLCRVL LNVIHECLKLRLEQRPAGEPSLLSIK QLVRECKEVLKGGLLMKQYYQFM LQEVLEDLEKPCDNIDAFEEDLHKM LMVYFDYMRSWIQMLQQLPQASHS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LKNLLEEEWNFTKEITHYIRGGEAQ AGKLFCDIAGMLVLKSTGSFLEFGLQ ESCAEFWTSADDSSASDEIIRSVIEIS RALKELFHEARERASKALGFAKML RKDLEIAAEFRLSAPVRDLDVLKS KQYVKVQIPGLENLQMFVPTLAE EKSIIQLLNAAAGKDCSKDSDDVL IDAYLLLTKHGDRARDESDSWGTV EAQPVKVVPQVETVDTLRSMQVDN LLLVVMQSAHLTIQRKAFQQSIEGL MTLCQEQTSSQPVIKALQQLKND ALELCNRISNAIDRVDMFTSEFDA EVDESESVTLQYYREAMIQGYNF GFEYHKEVVRLMSGEFRQKIGDKYI SFARKWMNYVLTKCESGRGTRPR WATQGFDFLQAIEPAFISALPEDDFL SLQALMNECIGHVIGKPHSPVTGLY LAIHRNSPRPMKVPRCHSDPPNPHLI IPTPEGFRGSSVPENDRLASIAAELQ FRSLSRHSSPTEERDEPAYPRGDSSG STRRSWELRTLISQSKDTASKLGPIE AIQKSVRLFEEKRYREMRRKNIIGQ VCDTPKSYDNVMHVGLRKVTFKW QRGNKIGEGQYGVYTCISVDTGEL MAMKEIRFQPNHKTIKETADELKI FEGIKHPNLVRYFGVELHREEMYIF MEYCDEGTLEEVSRGLQEHVIRLY SKQITIAINVLEHGIVHRDIKANIF LTSSGLIKLGDFGCSVKLNNAQTM PGEVNSTLGTAAAYMAPEVITRAG EGHGRAADIWSLGCVVIEMVTGKR PWHEYEHNFQIMYKVGGMGHKPPIP ERLSPEGKDFLSHCLESDPKMRWT ASQLLDHSFVKVCTDEE |
| 5160 | 10657 | A | 5472 | 3 | 425 | |
| 5161 | 10658 | A | 5473 | 1 | 234 | |
| 5162 | 10659 | A | 5474 | 3 | 260 | |
| 5163 | 10660 | A | 5475 | 3255 | 3467 | LNKNLGLIFFFFFFFFFETASRSVTR LEYSGSILAHCELRLPGSRHSPVVS TWEAEAGELPEPRRQRLR |
| 5164 | 10661 | A | 5476 | 1 | 4497 | |
| 5165 | 10662 | A | 5477 | 2 | 891 | |
| 5166 | 10663 | A | 5478 | 1 | 9786 | |
| 5167 | 10664 | A | 5479 | 27 | 13959 | VPFSVAAAEEPAQPARAARPRPGRS PGAAPPQLAMDPPRPALLALLALPA LLLLLLAGARAEEMELENVSLVCPK DATRFKHLRKYTYNYEAESSGVP GTADRSATRINCKVELEVPLCSFI LKTSQCILKEVYGFNPEGKALLKKT KNSEEFAAAMSRYELKLAIEGKQV FLYPEKDEPTYILNIKRGIIISALLVPP ETEEAKQVFLDVTYGNCSHTFTV KTRKGNVATEISTERDLGQCDRFKP IRTGISPLALIKGMTRPLSTLISSQS CQYTLDAKRKHVAEAIKCEQHLFL PFSYKNKYGMVAQVTQTLKLEDTP KINSRFFGEGTKKMGLAFESTKSTS PPKQAEAVLKTQVELKKLTISEQNI |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | QRANLFNKLVTLELRGLSDEAVTSL PQLIEVSSPITLQALVQCGQPQCSTH ILQWLKRVHANPLLIDVVTYLVALI PEPSAQQLRIFNMARDQRSRATLY ALSHAVNNYHKTNPTGTQELLDIA NYLMEQIQDDCTGDEDYTYLILRVI GNMGQTMEQLTPELKSSILKCVQST KPSLMIQAAIQALRKMEPKDKDQ EVLLQTFLDDASPGDKRLAAYLML MRSPSQADINKIVQILPWEQNEQVK NFVASHIANILNSEELDIQDLKKLVK EVLKESQLPTVMDFRKFSRNYQLY KVSIPS LDPASAKIEGNLIFDPNNY LPKESMLKTTLTAFGFASADLIEIGL EGKGFEPTEALFGKQGFPPDSVNK ALYWVNGQVPDGVSKVLVDHFGY TKDDKHEQDMVNGIMLSVEKLIKD LKSKEVPEARAYLRILGEELGFASL HDLQLLGKLLLMGARTLQGIPQMI GEVIRKGSKNDFFLHYIFMENAFEL PTGAGLQLQISSGVIAPGAKAGVK LEVANMQAELVAKPSVSVEFVTNM GIIIPDFARSGVQMNTNFFHESGLEA HVALKPGKLFKIIPSPKRPVKLLSGG NTLHLVSTTKTEVIPPLIENRQSWSV CKQVFPGLNYCTSGAYSNASSTD SA SYYPLTGDTRLELELRPTGEIEQYSV SATYELQREDRALVDTLK FVTQAE GAKQTEATMTFKYNRQSM T L S SEV QIPDFDVDLG TILRVNDESTEGKTS YRLTLDIQNKKITEVALMGHLSCDT KEERKIKGVISIPRLQAEARSEILAH WSPAKLLLQMDSSATAYGSTVSKR VAWHYDEEKIEFEWNTGTNVDTKK MTSNFPVDLSDYPKSLHMYANRLL DHRVPQTDMTFRHVGSKLIVAMSS WLQKASGSLPYTQTLQDHLNSLKE FNLQNMGLPDFHIPENLFLKSDGRV KYTLNKNLSLKIEIPLPFGGKSSRDLK MLETVRTPALHF KSVGFHLP SREFQ VPTFTIPKLYQLQVPLLGVLDLSTN VYSNLYNWSASYS GGNTSTDHFSL RARYHMKADSVVDLLSYNVQGS G ETTYDHKN T FT LSCD GSLRHKFLDS NIKFSHVEKLGNNPVSKGLLIFDASS SWG PQMSASVHLD SKKKQH L FVKE VKIDGQFRVSSFYAKGT YGLSCQRD PNTGRLNGESNLRFNSSYLQGTNQI TGRYEDGTLSTSTSDLQSGIHKNTA SLKYENYELTLKSDTNGKYKNFAT SNKMDMTFSKQNALLRSEYQADYE SLRFFSLLSGSLNSHGLELNADILGT DKINSGAHKATLRIGQDGISTSATT NLKCSLLVLENELNAELGLSGASM KLTTNGRFREHNAKFSLDGKAALT ELSLGSAYQAMILGVDSKNIFNFKV SQEGLKLSNDMMGSYAEMKFDHT NSLNIAGLSLDFSSKLDNIYSSDKFY |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|--------|-------------------------------------|---|--|--|
| | | | | | | KQTVNLQLQPYSLVTTLNSDLKYN ALDLTNNGKLRLEPLKLHVAGNLK GAYQNNKIKHIYAISSAALSASYKA DTVAKVQGVFEFSHRLNTDIAGLAS AIDMSTNYNSDSLHFSNVFRSVMAP FTMTIDAHTNGNGKLALWGEHTGQ LYSKFLLKAEPLAFTFSHDYKGSTS HHLVSRKSISAALHKKVSALLTPAE QTGTWKLKTQFNNNEYSQDLDAY NTKDKIGVELTGRTLADLTLLDSPI KVPLLLSEPINIIDAEMRDAVEKPQ EFTIVAFVKYDKNQDVHSINLPFFET LQEYFERNROTIIVVLENVQRNLKH INIDQFVRKYRAALGKLPQQANDY LNSFNWERQVSHAKEKLTALTKKY RITENDIQIALDDAKINFNEKLSQLQ TYMIQFDQYIKDSYDLHDLKIAIANI IDEIIEKLKSLDEHYHIRVNLVKTIH DLHLFIENIDFNKSGSSTASWQNV TKYQIRIQIQEKLQQLKRHIQNIDIQ HLAGKLKQHIEAIDVRVLLDQLGTT ISFERINDVLEHVKHVFVINLGDVEV AEKINAFRAKVHELIERVEVDQIQ VLMDKLVELAHQYKLLKETIQKLSN VLQQVKIKDYFEKLVGFIDDAVKK LNELSFKTFIEDVNFKFLDMLIKKLS FDYHQFVDETNDKIREVTQRLNGEI QALELPQKAEALKLFLEETKATVA VYLESQDTKITLIINWLQEALSSAS LAHMKAKFRETLEDTRDRMYQMDI QQELQRYLSLVGQVYSTLVTYISD WWTLAAKNLTDFAEQYSIQDWAK RMKALVEQGFTVPEIKTILGTMPAF EVSLQALQKATFQTPDFIVPLTDLRI PSVQINFKDLKNIKIPSRFSTPEFTIL NTFHIPSFTIDFVEMKVKIIRTIDQML NSELQWPVPDIYLRDLKVEDIPLARI TLPDFRLPEIAIPEFIPTLNLNDFQVP DLHIPEFQLPHISHTIEVPTFGKLYSI LKIQSPLFTLDANADIGNGTTSANE AGIAASITAKGESKLEVLNFDQAN AQLSNPKINPLALKESVKFSSKYLR TEHGSEMLFFGNAIEGKSNTVASLH TEKNTLELSNGVIVKINNQLTLDN TKYFHKLNIPKLDSSQADLRNEIKT LLKAGHIAWTSSGKGSWKWACPRF SDEGTHESQISFTIEGPLTSFGLSNKI NSKHLRVNQNLVYESGSLNFSKLEI QSQVDSQHVGHSVLTAKGMALFGE GKAEFTGRHDAHLNGKVIGTLKNS LFFSAQPFEITASTNNEGKLVKVRPL RLTGKIDFLNNYALFLSPSAQQASW QVSARFNQYKYNQNFSAAGNNENIM EAHVGINGEANLDFLNIPLTIPEMRL PYTIITTPPLKDFSLWEKTGLKEFLK TTKQSFDSLVAQYKKNKHRHSIT NPLAVLCEFISQSIKSFDRHFEKNRN NALDFVTKSYNETKIKFDKYKAES |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | HDELPRTFQIPGYTVPVNVVEVSPF TIEMSAFGYVFPKAVSMPSFSILGSD VRVPSYTLILPSLELPVLHVPRNLKL SLPDFKELCTISHIFIPAMGNITYDFS FKSSVITLNTNAELFNQSDIVAHLLS SSSSVIDALQYKLEGTTTLTRKRGL KLATALSLSNKFVEGSHNSTVSLTT KNMEVSVATTTKAQIPILRMNFKQE LNGNTKSKPTVSSSMFEKYDFNSSM LYSTAKGAVDHKLSLESLSYFSIES STKGDVKGSVLSREYSGTIASEANT YLNSKSTRSSVKLQGTSKIDDIWNL EVKENFAGEATLQRIYSLWEHSTKN HLQLEGLFFTNGEHTSKATLELSPW QMSALVQVHASQPSSFHDFPDLGQ EVALNANTKNQKIRWKNEVRIHSG SFQSQVELSNDQEKALHDIAGSLEG HLRFLKNILPVYDKSLWDFLKL DV TTSIGRRQHLRVSTAFVYTKNPNGY SFSIPVKVLADKFIIPGLKLDLNSV LVMPTFHVPFTDLQVPCKLDFREI QIYKKLRTSSFALNPLTLPVVKFPEV DVLTKYSQPEDSLIPFEITVPESQLT VSQFTLPKSVSDGIAALDLNAVANK IADFELPTIIVPEQTIEIPSIFSVPAGI AIPSFQALTARFEVDSPVYNATWSA SLKNKADYVETVLDSTCSSTVQFLE YELNVLGTHKIEDGTLASKTKGTFA HRDFSAEYEDGKYEGLQEWEGKA HLNIKSPAFTDLHLRYQKDKKGIST SAASPAVGTVGMDMDEDDDFSKW NFYYSPQSSPKKLTIKTEL RVRES DEETQIKVNWEEEAASGLTSLKDN VPKATGVLYDYVNKYHWEHTGLT LREVSSKLRRNLQDHAEWVYQGAI REIDDIDERFQKGASGTTGT YQEWK DKAQNLYQELLTQEQASFQGLKD NVFDGLVRVTQEFHMKVKHLIDSLI DFLNFPRFQFPKPGIYTREELCTMF IREVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISMREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFGPSGVGWTVK YYEGEEKIVSLIKNLLVALKDFHSE YIVSASNFTSQLSSQVEQFLHRNIQ EYLSILTDPDGKGKEKIAELSATAQ EIKSQANATKKIISDYHQQFRYKLO DFSDQLSDYYEKFIAESKRLNDLSI QN\YHTFLDYTSREFNWKKLAIQPQ SLNPYMKLAPGELYHPLIFLKEIFN LFFFSNLNFSHRHRKNCKLPILIKPY SEPALQ |
| 5168 | 10665 | A | 5480 | 2 | 316 | |
| 5169 | 10666 | A | 5481 | 2 | 401 | |
| 5170 | 10667 | A | 5482 | 126 | 415 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5171 | 10668 | A | 5483 | 3 | 499 | |
| 5172 | 10669 | A | 5484 | 1 | 241 | |
| 5173 | 10670 | A | 5485 | 12 | 308 | |
| 5174 | 10671 | B | 5486 | 394 | 565 | MSAEERLRSSGVLSQKVIAHSLGFD KHGNRLGRGKGYDAYLKRCLQH QEVKPYTLALAFKEQICLQVPVNEN DMK* |
| 5175 | 10672 | B | 5487 | 674 | 807 | MSAEERLRSSGVLSQKVIAHSEYQK SKRISIFLSMQDEIETEEIHKDIFQRGK ICFLPSVRVPEQSHGYGLGFDKHGN RLGRGKGYDAYLKRCLQHQEVK PYTLALAFKEQICLQVPVNENDIK* |
| 5176 | 10673 | A | 5488 | 113 | 339 | |
| 5177 | 10674 | A | 5490 | 2 | 388 | FLFFFEMESRSVAQAGVQWCDLG SLQPPPPGLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVVGQAGLELLAPS DPPA |
| 5178 | 10675 | C | 5491 | 197 | 415 | MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF* |
| 5179 | 10676 | A | 5492 | 768 | 1081 | KGVLFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA |
| 5180 | 10677 | A | 5494 | 305 | 477 | |
| 5181 | 10678 | A | 5495 | 1 | 903 | |
| 5182 | 10679 | A | 5496 | 111 | 295 | KPATSVPVIVCVCSSAKPELPLCPAT YTEHHAGQPHWWYHAAR/DLVSW K*QISQRGEINPH |
| 5183 | 10680 | A | 5497 | 1 | 505 | |
| 5184 | 10681 | A | 5498 | 3 | 345 | |
| 5185 | 10682 | A | 5499 | 1 | 1416 | |
| 5186 | 10683 | A | 5500 | 618 | 707 | |
| 5187 | 10684 | C | 5501 | 1729 | 2511 | MDIASTNTSNKSDTNMEQVPATND TIKRLESKLLKNQAKQQSESGRLSL GASRGSSVESLPPTSEGKRMSADMS EIEARIAATTGNGQPRRSIQDLTVT GTEPGQVSSRSSSPSRMITTSGPTS EKPTRSHPWTPDDSTDINGSDNSIP MAYLTLDHQLQPLAPCPNSKESMA VFEQHCKMAQEYMKVQTEIALLQ RKQELVAELDQDEKDQQNTSRLVQ EHKKLLDENKSLSTYYQQCKKQLE VIRSQQQKRQGT* |
| 5188 | 10685 | A | 5502 | 1 | 3489 | |
| 5189 | 10686 | A | 5503 | 1 | 246 | |
| 5190 | 10687 | A | 5504 | 40 | 124 | NVPQFTAKAPCKHEKCLNTNSPDLF EAC*DNIDQTAVSLTAPKTGKRK*R NKVQLS**PQFTAKAPCKHEKCLNT NSPDLFEAC |
| 5191 | 10688 | A | 5505 | 156 | 1001 | GIQQFGQYCLNMLQINQLLSKIKLA NPKEKTAMYLVELARFNRVQPQY KLLD*RGPAHSMFVSQSLGEQT WESEGSSIKKAQQA VGNKALTESTL |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | PKPI*KPPKSNVNNNPGCITPTVELN GLAMKRGRACHPQAIRSKAIPK**S *LQLSSHV*SEVS\FPIPKIFYVQLTV GNNEFFGEGKTRQAARHNAAMKA LQALQNEPI/LRKISSGMVNQERIW MMTK/HANKSEISLVFEIALKRNM VSFEVIKESGPPHMKSFVTRVSVGE FSAEGEGNSKK |
| 5192 | 10689 | A | 5506 | 175 | 411 | |
| 5193 | 10690 | A | 5507 | 198 | 381 | |
| 5194 | 10691 | A | 5508 | 137 | 346 | |
| 5195 | 10692 | A | 5510 | 3 | 136 | |
| 5196 | 10693 | A | 5511 | 2 | 673 | |
| 5197 | 10694 | A | 5512 | 1 | 257 | |
| 5198 | 10695 | A | 5513 | 1 | 712 | PRKT/PPAPH\DGDRKELPRTKLLPP API\STD*SQHADRGTEP/GPIRPSIEP GPPVQFGTSDKDSDLRLVVGDSLIA EKELPASVTEAIPVSRDWQLLGSGA ASAEPQSKNLD SGHC VPEHSSSGQR LYPEVFYGSAGPSSSQISGGAMDFH LAFSGGQGRHLEKGPDPGQSRSLGPE GTRSLGCPHPAEGVPLAPYPRGLYI DYKY/MKGERGGRRGGVLGLGPHFP SSPFPWSPVPGAVC |
| 5199 | 10696 | A | 5514 | 2 | 322 | |
| 5200 | 10697 | A | 5515 | 1 | 6470 | MSDRSGPTAKGKD GKKYSSLNLF TYKGSLEIQKPA\VAPRHGLQSLG KVAIARR/MRPPANLPSLKAENKGN DPNVSLVPKDG TGWASKQE QSDPK SSDASTAQPPESQPLPASQTPASNQP KRPPAAPENTPLVPSGVKSWAQAS VTHGAHGDGGRASSLLSRFSREEFP TLQAAGDQDKAAKERESAEQSSGP GPSLRPQNSTTW RDGGGRGPDELE GPDSKLHHGHDP RGGGLQPSGPPQFP PYRGMMPFMYPPYLPFP PPYPGPQG PYRYPTPDGPSRFRVAGPRGSGPP MRLVEPVGRPSILKEDNLKEFDQLD QENDDGWAGAHEEVDYTEKLKFS DEEDGRDSDEEGAEGHRDSQSASG EERPEADGKKGN SPNSEPTPKTA WAETSRPPETEPGPPAPKPLPPGDY PDRGGPPCKPPAPEDEDEAWRQRR KQSSSEISLAVERARRRREEEERM QEERRAACAEKLKRLDEKFGAPDK RLKAEP AAPAAPTSTAPPPAVPKE LPAPPAPPASAPTPEPEEPAQAP PAQSTPTPGVAAATLVSGGGSTSS TSSGSFEASPVEPQLPSKEGPEPPEE VPPPTTPPVKVEPKGDGIGPTRQPP SQGLGYPKYQKSLP PRFQRQQEQ LLKQQQHQWQQHQQGSAPTPVP PSPPQPVTLGAVPAPQAPPPPKALY PGALGRPPMPPMNFDP RWM MIPP YVDPRLQGRPPLEFYPPGVHPSGL VPRERSDSLGLSSEPFDRHAPAMLR ERGTPVDPKLA WVGDVFTATPAE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|--|---|--------|-------------------------------------|---|--|--|
| | | | | | | PRPLTSPRLRQAADDDKGMRSCTPP VPPPPPYLASYPGFENGAPGPPISR FPLEEPGPRPLPWPPGSDEVAKIQTP PPKKEPPKEETAQLTGPEAGRKLPA SRSGAGPPPPRRRESRTETRWGPRPG SSRGIPPEEPGAPPRRAGPIKKPPPP TKVEELPPKPLEQGDTPKPPKPDPL KITKGKLGPKETPPNGNLSPAPRL RRDYSYERVGPTSCRGRGRGEYFA RGRGFRGTYGGRGRGG/RSEFRSYR EFRGDDGRGGGTGGPNHPPAPRGR HASETRSEGSEYEEIPKRCRQSGSET GSETHESDLAPSDKEATPKEGTLT Q/VPLAPPPPGAPP\SPAPARFTC/RG GRRVFTPR/GVPSRRGRGGGR/PPPQ VCPGWSPPAKSLAPKKPPTGPLPPS KEPLKEKLIPGLSPVARGGSNGGS NVGMEDGERPRRRRHGRAQQQDK PPRFRRLKQERENAARGSEGKPSLT LPASAPGPEEALTTVTVAPAPPRAA AKSPDLNQNSDQANEWETASESS DFTSERRGDKEAPPPVLLTPKAVGT PGGGGGGA VPGISAMSRGDL SQRA KDLSKRSFSSQRP GMERQNR RP GP G GKAGSSGSSSGGGGGGPGGRTGPG RGDKRSWSPKNSRSPPEERPPGLP LPPPPSSSA VFRLDQVIHSNPA GI Q QALAQ LSSRQGSVTAPGGHPRHKP GPPQAPQGPSRPTRYEPQRVNSG LSSDPHFEEPGPMVRGVGGTPRDSA GVSPFPKRRERPPRKPELLQEESLP PPHSSGFLGSKPEGPGPQAESRD TG TEALTPHIWNRLHTATSRKSYRPTS MEPWMEPLSPFEDVAGTEMSQSDS GVDLSGDSQVSSGPCSQRSSPDGGL KGAAEGPPKRP GGSSPLNAVPCGP PGSEPPRRPPAPHDGDRKELPREQP LPPGPIGTERSQRTDRGTEPGPIRPS HRP GPPVQFGTSDKSDLR LVGDS LKAEKELTASVTEAIPVSRDWELLP SAAASAEPQSKNLD SGHCVPPESSS GQRLYPEVFYGSAGPSSSQISGGA MDSQLHPNSGG/FRPGTPSLHPYRS QPLYLPPGPAPPSALLSGVALKGQF LDFSTMQATELGKLPAGGVLYPPPS FLYSPAFCPSPLPDTSL LQVRQDLPS PSDFYSTPLQPGGQSGFLPSGAPAQ QMLLPM\VDSQLPVV\NFGSLPPAPP PAPPPLSLLPVGPALQPPSFVVRPQS SPSTGVLP*LARPFVYFGRTELHP VNIKPFRDF\QKLSSNLGGPGSSRT P\TGRRPSSLRFSGLNSRLQSRLS NLTSGVF\RNQAASTFYQAGLPHPD ALRWIPKPWERTG\RP\RDGPSRR\A AEEP\GSRGDKEP\GLPPPR |
| 5201 | 10698 | A | 5516 | 2 | 119 | |
| 5202 | 10699 | A | 5517 | 1 | 325 | FFFFF*DRVSLLLPKLECNGTISAHC NLRLPGSSD SPASASSSFTIHVAPLP |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | QLRHY*IFYDGTRSLYAG*YSQNLLI YSAPRQPQYHFKDMNKILDSIQRSY TKI |
| 5203 | 10700 | A | 5518 | 228 | 481 | QFFRNTIFF*DRVSLLLPKLECNSAIS AHHNLCPLGSSDSPASASRVAGITG TCHHTRLL\FVFLVETGFYHVSQSG LELLTSGD |
| 5204 | 10701 | A | 5519 | 175 | 431 | LIVKMPFLK*SWKIF*MSK**VMLIH *GFVFLFVCFF*DRVSLLLPRLECN GPISAHRLHLPDSSDSPASAYIKGF VRQLSHEE |
| 5205 | 10702 | A | 5520 | 257 | 453 | TKGGGYTQRTAIQFILFIYLFYI*DG VSLLLPRLE*NGAISAHCNHLPGSS DSQKKTCKNFCTQ |
| 5206 | 10703 | A | 5521 | 277 | 1230 | ISFHLSTFGAPSF F F F F F F E M E F S L L L P R LECN GAISAHRNLRLPGSSDSPASAS PVGWDYRHVHPRSANFV F F F S R D G VSPCWSGLVSNRPQMIPPSRPPKV LDTGLATMPGLCLANFCGRNRVSL MCPWSPELKQSTCLSLPKCWDYR RAAVPGLFILFFLRHRCPTLTQDEV QWCDHSSLPSTPEIKHPASASQSS WDQRHAPLHLANFYFYF*FFETES\ HSVT\RLLECSGAILAHCNLCPLGSSY SPAPAS*VAGTTGAH/RRLANFFVFL VEMGFHHVRQVDARSLDLVICLPR PPKVLGLQDVSHHRPAYF |
| 5207 | 10704 | A | 5522 | 1 | 467 | FFFLF*EGVSLLLPRLECSGAISA/HC NLHLPGSSDSPASASQEDGITGVRY HAWLIL/VFLVEIGFHHVGQADLKP *PQVIHPPLFFFLRQSFALVAQAGV QWCDLSSLQTPPPRVQGILLAQPE YL VAGFTGMRHHTRLFFFFAFLVET GFHPC |
| 5208 | 10705 | A | 5523 | 293 | 681 | QGTILIGLCPFDITPAIVDILLAFWHV R\CPRPTVSCFCKKVLLV*NFFFFF FFFETESCSVTRLECSGVILAHCNL RLPGSSDSHASASRVAETTGVRRHA WPIFVFLVETRFHHVGQAGLELLTS GD |
| 5209 | 10706 | A | 5524 | 274 | 321 | |
| 5210 | 10707 | A | 5525 | 2 | 733 | |
| 5211 | 10708 | A | 5527 | 1 | 3555 | MHYVLNSSSMETFVGEQNYEGSSR LCVCKRTREADDPSARDSVCEGVR ARFNICGINQIVLKCPIWGCENPAQ MGCPPVGKADRCGLLAN SATCEKG MFCHADLVGITPTVFPSHPRCKTTA SAKLACQQDVLDRQSLSSIDKNPS ERGQSQLSNPTDDSWKGRPYANQK LFASLLIKCVVQLELIQTIDNIVFYPA TSKKEDAEHMAAQQDITLDADIHI ETEDQGMKYMSSQHLFKLLDCLQ ESHFSKAFNSNYEQRTVLWRAGF KGKSKPNLLKQETSSLACCLRILFR MYVDENRRDSWEEIQRLLTVCS ALAYFITVNSESHREAWTSLLLLLL TKTLKINDEKFKAHASMYYPYLCEI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|--|---|--------|-------------------------------------|---|--|---|
| | | | | | | MQFDLIPELRAVLRKFFLRIGVVYKI WIPEEPSQARCRAILPGFECEAERRQ ERVVPATVRGWGSLLRFCIPTSSYN KCLLNMYCVPDPIAMELSDANLQT LTEYLKKTLDPDPAIRRPAEKFLESV EGNQNYPLLLLTLEKSQDNVIKVC ASVTFKNYIKRNWRIVEDPNKICE ADRVAIKANIVHMLSSPEQIQKQL SDAISIIGREDFPQKWPDLLTEMVN RFQSGDFHVINGVLRTAHSLFKRYR HEFKSNELWTEIKLVDAFALPLTN LFKICDNaALYAQKYDEEFQRYLPR FVTAIWNLLVTTGQEVKYDLLVSN AIQFLASVCERPHYKNLFEDQNTLT SICEKVIVPNMEFRAADEEAFEDNS EEYIRRDLEGSIDIDTRRRACDLVR GLCKFFEGPVTGIFSGYVNSMLQEY AKNPSVNWKKHDAIYLVTSLSK AQTQKHGITQANELVNLTEFFVNHI LPDLKSANAIMRSFSLQEAIPYIPT LITQLTQKLLAVSKNPSKPHFNHYM FEAICLSIRITCKANPAAVVNFEAL FLVFTEILQNDV/PSESVDQYRKQIFI LLFQRLQNSKTTKFIKSK*NHLDVL QK**KK\MFGMVLEKIIPEIQKVS NVEKKICAVGITKLLTECPMMMDTE YTKLWTPLLQSLIGLFELPEDDTIPD EEHFIDIEDTPGYQTAFSQLAFAGK KEHDPVGQMVNNPKIHLAQLSHKL STACPRSCGSSPVEDGVCIGAPRSP TASVCFPSLVGSINGPAPPPPPTVR TTSSGWHCGGACARKARRGPSGRS ALSRLDRSGPS |
| 5212 | 10709 | A | 5528 | 1 | 4611 | |
| 5213 | 10710 | A | 5529 | 58 | 3051 | CQLRSAAGVPSSSVSPRDPAMEL SDANLQTLTEYLKKTLDPDPAIRRP AEKFLESVEGNQNYPLLLLTLEKS QDNVIKVCASVTFKNYIKRNWRIV EDEPNKICEADRVAIKANIVHMLSL SPEQIQKQLSDAISIGREDFPQKW PDLALTEM\VNRFQSGDFHVINGVLR TAHSLFKRYRHEFK\SNELWTE\K LVLDALFALPLTYLFKATIELCSTH ANDASALRILFSSLILISKLFYSLNFQ DLPEFFEDNMETWMNMFHTLLTLD NKLLQTDDEEEAGLLELLKSQICDN AALYAQKYDEEFQRYLPRFVTAIW NLLVTTGQEVKYDLLVSNAIQFLAS VCERPHYKNLFEDQNTLTSICEKVI VPNMEFRAADEEAFEDNSEYIRRD LEGSIDIDTRRRACDLVRGLCKFFE GPVTGIFSGYVNSMLQEYAKNPSV NWKKHDAIYLVTSLSKAAQTQKH GITQANELVNLTEFFVNHLPLDKSA NVNEFPVLKADGIKYMIFRNQVPK EHLLVSIPLLINHLQAGSIVVHTYAA HALERLFTMRGPNNATLFTAAEIAP FVEILLTNLFKALTLPGSSENEYIMK |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me- thod | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|-------------|-------------------------------------|---|--|---|
| | | | | | | AIMRSFSLLQEAIIPIYIPTLITQLTQK LLAVSKNPSKPHFNHYMFEAICLSIR ITCKANPAAVVNFEEALFLVFTEILQ NDVQEFIPYVFQVMSLLLETHKNDI PSSYMALFPHLLQPVWLWERTGNIPA LVRLQAFLEGRSNTIASAAADKIP GLLGVFQKLIASKANDHQGFYLLNS IIEHMPPEVDQYRKQIFILLFQRLQ NSKTTKFIKSFLVFINLYCIKYGALA LQEIFDGIQPKMFGMVLEKHIPEIQK VSGNVEKKICAVGITNLLTECPPMM DTEYTKLWTPLLQSLIGLFELPEDD TIPDEEHFIDIEDTPGYQTAFSQLAF AGKKEHDPVGGQMVNNPKIHLAQSL HMLSTACPGRVPSMVSTSLNAEAL QYLQGYLQAASVTLL |
| 5214 | 10711 | A | 5530 | 1 | 396 | |
| 5215 | 10712 | A | 5531 | 1 | 1095 | |
| 5216 | 10713 | A | 5532 | 1 | 1077 | |
| 5217 | 10714 | A | 5533 | 1 | 986 | |
| 5218 | 10715 | B | 5534 | 214 | 975 | MEVKTKARELRDECTSLSSRFDQLE ERVLVMENQMNQMKQEEKFREKRI KRNEQSLQEIWDYVVKRPNLRVIGVP ESDGENGTKELENTLQDIIQENFPNL ARKANIQIQTQRMPPQRYSSRRATP RHIIVRFTKVEMKETMLRAAREKG RVTHKGKPIRLTADLSAETLQAKRE WGPIFNILKEKNFQPRISYPAKLSFIS EGEIKSFTDKQMLRDFVTTTPALKE LLKEALNMERNNQYQHCKNMPNC KDHPG* |
| 5219 | 10716 | A | 5535 | 3 | 1135 | |
| 5220 | 10717 | A | 5536 | 1 | 1023 | |
| 5221 | 10718 | A | 5537 | 2 | 2747 | LHLWGQGTDKQKDSSNLCRLKCP LTALKRAVVLPARSWRSENGQTAS SKGKLTTRKDIYTENPSVHHHHQRP KVDKTTKMGKKQNRKTGNSKKQS ASPPPKERSASPPPKERSSSPATEQS WREN/DLFDDELRAEGFKRSNYSE LWEDIQTKGKEVENFEKNLEECITRI TNTEKCLKELMELKTKARELCEEC RSLRSRCDQLEERVSAMEDEVKMN EMNEMKREGKFREKRIKRNEQSLQ EIWDYVVKRPNLRLTGVPESDGENG TKLENTLQDIIQENFPNLARQANVQI QEIQRTPQRYSSRRATPRHIIVRFTK VEMKEKILRAAREKGRVTLKGKPIR LTADLSAETLQARREWGPIFNILKE KNFQPRISCPAKLSFISEGEIKYFTDK QMLRDFVTTKPALQELLKEALNME RNNRSPSSSPATEQSWMENDFDEL EEGFRRSNYSELREDIQTGKKEVEN FEKNLEECITRITNTEKCLKELMELK TKARELREECRSLRSRCDQLEERVS AMEDEMNMKREGKFREKRIKRNE QSLQEIWDYVVKRPNLRLIGVPESDV ENGTKLENTLQDIIQENFPNLARQA NVQIQEIQRTPHRFSSRRATRNLI |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | RFTKVEMKEKMLRAAREKGRVTH KGKPIRLTADLLAETLQARREWGPI FNILKEKNFQPRISYPAKLSFISEGEI KYFTEKQMLRDFVTTSPALEELLKE ALNMERNNRRTTRQKVNKDIQELNS ALHQADLIDISRTLHPKSTEYTFSSA PHHTYSKIDHIVGSKALLSKCKRTEI ITKCLSDHSAIKLELRIKKLTQNCCTT TWKLNNLLNDYWVQNEMKAEIK MFFENNENKDDTTYQNLWDTFKAV CRGKFIALNAHKRKQKRSKTDLTLS QLKELEKEEKHIQKLAEGKK |
| 5222 | 10719 | A | 5538 | 99 | 432 | |
| 5223 | 10720 | A | 5539 | 100 | 732 | |
| 5224 | 10721 | A | 5540 | 242 | 1300 | NPRRSGHSLEAKLRDSSSYSELLRDIL QKHEAVHMEALDELYEALAETLM AKESTQGHRSYLLPSGGSVTLSEST AIISHGTTGLVTWDATLYLAEWAIE NPAAFTNRTVLELGSGAGLTGLAIC KDVPPPGIHLQRTCHSRVLEQLRGN VPS\NGLSLEADITAKLDSRVTVVAQ LDWDVATVHQLSAFQPDVVIAADV LYCPEAIMSLVGVLRRLAACREDQ RAPEVYVAFTVRNPETCQLFTTELA PSTCEGVLSLSHLTDKDIRTHRGQA TLELLQTAARPPGSRASTIHPSLPMP RASAPAPPEHSPSWQPCAQMHPQQ PLPAHRDTPVPVHVGPVNYRA NKQAST |
| 5225 | 10722 | A | 5541 | 3 | 167 | |
| 5226 | 10723 | A | 5542 | 2 | 378 | |
| 5227 | 10724 | A | 5543 | 3 | 359 | |
| 5228 | 10725 | A | 5544 | 15 | 347 | |
| 5229 | 10726 | B | 5545 | 141 | 371 | DFGYFYGSSYVAAPDSSRTPGLSRS RDGLLVAKLDLNLCCQQVNDVWNF KMTGRYEMYARELAEAVKSNSPT IVKE* |
| 5230 | 10727 | A | 5546 | 1 | 1154 | MAGAEWKSLEECLEKHLPLPDLOE VKRVLYGKELRKLDLPREAFEAS REDFELQGYAFEAAEEQLRRPRIVH VGLVQNRIPLPANAPVAEQVSALHR RIKAIVEVAAMCGVNIICFQEAWTM PFAFCTREKLPWTEFAESAEDGPTT RFCQKLAKNHDMVVVSPILERDSE HGDVLWNTAVVISNSGAVLGKTRK NHIPRVGDFNESTYYMEGNLGHVP FQTQFGRIAVNICYGRHHPLNWLM YSINGAEIIFNPSATIGALSESLWPIE ARNAAIANHCFTCAINRVGTEHFP NEFTSGDGKKAHQDFGYFYGSSYV AAPDSSRTPGLSRSRDGLLVAKLDL NLCCQQVNDVWVKFITGRYEMYAR ELAEAVKSNSPTIVKE |
| 5231 | 10728 | A | 5547 | 424 | 604 | |
| 5232 | 10729 | A | 5548 | 52 | 318 | |
| 5233 | 10730 | A | 5549 | 3 | 148 | |
| 5234 | 10731 | A | 5550 | 258 | 458 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5235 | 10732 | A | 5551 | 1 | 217 | |
| 5236 | 10733 | A | 5552 | 246 | 361 | |
| 5237 | 10734 | C | 5553 | 69 | 254 | MDHLYNXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXEIQXXXXXERERNKN PFPAGDDIISRGVVGQ* |
| 5238 | 10735 | A | 5554 | 32 | 169 | NPVPPYPPLCPALVFFLLLIYLLIY*PS PLLRMSAPAGKGFLFLSL |
| 5239 | 10736 | A | 5555 | 417 | 490 | |
| 5240 | 10737 | A | 5556 | 2 | 121 | |
| 5241 | 10738 | A | 5557 | 69 | 398 | |
| 5242 | 10739 | A | 5558 | 2 | 732 | GRVPSQCGWIRMRSRSCREDQKPG MDDQRDLISNNEQLSMLGRRPGAP ESKCSRGCPLHSAFSILVTLVVQA INAYFLYH*HGRDLKLTVPQNLQ LENL\RMKLP\KPPKPVSKMRMATP LL\MQALPMGALPQGPMPQATKYG NMTEDHVMHLLQNADPLKVYPPL KGSFPENLRHLKNTMETIDWKVFES WMHHWLLFEMSRHSLEQKPTDAPP KESLELEDPSGLGVTKQDLGPVPM |
| 5243 | 10740 | A | 5559 | 2 | 359 | |
| 5244 | 10741 | A | 5560 | 2444 | 2755 | DYFFEMESCSVAQAGVQWRDL GSLQPPPPSSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVQQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS |
| 5245 | 10742 | A | 5561 | 1724 | 1941 | AHLLYEWIFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPGSQSDSPAS ASWVAGITGACHHARHEWNFKC |
| 5246 | 10743 | A | 5562 | 2 | 362 | |
| 5247 | 10744 | A | 5563 | 138 | 236 | |
| 5248 | 10745 | A | 5564 | 1 | 278 | |
| 5249 | 10746 | A | 5565 | 80 | 591 | RGCKREGLSMSSLIRRVISTAKAPG A\IGPPTVQAVLV\DRTHLHFRDQIG HGPLPSWTSLCPGGVAGRSLNKL KNMGEIPESLPGCDFATNVVKTTCSS GLDINDLQLLFNEILQTVFSRSNFPA RAAYPSWLLLPQKGSRIEIAVAIQ GPLTTAFILSGDPCCVWDC |
| 5250 | 10747 | A | 5566 | 141 | 340 | |
| 5251 | 10748 | A | 5567 | 209 | 386 | |
| 5252 | 10749 | A | 5568 | 1 | 346 | |
| 5253 | 10750 | A | 5569 | 160 | 391 | |
| 5254 | 10751 | A | 5570 | 101 | 332 | |
| 5255 | 10752 | A | 5571 | 500 | 752 | |
| 5256 | 10753 | A | 5572 | 2 | 82 | |
| 5257 | 10754 | A | 5573 | 3 | 165 | |
| 5258 | 10755 | A | 5574 | 1 | 219 | |
| 5259 | 10756 | A | 5575 | 1 | 327 | |
| 5260 | 10757 | A | 5576 | 2 | 160 | |
| 5261 | 10758 | A | 5577 | 1 | 189 | QQLRHPDLHLQRRSQAQQHQGGQ DS*AQMLCRVPTVPSTTCGRTVSLP LPPKTQGHPHDLDP |
| 5262 | 10759 | A | 5578 | 2 | 224 | |
| 5263 | 10760 | A | 5579 | 1 | 1392 | |
| 5264 | 10761 | A | 5580 | 1 | 1272 | PGCGRPRAFSLNIAIDIEKRGFTSHF VRQTPSPSPNNL*YLIYRRYRQFHA |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|--------|-------------------------------------|---|--|--|
| | | | | | | LQSKLEERFGPDSKSSALACTLPTLP GRRPLPSCCCRAAVRIPALNAYMK VPVGLATLARGRALPPWDPLQGS CLWSLSTQSQPSVSPDLCAWSLVR* PRQALGARVLDVRIFFYQSPYDSEQ VPQALRRLRPTRKV*VTSPWAST WPEPAAPRAEVTAPTLARLSHCNF KAGDVIFLLSRINKDWLEVSSEVRM EVRKLVFVKILKDFPEEDDPTNWL CYYYEDTISTIKSVAWEGGACPAFL PSLRPLPTSPSHGSLSHSKAPSGSQ MSHNAVTSHQRPWPQPHSPFP PTLKDLELTR*GAGNGAGELDTLD AEGDLVRLLSDEEDVALMVRQARGL PSQKRLFPWKLHITQKDNRYRYNT MP |
| 5265 | 10762 | A | 5581 | 437 | 728 | |
| 5266 | 10763 | A | 5582 | 570 | 1648 | TQPGTGWARLSTCSLGPSPTMAVA QQLRAESDFEQLPDDVAISANIADIE EKRGFTSHFVFVIEVKTKGGSKYLI YRRYRQFHALQSKLEERFGPDSKSS ALACTLPTLPKVVYGVKQEIEM RIPALNAYMKSLLSLPVWVLMDED VRIFFYQSPYDSEQVPQALRRLRPR TRKVKSVPQGNVDRMAAPRAEA LFDFTGNSKLELNFKAGDVIFLLSRI NKDWLEGTVRGATGIFPLSFVKILK DFPEEDDPTNWLRCYYYEDTISTIK DIAVEEDLSSTPLLKDLELTRREFQ REDIALNYRDAEGDLVRLLSDEEDV ALMVRQARGLPSQKRLFPWKLHIT QKDNRYRYNTMP |
| 5267 | 10764 | A | 5583 | 1705 | 2233 | |
| 5268 | 10765 | A | 5584 | 1 | 354 | |
| 5269 | 10766 | A | 5585 | 270 | 390 | |
| 5270 | 10767 | A | 5586 | 3 | 132 | |
| 5271 | 10768 | A | 5587 | 234 | 362 | |
| 5272 | 10769 | A | 5588 | 1 | 402 | |
| 5273 | 10770 | A | 5589 | 2 | 509 | |
| 5274 | 10771 | A | 5590 | 3 | 1607 | SPRPGIPRCFHLVISTEHRRVMTEFG LSWVFLVAIFKGVQCEVQLVESGG DLVQPGGSLRLSCAASGFTSSYAM HWVRQAPGKGLKYVSGISSNGRRT YYANSVKGRFTISRDNKNTLYLQ MGSRAEDMAVYYCARGGDHIVP AAVAPFHMDVWGQGTIVTVSSASP TSPKVFPLSLCSTQPDGNVVIACLP PGLLPAGATQCDLERKRTGRDRQK LPTQPGCLRGPVHHEQPADPAGHT VPSRQVRDMPREALHESQPGCDCA LPSSLNSTYIPISLNSTYIPISLMLPPPT VTAPTGPSKDLFLGSKATFTCTLP LRDASGVTFTWDALKVGKSAVQGP P*RRDLGCYCYSVSSVLPGCAEAH GTHGEGPSLWHCWYPESKDPA*PP TLFKIRGNTFPGPRFHL\PPPSEGAG PWNELVTLATCLGIGLSAPRMLLVC |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|--------|-------------------------------------|---|--|---|
| | | | | | | WVAGGHRSLREKYLTWASRQKP SQGTTTFAVTSILRVAEDWKKGD TFSCMVGHEALPLAFTQKTIDRLAG KPTHVNVSVVMAEVDGTCY |
| 5275 | 10772 | A | 5592 | 2 | 315 | |
| 5276 | 10773 | A | 5593 | 245 | 455 | |
| 5277 | 10774 | A | 5594 | 1 | 2863 | MIFPAESSCALPQEGSAGPGSPGSAP PSRKRSWSSEESNQATGTSRWDG VSKKAPRHLSVPCTRPREARQEAE DSTSRLSAESGETDQDAGDVGPDP PDSYYGLLGTLPQEQALSHICSLPSE VLRHVFAFLPVEDLYWNLSLVCHL WREIISDPLFIPWKKLYHRYLMNEE QAVSKVDGILSNCGIEKESDLCVLN LIRYTATTKCSPSVDPERVLWSLRD HPLLPEAEACVRQHLPDLYAAAGG VNIWALVAAVVLLSSSVNDIQRLLF CLRRPSSTVTMPDVTETLYCIAVLL YAMREKGINISNSKKTITLTHEQQLI LNHKMEPLQVVKIMAFAGTGKTST LVKYAEKWSQSRFLYVTFNKSIAK QAERVFPNSVICKTFHSMAYGHGR KYQSKKKLNLFKLTPFMVNSVLAE GKGGFIRAKLVCKTLENFFASADEE LTIDHVPWCKNSQGGQRMVEQSE KLNGVLEASRLWDMRKLGECTEE AHQMTHDGYLKLWQLSKPSLASFD AIFVDEAQDCTPAIMNIVLSQPCGKI FVGDPHQIYTFRGAVNALFTVPHT HVFYLTQSFRFGVEIAYVGATILDV CKRVRKKTLVGGNHQSGIRGDAKG QVALLSRTNANVFDEAVRVTEGEF PSRIHLIGPEEERRKREYPPGLGALE GRTQVTGTRKKQAQSESGTRFPPEK GELVLLSSHDEGENLVKDKFIRRW VHKEGFSGFKRYVTAEDKELEAKI AVVEKYNIRIPELVQRIEKCHIEDLD FAEYILGTVHKAKGLEFDTVHVLD DFVKVPCARHNLQPLPALR\VEPFS\ EDEWNLLYVAVTRAKKRLIMTKS LENILTLAGEYFLQAE LTSNVLKTG VVR\CCVG\QCENNAIPVDTVLTMMK L\PIY*ATGK\ENKGGYLCHSCAEQ RIGPLAFLTASPEQVRAMERTVENI VLPRHEALLFLVF |
| 5278 | 10775 | A | 5595 | 3 | 613 | |
| 5279 | 10776 | A | 5596 | 2 | 1419 | PPHLLSPFVAAPRARATAGFTLS ASAMQEIAHLQAGQCGNQIGAKFW EVISDEHGIDPTGTYHGDSDLQLERI NVYYNEATG\GNYVPRAVLVDLEP GTMDSVRSFGPGQIFRPNFVFGQS GAGNNWAKGHYTEGAELVDAVLD VVRKEAESCDCLQGFQLTHSLGGG TGSGMGTLISKIREFPDRIMNTFS VVPS\PKCQDTVVEPYNATLSVHQL VENTDETYCIDNEALYDICFRTLKL TTPTYGDLNHLVSA TMSGVTTCLRF PGQLNADLRKLAVNMVFPRLHFF |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | MPAFAPLTSRGSQQYRGLTVPELTQ QMFDANKMMAACDPRHGRYLTVA AVFRGRMSMKEVDEQMLSVQSKN SSYFVEWIPNNVKTA VCDIPPRGLK MAVTFIGNSTAIQELFKRISEQFTAM FRRKAFLHWYTGE GMDMEFTEAE SNMNDLVSEYQQYQDATAEQGEFE EEAEEVA |
| 5280 | 10777 | A | 5603 | 1 | 384 | |
| 5281 | 10778 | A | 5604 | 185 | 700 | |
| 5282 | 10779 | A | 5605 | 1 | 414 | |
| 5283 | 10780 | A | 5606 | 3 | 138 | |
| 5284 | 10781 | A | 5607 | 1 | 433 | NNPDFKAGV\MALPTL\LQIQRHDD YLVMLKAIRILVQERLTQDAVAKA NQTKGLPVALDKHILGFDTGDAV LNEAAQILRLLHIEELRELQTKINEA IVAVQAIHFVHVWWSKCHILGGGS PENWVCSRDLPLLIATFFFNKV |
| 5285 | 10782 | A | 5608 | 1 | 459 | |
| 5286 | 10783 | A | 5609 | 118 | 375 | VAVVQIIFLPVFIAEKYKDLVPDnsk TADNATKNAEPLINLDVNNPDFKA GVMALANLLQIQRHDDYLVMLK\A IRILVQERLTQD |
| 5287 | 10784 | A | 5610 | 344 | 513 | |
| 5288 | 10785 | A | 5611 | 3 | 116 | |
| 5289 | 10786 | A | 5612 | 3 | 869 | HEVFSRPRPGEPNREAGTMFRRRLT VLDYHNPAFGNCKDETEFRNFIVW LEDQKIRHYKIEDRG\NLRNHSSDW PK\FFEKYLRDVNCPFKIQDRQEI DWLLGFAVRPEYG\DNAEKYKDLV P\DNSK\TADNAPKNAEPWINLDVN NPDK\AGVMALG*PAFRFQRHDD\ FLVNA*RQFRIWVQE\RLTQDA\VA KAKSNKKRALPVALAQTHILGFD\T GDASSLMKLEILRIACTYEELREL DQKSTKAIVAVQAIYC*SQRQDHRL GKSLEDEHFEDLQLSPLL |
| 5290 | 10787 | A | 5613 | 298 | 403 | |
| 5291 | 10788 | A | 5614 | 3 | 611 | |
| 5292 | 10789 | A | 5615 | 192 | 340 | |
| 5293 | 10790 | A | 5616 | 187 | 361 | |
| 5294 | 10791 | A | 5617 | 187 | 385 | |
| 5295 | 10792 | A | 5618 | 2 | 340 | |
| 5296 | 10793 | A | 5619 | 1 | 702 | EKYIQLVRQRALEGALGNTIYKSQ TAKGTPQETEGTSSGSKSNVRSGR VPSGRMV\IHSHPAEVT*E*TRVH WIWQS*CQGESWKQVPFLCHSGS* RNALL\CLRHDVDALLWQPHSSKQ DDMWEHIATFNALGYVQASKRDK KFFACAPNYSYAALCECLRRVFIYR QPAPMSTVLNKKGRQA\VGQVAK QQVASLETNDPNLGIQATNERLFV LTTKNLFLIKVNTEN |
| 5297 | 10794 | A | 5620 | 3 | 357 | |
| 5298 | 10795 | A | 5621 | 1 | 1926 | |
| 5299 | 10796 | A | 5622 | 1 | 362 | LQTSDEETGFSCLEFYVCAATSFVL VCIINNWSCKAD*DTRWTFRIKIGR |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | T/SVVVDLLYWRDINITGVVFGATLFL LLSLTVFSIVSVTAYIALALLSVTISF TIYKGVSHAIPKSDEGHPF |
| 5300 | 10797 | A | 5623 | 247 | 533 | KSFPGWQTYFSCGWVGCGLGRGS QNASPPASPLPQLPPG*RRSWPLRG TACRSWSALSOWAAGLYHPPRMPP LMWEAGAGSPGELRGTRIRER |
| 5301 | 10798 | A | 5624 | 128 | 667 | |
| 5302 | 10799 | A | 5625 | 12 | 3756 | VPRLSRPSPSQSSPTPTTARGSETRP RRRRQQLQHHLHPPAMEDLDQSPL VSSSDSPRPQPAFKYQFVREPEDEE EEEEEEEEDEDEDLEELVLERKPA AGLSAAPVPTAPAAAGAPLMDFGND FVPPAPRGPLPAAPPVAPERQPSWD PSPVSSTVPAPSPLSAAAVSPSKLPE DDEPPARPPPPPPASVSPQAEPVWTP PAPAPAAPSTPAAPKRRGSSGSVD ETLFALPAASEPVIRSSAENMDLKE QPGNTISAGQEDFPSVLLETAASLPS LSPLSAAAFKEHEYLGNLSTVLPT GTLQENVSEASKEVSEKAKTLLIDR DLTEFSELEYSEMGSFSVSPKAESA VIVANPREEIIIVKNKDEEEKLVSNNI LHNQQELPTALTKLVKEDEVVSSEK AKDSFNEKRVAVEAPMREEYADFK PFERVWEVKDSKEDSDMLAAGGKI ESNLESKVDDKCFADSLEQTNHEK DSESSNDDTSFPSTPEGIKDRSGAYI TCAPFNPAATESIATNIFPLLGDPTSE NKTDEKKIEEKKAQIVTEKNTSTKT SNPFLVAAQDSETDYVTTDNLT TEEVVANMPEGLTPDLVQEACESEL NEVTGKIA YETKMDLVQTSEVMQ ESLYPAAQLCPSFESEATPSPVLPD IVMEAPLNSAVPSAGASVIQSSSPL EASSVNYESIKHEPENPPPYEEAMS VSLKKVSGIKEEIKEPENINAALQET EAPYISACDLIKETKLSAEPAPDFSD YSEMAKVEQVPDHSSELVEDSSPDS EPVDLFSDDSIPDVPQKQDETVMV KESLTETSFESMIEYENKEKLSALPP EGGKPYLESFKLSLDNTKDTLLPDE VSTLSKKEKIPLQMEELSTAVYSND DLFISKEAQIRETETFSOSSPIIIDEF PTLISSKTDSFSKLAREYTDLEVSHK SEIANAPDGAGSLPCTELPHDLSLK NIQPKVEEKISFSDDFSKNGSATSKV LLLPPDVSALATQAEIESIVKPKVLV KEAEKKLPSDTEKEDRSPSAIFSAEL SKTSVVDDLLYWRDIKKTGVVFGA/ SAVFLLSLTVF\SIVSVTAYIALAL LSVT\ISFRIYKGVIAIQKS\DEGHP FRAISGNL/ESCLYLRELGSGRYSNS\ ALGSMWNCTVKGNFRAPSFSSWM DLVDSL/RSFAVLMWVFTYVGCGLG LMVLDTTGFWALNF/ISSSGSWLIYE RHQAQ\IDH\YGLANKNVKDAMA KIQAKIPG\LRKAE |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5303 | 10800 | A | 5626 | 2 | 436 | RRQFEERQQEMEHVYELLENKMQL LQESRLAKNEAARMAALVEAEKE CNLELSEKLKGVTKNWEDVPGDQV KPDQYTEALAQRDK*VPSVFLRL SFAHSQGIQQLSCSLSRT/RQ*ELHY F*DFMGPQPKTFFSGLNFQWYPL |
| 5304 | 10801 | A | 5627 | 3 | 309 | |
| 5305 | 10802 | B | 5628 | 454 | 645 | MTCKKENFSLKLLIYFLEERMQQK YEASREDIYKRNTTELKVEVESLKRE LQDKKQPSGLKPWA* |
| 5306 | 10803 | A | 5629 | 1 | 294 | |
| 5307 | 10804 | A | 5630 | 14 | 228 | |
| 5308 | 10805 | A | 5631 | 201 | 350 | |
| 5309 | 10806 | A | 5632 | 262 | 626 | PSARPHCFGLEAMHARSLPCWNCS SRLLILAFS/WGSE/CCTRKPRIIDV VYNASNNELVRTKTLVKNCIVLIDS TPYR\QWYESH\YALPLGRKKGAKL TPEEEELNKKRSKKIQKKYDERKE NAKISSLLEEQQQKLLACIASRPK QCGRADGYVLEGKELEFYLRK\KA RKRQINPCFVFTHGNRGVYCFVPTF MLPEYMTVFSAIFPCPAKLIWGGGL QPLALTSASYCPETGSPHC |
| 5310 | 10807 | A | 5633 | 3 | 452 | |
| 5311 | 10808 | A | 5634 | 26 | 477 | NSTDSETHHGARLLPDKTNVCAA WGKVGAGAHAGYGAELERMFLSF PT\TKTYFPHFDLASHG\SAQVKG/HT GKKVADALTNAVANVDDMPN\AL SALSDLHAHKLRVDPVNFKLLSHCL AGGPWAAHLPRPSSTPGGATPSLEQ SSWASC |
| 5312 | 10809 | A | 5635 | 1 | 147 | |
| 5313 | 10810 | A | 5636 | 1 | 503 | AAAAARAAGTAGPWRSAARLPALP ASSLGAAAMAASAKRKQEEKHLK MLRDMTGLPHNRKCFDCDQRGPTY VNMTVGSFVCTSCSGSLRG*NPPHR VKSISMTTFTQOEIEFLQKHGNEVC PPEQAKVVASVHASISGSSASSTSS TPEVRPLKSLLGDSAPTLHLN |
| 5314 | 10811 | A | 5637 | 272 | 360 | |
| 5315 | 10812 | A | 5638 | 1 | 1934 | WRRRRRLSRLCRLVWPVSPRTTAP GPRRAQYSQAAAAGSGAGGARRR RAAAAAARAAGTAGPRRSAARLPA LPASSLGAAAMAASAKRKQEEKHL KMLRDMTGLPHNRKCFDCDQRGPT YVNMTVGSFVCTSCSGSLRGLNPPH K/VGKSISMTTFTQOEIEFLQKHGNE VCKQIWLGLFDDRSSAIPDFRDPQK VKEFLQEKYEKKRWYVPPEQAKVV ASVHASISGSSASSTSTPEVKPLKS LLGDSAPTLHLNKGTPSQSPVVGRS QGQQQEKKQFDLLSDLGSDIFAAPA PQSTATANFANFAHFNHAAQNSA NADFANFADFQSSGSSNFGGFPTA SHSPFQPTTGGSAASVNANFAHFD NFPKSSSADFGTFNTSQSHQTASAV SKVSTNKAGLQTADKYAALANLDN |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IFSAGQGGDQGSFGTTGKAPVGSV VSVPSQSSASSDKYAALAE LDSVFS SAATSSNAYTSTSNASSNVFGTVPV VASAQTQPASSSVAPFGRTPSTNPF VAAAGPSVASSTNPFQTNARGATA ATFGTASMSMPTGFGTPAPYSLPTS FSGSFQQPAFPAQAAFPQQTAFSQQ PNGAGFAAFGQTKPVVTPFGQVAA AGVSSNPFMTGAPTQGFTGSSSTN PFL |
| 5316 | 10813 | A | 5639 | 1 | 307 | |
| 5317 | 10814 | A | 5640 | 957 | 3132 | GEEEPLWQGSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR *PLGPWCRRKKKGAEEEKPKRRR QEKQAACPFYNHEQMGLLRDEALA EVKDMEQLLALGKEARACPYYGSR LAIPAAQLVLPYQMLLHAATRQA AGIRLQDQVVIIDEAHNLIDTITGMH SVEVSGSQLCQAHSQQLQYVERYG KRLKAKNLMYKQILYLLEKFVAV LGGNIKQNPNTQSLSTGTTELKTIN DFLFQSQIDNINLFKVCVPAPQMK HGHCRNLNPKLVTQISNSDCPRVQRY CEKSMISRKLFGFTERYGAVFSSRE QPKLAGFQQFLQSLQPRTEALAAP ADESQASTLRPASPLMHIQGFALAAL TTANQDGRVILSRQGSLSQSTLKFL LLNPAVHFAQVVKECRAVVIAGGT MQPVSDFRQQLACAGVEAERVVE FSCGHVIPPNDILPLVICSGISNPLE FTFQKRELPMMDDEVGRILCNLCG VVPGGVVCFFPSYEYLRQVHAHWE KGGLLGRLAARKKIFQEPKSAHQV EQVLLAYSRCIACGQERGQVTGA LLSVVGGKMSEGINFSDNLGRCV VMVGMPFPNIRSAELQEKMAYLDQ TLPRAPGQAPPKALVENLCMKAV NQSIGRAIRHQKDFASVVLLDQRYA RPPVLAKLPAWIRARVEVKATFGPA IAAVQKFLQVYGTSLPLNHL SKLQD TFYPNTS NYAKGR |
| 5318 | 10815 | A | 5641 | 1 | 1668 | |
| 5319 | 10816 | A | 5642 | 947 | 2782 | GEEEPLWQGSAGLPWLPAEPLCK* RREKPRFCAAYQRPLCGHAEKQAR/ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYYGSR LAIPAAQLV VLPYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSQL CQAHSQQLQYVERYGKRLKAKNL MYLKQILYLLEKFVAVLGGNIKQNP NTQSLSTGTTELKTINDFLFQSQIDN INLFKVQRYCEKSMISRKLFGFTER YGAVFSSREQPKLAGFQQFLQSLQ RTTEALAAPADESQASTLRPASPLM HIQGFALAALTTANQDGRVILSRQGS LSQSTLKFLLLNPAVHFAQVVKECR AVVIAGGTMQPVSDFRQQLACAG |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | VEAER\VVEF/SCGHVIPPDNILPLVI CSGISNQPLEFTFQKRELPMIFQEP KSAHQVEQVLLAYSRCIQACGQER GQVTGALLSVVGGKMSEGINFSD NLGRCVVMVGMPPFNIRSAELQEK MAYLDQTLPRAPGQAPPKALVEN LCMKAVNQSIGRAIRHQKDFASVV LLDQRYARPPVLAKLPWIRARVE VKATFGPAIAAVQKFHREKSASS |
| 5320 | 10817 | A | 5643 | 1143 | 3233 | GEEEPLWQGCSAGLPWLPAEPLCK* RREKPRFCAAYQRPLRGHAEEKQAR\ KKKGAEEEKPKRRRQEKQAACPFY NHEQMGLLRDEALAEVKDMEQLL ALGKEARACPYRSRLAIPAAQLV VLSYQMLLHAATRQAAGIRLQDQV VIIDEAHNLIDTITGMHSVEVSGSIQ LCQAHSQLLQYMERYGKRLKAKN LMYLKQILYLLEKFVAVLGGNIQ NPNTQSLSQTGTTELKTINDFLFQSQI DNINLFKVQRYCEKSMISRKLFQFT ERYGAVFSSREQPKLAGFQQFLQSL QPRTEALAAPADESQASVPQPASP LMHIEGFLAALTANQDGRVILSRQ GSLSQSTLKFULLNPAVHFAQVVKE CRAVVIAGGTMQPVSDFRQQLLAC AGVEAERVVEFSCVFGPSLALTIGH VIPPDNILPLVICSGISNQPLEFTFQK RELPMMDDEVGRILCNLCGVVPGG VVCFFPSYEYLRQVHAHWKGGLL GRLAARKKIFQEPKSAHQVEQVLL AYSRCIQACGQERGQVTGALLSV VGGKMSEGINFSDNLGRCVVMVG MPFPNIRSAELQEKMAYLDQTLPR PGQAPPKALVENLCMKAVNQSIG RAIRHQKDFASIVLLDQRYARPPVL AKLPWIRARVEVKATFGPAIAAV QKVSPTFFFLRASPPRDHISHCLLSA QFHREKSASS |
| 5321 | 10818 | A | 5644 | 3 | 744 | |
| 5322 | 10819 | A | 5645 | 40 | 126 | |
| 5323 | 10820 | C | 5646 | 187 | 366 | MDERDSHCPYLLSSETTAKGTGLAE SAGKEDPVELDSSLEARVRRRPPST SMPLTSAPC* |
| 5324 | 10821 | A | 5647 | 1 | 382 | TADCAKPVPLAVVSLDSRYGQWES RSSIHA\VTN*ASSSSSSSSSSSF\SR\ YPRFIEFIHFDIQSTGQ/RITSR*HPPR/ DLRDALF*LNSLIPLVRTSSKSAARR RP\GEAPRGTA VPGADPAGGTRPR |
| 5325 | 10822 | A | 5648 | 3 | 684 | QGPRAALGALFPCWAPGKYVHGV RAKHPRATARAPRGSP/LPPHRVSE KTIRVVVFHRRPAGPADPAPGPSRG HRGGAG/EPPTYSTPLMSLHRARLE SSSTGSSFPADSAKPVPLAVVSLDSR *GQWESRSSIHA\VTN*ASSSSSSSS SS\FSR\YPRFIEFLHFDIQSTGQ/RIT SRQHPPR/DLRDALF*LNSRIPLVRTS SKSAARRR\GEAPRGTAAPGADPA GGP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|--|---|--------|-------------------------------------|---|--|--|
| 5326 | 10823 | A | 5649 | 2 | 331 | |
| 5327 | 10824 | A | 5650 | 3 | 340 | |
| 5328 | 10825 | A | 5651 | 1 | 94 | |
| 5329 | 10826 | A | 5652 | 2 | 496 | ASMGCSPLLSLLSLLVGAWLKLGH* TAGHAGGAGKGDGALRPGGREGP EAPLPASGMRLQPPAGEVALGAQG ASPPCAFNFLWNLSIQAQLRRVRG QGCSWRWLVLAAQAEELLGDPALV PTRRQPVGRAAPAPAASSLCCADPA GREVTQVVVVQVVVNSSS |
| 5330 | 10827 | A | 5653 | 3 | 997 | |
| 5331 | 10828 | A | 5654 | 3 | 131 | |
| 5332 | 10829 | A | 5655 | 112 | 289 | |
| 5333 | 10830 | A | 5656 | 35 | 5228 | LDPLGRMVMGIFANCIFCLKVKYLP QQQKKKLQTDIKENGKGSFSLNPQ CTHIILDNADVLSQYQLNSIQKNHV HIANPDIWKSIREKRLLDVKNYDP YKPLDITPPPDQKASSEVKTEGLCP DSATEEEDTVELTEFGMQNVEIPHL PQDFEVAKYNTLEKVGMEGGQEA VVVELQCSRDSRDCPFLISSHFLDD GMETRRQFAIKKTSEDASEYFENYI EELKKQGFLREHFTPEATQLASEQ LQALLLEEVMNSSTLSQEVSDLVE MIWAEALGHLEHMLLKPVNRISLN DVSKAEGILLVKAALKNGETAEQ LQKMMTEFYRLIPHKGTMPKEVNL GLLAKKADLCQLIRDMVNV CETNL SKPNPPSLAKYRALRCKIEHVEQNT EEFLRVRKEVLQNHHSKSPVDVLQI FRVGRVNETTEFLSKLGNVRPLLHG SPVQNI VGILCRGLLLPKVVEDRGV QRTDVGNL GSGIYFSDSLSTSIKYSH PGETDGTRLLICDVALGKCMDLH EKDFSLTEAPPGYDSVHGVSQ TASV TTDFEDDEFVYKTNQVKMKYIIF SMPGDQIKDFHPSDHTLEEYRPEF SNFSKVEDYQLPDAKTSSSTKAGLQ DASGNLVPLEDVHIKGRIIDTVAQVI VFQTYTNKSHVPIEAKYIFPLDDKA AVCGFEAFINGKHI VGEIKEKEEAQ QEYLEAVTQGHGAYLMSQDAPDVF TVSVGNLPPKAKVLIKITYITELSILG TVGVFFMPATVAPWQQDKALNEN LQDTVEKICIKEIGTKQSFSLTMSIE MPYVIEFIFSDTHELKQKRTDCKAVI STMEGSSLDSSGFSLHIGLSAAYLPR MWVEKHPEKESEACMLVFQPDLD VDLPDLANESEVIICLDCSSMEGVT FLQAKEIALHALSLVGEKQKVNIIF GTGYKELFSYPKHITSNTAAAEFIM SATPTMGNTDFWKT LRYLSLLYPA RGSRNILLVSDGHLQDESLTLQLVK RSRPHTRLAFACGIGSTANRHVLRIL SQCGAGVFEYFNAKSKHSWRKQIE DQMTRLCSPSCHSVSVKWQQLNPD APEALQAPAQVPSLFRNDRLLVYGF IPHCTQATLCALIQEKEFCTMVSTTE |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | LQKTTGTMIHKLAARALIRDYEDGI LHENETSHEMKKQTLKSLIKLSKE NSLITQFTSFVAVEKRDENESFPDI PKVSELIKEDVDLPYMSWQGEF QEA VRNQSLLASSEWPELRLSKRK HRKIPFSKRKMELSQPEVSEDFEED ALGVLPFTSNLERGRVEKLLDLS WTESCKPTATEPLFKKVSPWETSTS SFFPILAPAVGSYLTPTTRAHSPASL SFASYRQVASFGSAAPPRQFDASQF SQGPVPGTCADWIPQSASCPTGPPQ NPPSAPYCGIVFSGSSLSSAQAPLQ HPGGFTTRPSAGTFPELDSPLHFSL PTDPDPIRGFGSYHPSAYSPFHFQPS AASLTANLRLPMASALPEALCSQSR TTPVDLCLLEESVGSLEGRCPVFAP QSSDTESEDELSEVLQDSCFLQIKCDT KDDSI PCFLEVKEEDEIVCTQHWQD AVPWTELLSLQTEGFWKLTPELG LILNLNTNGLHSFLKQKGIQSLGVK GRECLLDLIA TMLVLQFIRTRLEKE GIVFKSLMKMDDPSISRNPWAF EAI KQASEWVRRTEGQYPSICPRLELGN DWDSATKQLLGLQPISTVSPHRLV HYSQG |
| 5334 | 10831 | A | 5657 | 10 | 82 | |
| 5335 | 10832 | C | 5658 | 189 | 396 | MVHPAGPLASQXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXELWLHHLSSSS * |
| 5336 | 10833 | C | 5659 | 54 | 485 | MXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXRPEDFATYYCQ QNYISPLTFGGGTVKVEIXRTVAAPS VFIFPPSX* |
| 5337 | 10834 | A | 5660 | 5 | 417 | |
| 5338 | 10835 | A | 5661 | 3 | 398 | |
| 5339 | 10836 | C | 5662 | 12 | 451 | MXXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXXXXXXXXXX XXXXXXXXXXXXXXXXXFFSSYYCQ QSYVSPFTFGPGTKVDIKRTVAAPS VFIFPPSDEQ* |
| 5340 | 10837 | A | 5663 | 3 | 679 | AWWNSETPAQLLFLLLWLPTYTSG EIVLTQAPGTLSPGERATLSCRAS QTIGSTYLAWYQQRPGQAPRFLIYG ASSRATGIPDSSSSSSSSSSSSSSSS SSSSSSSSSSQYYTSPFTFGGGTKV EIRRTVAAPSVFIFPPSDEQLKSGTA SVVCLLNNFYPREAKVQWKVDNA LQSGNSQESVTEQDSKDYSLSSST LTLSKADYEKHKVYA\CEVTHQG |
| 5341 | 10838 | B | 5664 | 94 | 321 | XDRVTTTCQATQDIGNYLNWYQHK PGKAPNLLIYDASNLETGVPSRFSG RSGTHFTFTISSLPEDIATYYCQQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | YX* |
| 5342 | 10839 | A | 5665 | 3 | 764 | AWLESISPTMRVPAQLLGLLLWIP GSVADIMMTQTPLSLSVSPGQSASIS CKSSQSLLHSDGKTHVYWYLQKPG QSPQLLIYEVSSRFSGVDPDRFSGSGS GTDFTLKITRVEAEDVGVIYCQQY NSYLLFTFGPGTKVDIKRTVAA\PSV FIFPP\SDEQLKSGTASVVCLLNNFL FPARRAKVQWEGGINALQSGNSQEC VTE\QDSKGSTYSLASSTLTVSKADY EKHKVYACEVTHQGLSSPVTKSFN RGEC |
| 5343 | 10840 | A | 5666 | 1 | 534 | RRPRREPWKPQRSFSSSCYS/ELPDT TGEIVLTQSPGTLSPGERATLSCR ASQSVSNYYLAWYQQKPGQAPRLI IYDTSSRATGIPDRFSGSASGTDFTL TISRLEPEDFAVYYCQQYGSSPPMY TFGQGTKLEIKRTVAAPSVFIFPPSD EQLKSGTASVVCLLNNFYPREAKV QW |
| 5344 | 10841 | A | 5667 | 184 | 621 | LHECISVLFPISDTTGEIVLTQSPATL SLSPGERATLSCRASQSVNNYYLA WYQQKPGQPPRLIYDASNRITGIP ARF\SGSGSGTEFTFHHSAAACSLKDF CSLFTVQQLINWASDSPLGQGTRL GD/IKRTVAAPSVFIFPPSDE |
| 5345 | 10842 | A | 5668 | 156 | 364 | |
| 5346 | 10843 | A | 5669 | 2 | 2143 | SSDGSWWTGFQWREWROAGRSVN SWDNPKEVRASSKDKSRGSIQEA MRMQSSAKLLCSAWTLAYSIAVRT LSSDSEGQPLVIHRQTGSGEDLQQ TPTDLQLRVLTIRKTNKQKGHPHQ NPISRRQEITKIRAELKKIETQKPFK KINESRSWFFKINKIDRLLARLIKK KIEKNQIDAINKDKGNITNPTEIQT TIREYYKHL YANKLEHLEEMDKFL DIYTLPRLNQEEVESVNRPIGSEIE AIINSLPTKKSPGPDRFTAELYQRYK EELVPFLLKLFQSIEKEGILPNSFYEA SIILISKPGRDTTKENFRPISLMNID AKILNKILANQIQHHKLIHHHQV GFIPGMQGWFNILKSINVIHHINRTK DKNHMIISIEAEKAFDKIQPFMLKT LNKLGIDGTLYLTYLKIIRAIYDKPTA NIILNGQKLEAFPFTGTROGCPLSP LLFNIVLEALARAIQKEKEIGIQLG KEDVKLSLFADDMIVYLENPIVSAQ NLLKLISNFSEVSGYKINVQKSQAFL YTNNRQTESQIMSELPFTIASKRIKY LGIQLTRDVKDLFKENYKPLLNEIK EDTNKWKNIPCSWIGRINIVKMAIL PKTLNQKFSYWFRVKNHYIHQRTFP LKETEFNTIATLYNGASP/RTAPKST GTNGHQASGLPRF*RIAFCSALVKS KRKLYQGYLPGQTDREEGVSWCP GGP |
| 5347 | 10844 | A | 5670 | 1 | 2781 | |
| 5348 | 10845 | A | 5671 | 1 | 2988 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5349 | 10846 | A | 5672 | 1 | 3516 | |
| 5350 | 10847 | A | 5673 | 1 | 2850 | |
| 5351 | 10848 | A | 5674 | 1 | 2850 | |
| 5352 | 10849 | A | 5675 | 1 | 3087 | |
| 5353 | 10850 | A | 5676 | 1 | 3111 | |
| 5354 | 10851 | A | 5677 | 1 | 2742 | |
| 5355 | 10852 | A | 5678 | 1 | 3474 | |
| 5356 | 10853 | B | 5679 | 1 | 3264 | MGDFNTPLSTLDRSMRQKVNKDTQ ELNSALHQADLIDIYRTLHPKSTEYTF FFSAPHHTYSKTDHIVGSKALLSKC KRTEIITNCLSDHSAIKLELRKLNLTQ NRSTTWKLNNQLLNDYWAHNEMK AEIKMFFETNENKDTTYQNLWDTF KAVCRGKFIALNAHKRKQERSKIDT LTSQLEKEKQEQTHSKASRRQEIT KIRAELEIETQKILQKINESRSWFF ERINKIDRPLARLIKKKREKNQIDAI KNDKGDITDPTIEQNTIREYYKHL YTNKLENLEEMDKFLDTYTLPRLN QEEVESLNRPTGPEIVAINSLPTKK SPGPDGFTAKFYQRYKEELVPFLK LFQSIEKEGILPNSFYEASILIPKGR DTTKKENFRPISLMNIDAKILNKILA KRIQQHIKKLIHHDQVGFIPGMQGW FNIHKSINVIQHINRPKDKNHMISID AEKAFDKIQPFMLKTLNKLIGDGT YFKIISAIYDKPTANIILNGQKVEAFP LKTGTRQGCPLSPLFNIVLEVLAR AIRQEKEIKGIQLGKEEVKLSLFADD MIVYLENPVSAQNLLKLISNFSKVS GYKINVQKSQAFLYTNNRQTESQIM SELPFTIASKRIKYLGIQLTRDVKDL FKENYKPLLKEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAIPIK LPMTFFTELEKTTLKFIWNALITKSI LSQKNKAGGITLPDFKLYYKATVT KTAWYWYQNRDIDQWNRTEPSEIT PHIYNLYFDKPEKNKQWGKDSLLN KWCWENWLAICRKLKLPFLTPYT KINSRWIKDLNVRPKTIKTLEENLGI TIQDIGMGKDFMSKTPKAMATKAK IDKWDLIKLSFCTAKQTTIRVNRQ PTKWEKIFATYSSDKGLISRIYNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIREMQIK TTMRYHLTPVRMAIKKSGNNRTW EYNILCSLVPLLCALLWLHLDHHL KEDRTKHLTASDNLEKTELSRWKE RALLYEHRVLRPAIDSQHSAPRRI QGHLVCGSDLTGFMDDVAVILIDVS PF* |
| 5357 | 10854 | A | 5680 | 1 | 3780 | |
| 5358 | 10855 | A | 5681 | 1 | 3290 | MGELITPLSTLDRSTRQKVNKDTQE LNSALHQGDLIDIYRTLHPKSTEYTF FSAPHHTYSKIDHILGSKALLSKCKR TEIITNYLSDHSAIKLELRKLNLTQN RSTTWKLNNLLLNDYWIHNEMKAE |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | IKMFFETNENKDTTYQNLWDAFKA VCRGKFIALNAHKRQERSKIDTLT SQLKELEKQEQTHSKASRRQEITKIR AELKEIETQKTLOKINESRSWFFERI NKIDRPLARLIKKKREKNQIDTIKND KGDIATNPTEIJQTTIREYYKHLNAN KLENLEEMDKFLDTYTLPRLNQEE VESLNRPIITGAEIVAIINSLPTKKSPG PDGFTAESYQRYKEELVPFLLKLFQ SIEKEGILPNSFYEASIIIPKPGRDTT KKENFRLISLMNIDAKILNKILANRI QQHIKKLIHHDQVGFIPGMQGWFN RKSINVIQHINRAKDKNHMIIISIDAE KAFDKIQQPFMLKTLNKLIGIDGTYF KIIRAIYDKPTANIILNGQKLEAFPLK TGTRQGCPLSPLLFNIVLEVLAIR QEKEIKGIQSGKEEVKLSLFADDMI VYLENPIVSDQNLLKLISNFSKVSGY KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLTRDVKDLFK ENYKPLLKEIKEDTNKWKNIPCSW VGRISIVKMAILPKVIYRFSAIPIKLP MTFFTELEKTTLKFIWNQKRARIAK AILSQKNKAGGITLPDFKLYYKATV TKTARYWYQNRDIDQWNRTEPSEI TPHIYNLYLIFDKPEKNKQWGKDSL F NKWCWENWLAICRKLKLDPFLTPY TKINSRWIKDLNIRPKTIKTLEENLG STIQDIGMGKDFMSKTPKAMATKD KIDIWDLIKLSFCTAKETTIRVNGQ PTKWEKIFATYSSDKGLISRICNELK QIYKKKTNNPIKKWAKDMNRHFSK EDIYAAKKHMKKCSSSLAIRQMCIK TTMRYHLTP/VKFRSTSHQSP*REAR GPGPLANAGSPGLRQIPETCHLKHP LGMLLLSHHSALSATHNPTPCKLQS SVMFTTSAAMLSDPWGLRKGLGRE MFSCKTTEGNQLEAGAAEQSLYAL PKPSDLQT |
| 5359 | 10856 | A | 5682 | 1 | 3780 | |
| 5360 | 10857 | A | 5683 | 1 | 2877 | |
| 5361 | 10858 | A | 5684 | 1 | 3126 | |
| 5362 | 10859 | A | 5685 | 3 | 3244 | |
| 5363 | 10860 | A | 5686 | 1540 | 3288 | SSSLHPWDARLVQYTQINKCNPAY KQSQRQKPHYYYQLEAFPLKTGTRQ QPFMLKT/LYSIVLEVLAIRQKKE IKGIQLGKEEVKLSLFADDMIVYLE NPIVSAQNLLKLISNFSKVSGYKINV QKSQAFLYTKNRQTESQIMSELPFTI ASKRIKYLGIQLTRDVKDLFKENYK PLLKEIKEDTNKWKNIPCSWVGRIN IVKMAILPKVIYRFNAIPIKLPMTFFT ELEKTTLKFIWNQKRARIAKSILSQK NKVGGITLPDFKLYYKATVTKTAW YWYQNRVIDQWNRKEPSEITPHY NYLIFDKPEKNKQWGKDSLFWKWC WENWLAICRKLKLDPFLTPYTKINS RWIKDLNVRPKTIKTLEENLGITIQD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=/possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | IGMGKDFMSKTPKAMATKAKIDK WDLIKLSFCTAKETTIRVNRQPTT WEKIFTTYSSDKGLISRIYNELKQIY KKKTNNPIKKWVKDMNRHFSKEDI YAAKKHMKKCSSLAIEMQIKTT MRYHLPVRMAIHKSGNNRCWRG CGEIGTLLHCWWDCCLVQPLWKS VWRFLRDLELEIPFDPAIPLLG IYPNDYKSCCYKDTCT |
| 5364 | 10861 | A | 5687 | 1182 | 3406 | YQSLAETQPKKENFRPISLMNIDAKI LNKILAKRIQQHIKKLIHHDQVGFIP GMQGWFNIRKSINVTQHINRAKDK NHMIISIDAEKAFDKIQQPFMLKTLN KLGIDGTYFKIIRAIYDNPTANIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIQEKEIKGIQLGKEEVK LSLFADNMIVYLENPIVSAQNLLKLI SNFSKVSGYKINVQKSQAFLYTNNR QTESQIMSQLPFTIASKRIKYLGIQLT RDVKDLFKENYKPLLKEIKEDTNK WKNIPCSGVEGRINIVKMAILP/KELE KTTLKFIWNQKRAHIAKSILNQKNK AGGITLPDFKLYYKATVTKTAWYW YQNRDIDQWNRTEPSEITQHIYSYLI FDKPEKNKQWGKDSL FNKWCWEN WLAICRKLKLDPPFLTPYTKINSRWI KDLNVRPKTIKTLEENLGITIQDIGM GKDFMSKTPKAMATKDKIDKWDL VKLKSFCTAKETTIRVNRQPTKWEK IFATYSSDKGLISRIYNELKQIYKKK TNNPIKKWAKDMNRHFSKEDIYAA KKHMKKCSSLAIEMQIKTTMRY HLPVRMAIHKSGNNRCWRGCGE TGTLHCWWDCCLAQPLWKS VWRFLRDLELEIPFDPAIPLLG IYPNDYKSCCYKDTCTRMFIAALFTIAKTWNQP KCPTIIDWIKKMWHIYTMEYYAAIK NDEFVSFVGTWMKLEIILSKLSQEQ KTTHRIFSLIGGN |
| 5365 | 10862 | A | 5688 | 1 | 7578 | |
| 5366 | 10863 | A | 5689 | 16775 | 19999 | KMIKGISPPIPQKYKTTIREYYKHLY ANKLENLEEMDKFLDTYTLPRLNQ EEVESLNRSGTSEIEAINSPTKKS P GPDGFTAIFYQRYKEELVPFLLKLF QSIEKEGILPNSFYESSILIPKGRDT TKKENFRPISPISLMNIDAKILNKILA KRIQQHIKKLMHHDQVGFIPGMQ G WFNIRKSINVIQHINRAKDKNHMIIS IDAEKAFDKIQQPFMLKTLNKL GIDGTYFKIIRAIYDKPTANIILNG QKLEAFPLKTGTRQGCPLSPLLFNIV LEVLARAIQEKEIKGIQLGKEEVKLS LFA DDMIVYVENPIVSAQNLLKLSNFS KVSGYKINVQKSQAFLYTNNRQTE SQIMSELPFTIASKRIKYLGIQLTRD VKDLFKENYKPLLKEIKEDTNKWK NIPCSWVGRINTVKMAILPKVIYRF NAIPIKLPMPPFFTELEKTTLKFIWNQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | KRARIAKSILRQKNKAGGITLPDFK LYYKATVTKTAWYWYQNRDIDQW NRTEPSEITPHIYNYLIFHKPEKNKQ WGKDSL FNKWCWENWLAICRKLK LDPFLTPYTKINSR WIKDLNVRPKTI KTLEENLGITIQDIGMGKDFMSKTP KAMATKDKIDK WDLIKLSFCTAK ETTITVNRQPTKWEKIFATYSSDKG LISRIYNELKQIYK\KKTNNPIKKWA RDMNRHFSKEDIYAAKKHMKKCSS SLAIREMQIKTTMRYHLPVRMAII KKSGNNRSWYFEKINKIDRLRLI KKKREKNQIDA KNDKG DITTDPTET QTTTREYYKHL YANKLENLEEMDK FLDTYNLPRLKQEEVESLNRPIRGSE IVAIINSLPTKKSPGPDGFTAIFYHR YKEELVPLLLKLFQSIEKEVLPNSF YEASIIIPKPDRTAKKENFRPISLM NIDAKILNKILANRIQQHIKKLIHHD QVGFIPGMQGWFNIRKSVNVIQHIN RTKDKNHMII SIDA EKSFDKIQQHF MLKTLNKL GIDGSYLKI RATYDKP TANIILNGQKLEAFPLKTGTRHGCP LSPLLFNIVLEVLARAIRQEKEIKGIQ LGKEEVKLSLFIDDMIVYLENPIISA QNLLKLISNFSSLRIQNQCTKITSILV HQ |
| 5367 | 10864 | A | 5690 | 78 | 308 | |
| 5368 | 10865 | A | 5691 | 1 | 611 | GASLGGFLAQKFAEYTHKSPRVHSL ILCNSFSDTSIFNQWTANSFWLMP AFMLKKIVLGNFSSGPVDPMMADA IDFMVDRLES LGQSELASRLTLNCQ NSYVEPHKIRDIPVTIM\DVFDQSAL STEAKEEMVQA\YPNA\RAHLKTG GNFPYLCRSAEGNLMVQIHLLOFH GTKYAAIDPSMVSAEELEVQKGS GISQEEQ |
| 5369 | 10866 | A | 5692 | 3 | 301 | |
| 5370 | 10867 | A | 5693 | 75 | 361 | |
| 5371 | 10868 | A | 5694 | 3 | 356 | |
| 5372 | 10869 | A | 5695 | 1 | 583 | SPLAAKSPPSLHLE/AFKNITSSSPE RHIFGEDRVVSEQPQVGTLEERNV VEALTGSAASRLRGGTSSRRLSSTP LPKAKRSLESEMYLEGLGRSHIASP SPCPDRMPLSPPTESRHSSSIPPVSSP PEQKVGLYRRQTELQDKSEFSDVD KLAFKDNEEFESSFECVDQKQIEEQ KEEEKIREQQVKERRQR |
| 5373 | 10870 | A | 5696 | 306 | 4412 | RLMMAQSNMFTVADVLSQDELRLK KLYQTFKDRGILDTLKTQLRNQLIH ELMHPVLSGELQPRISVEGSSLLIG ASNSLVADHLQRCGYEYSLSVFFPE SGLAKEKVFTMQDLLQLIKINPTSSL YKSLVSGSDKENQKGFMLHFLKEL AEYHQAKESCNETQTSSTFNRRDS LAEKLQLIDDQFADAYPQRIKFESL EIKLNEYKREIEEQLRAEMCQKLKF FKDTEIAKIKMEAKKKYEKELTMF |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | QNDFEKACQAKSEALVLRKSTLE RIHKHQEIETKEIYAQRQLLLKDMD LLRGREAELKORVEAFELNQLQE EKHKSITEALRRQEQNIKSFEETYDR KLKNELLNFHRLHGVCLALGILI*L WQVLEFGGSSPQECFYFLLEPKGQL VTAGKGK*NCENVPFGIANPDIMLL AVGSQDCA*SLSTKVLTLVGGGQM VQVDWK*PSDYHLGLSLLCAV*I*F TPLLFSVETN*KVIAFSK*PYDNTT LHFV*LSFGTQFIGSRKGFTGHFMFR GYIPGFSIEDFEVYKLSCLAPSGAPV P*ISSCTDNSLSRKMPPEELIFSHSDS\ RYQLELKDDYIIRTNRLIEDERKNK EKA VHLQEELIAINSKKEELNQSVN RVKELELELESVKAQSLAITKQNHM LNEKVKEMSDYSLLKEEKLELLAQ NKLLKQQLEESRNENLRLLNRLAQ APELAVFQKELRKA EKAIVVEHEEF ESCRQALHKQLQDEIEHSAQLKAQI LGYKASVKS LTTQVADLKLQKQT QTALENEVYCNPKQSVIDRSVNGLI NGNVVPCNGEISGDFLNNPFKQENV LARMVASRITNYPTAWVEGSSPDS DLEFVANTKARVKELQQEAEERLEK AFRSYHRRVIKNSAKSPLAAKSPPS LHLLEAFKNITSSSPERHIFGEDRVV SEQPQVGT LKEERN DVVEALTGSE ASRLRGGTSSRRLSSTPLPKAKRSL ECEMYLEGLGRSHIASPSPCPDRMP LPSPTESRHLSIPPVSSPPEQKVGLY RRQTELQDKSEFSDVDKLAFKDNE EFESSFEFNSFNYENTLTSKYVAKW LCWELHRILLGKGAPSYFGFSSRAP VSCPHTALPFFVLVLLLRTHGTIVPH AAAGNMPRQLEMGG LSPAGDMSH VDAAAAAVPLSYQHPSVDQKQIEE QKEEEKIREQQVKERRQREERRQSN LQEVLERERRELEKLYQERKMIEES LKIKIKKELEMENELEMSNQEIKDK SAHSENPLEKYMKIIQQEQDQESAD KVPVPWAGQSVGGGHPGLPWLNFL GRESVFSIEDKKSSK K MVQEGSLVD TLQSSDKVERHCIDPLWRTQQQGTI LEAETGSPDIEPASAFDLRLPLSL |
| 5374 | 10871 | A | 5697 | 3 | 721 | |
| 5375 | 10872 | A | 5698 | 3 | 265 | |
| 5376 | 10873 | A | 5699 | 2 | 216 | |
| 5377 | 10874 | A | 5700 | 3 | 268 | |
| 5378 | 10875 | A | 5701 | 2 | 465 | |
| 5379 | 10876 | A | 5702 | 1 | 196 | |
| 5380 | 10877 | A | 5703 | 2 | 213 | |
| 5381 | 10878 | A | 5704 | 1 | 438 | LQTWGPKQVC/SFFRRGGFEERVLL KNIRENGITGALLPCLDESRFENLGV SSLGERKKLLSYIQLRVQIHVDTMK\ VGYLAGCLVHALGEKQPELQISERD VLCVQIAGLCHDLGHGPF SHMFDG RFIPLARPEVKWTVCIHTVNSQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| 5382 | 10879 | A | 5705 | 2 | 1925 | |
| 5383 | 10880 | A | 5706 | 330 | 590 | |
| 5384 | 10881 | A | 5707 | 3 | 139 | |
| 5385 | 10882 | A | 5708 | 2 | 126 | |
| 5386 | 10883 | A | 5709 | 1 | 157 | |
| 5387 | 10884 | A | 5710 | 85 | 489 | EKPLRWDSHLSCMLCWQAGFEAEQ KVS GSSRKLAI SHALLEMLTPPPAG AMIPPPPSLPGPPRPGMMPVAPHMG GPPMMPMMGPPPPGMMPPVGPAPG MRPPMGGHMPMPMPGPPVTRPPARP MMVPTRPGMTRPDR |
| 5388 | 10885 | A | 5711 | 235 | 874 | VVRRSGFLFCLFVFLSSMNSASVD GHLSGCRLFLFLSPLFRFYCDYCDT/ YLSPHDSPSVRQTHCSGK\KHIENV KDYYQK\WMEK\QSQSL\DKTTAA FQQGKIPPTPFSAPPP\AGA\MIPPPK /SFPGPSPLV*MPKHPHMGPPFW MPPMMGPSFLLGDGWPVG\PASGEL RP\PMG\GHYCQLIAWGPPMDVGPS CPFH*WCPLGPGMTRPDR |
| 5389 | 10886 | A | 5712 | 2 | 406 | FRSPADPPVHCDKE*VLEVQREDED YHDSAKEKDEEDDSITRLLEFELEA YLSHNDYDGIKKLLQQLFLKAPVN TAELTNFLIQQNHIGSVIKHTDVS*D SIDDMDEDEAFGFISLLNLPDRKGT QCGEQIQE |
| 5390 | 10887 | A | 5713 | 3 | 379 | AVERGVPHFPDSPVQRDEEEKEVD TEDDDDDSDQEKDDENALDEEV NIEFVAYSLSYNDYDGIKKLLPQLFI AAPVNTAKLPDLLIQQNHIGSAIKQ TDVSEDSNDDMDEEEASYSIDRLYN |
| 5391 | 10888 | B | 5714 | 65 | 188 | MWGFRIPADALIQRDEEEKEVLNE DEDDDDSDKEKDEEDRX* |
| 5392 | 10889 | A | 5715 | 3 | 365 | |
| 5393 | 10890 | A | 5716 | 3 | 356 | |
| 5394 | 10891 | A | 5717 | 1 | 168 | |
| 5395 | 10892 | A | 5718 | 281 | 422 | |
| 5396 | 10893 | A | 5719 | 1 | 107 | |
| 5397 | 10894 | A | 5720 | 3 | 291 | |
| 5398 | 10895 | A | 5721 | 1 | 1260 | WRTAAFWAFTVFLGDIILLTDVVIH EDQWIGETVLQSTFSSQLLNLSYS SIQPEEYSSVVCVVQLDLLAYVSS KHSYLRDLPPRQPQRVNSIDFVIEL EHLQPDVLVHGSKELLDFITLITEG S/VYSYRGQKQ\KKVMLTV\DQAQG QHYALVLWGSWGQPGYPQLQRKK GYIWEFKYLFVQCNYTLENLELHTT PWSSCECLFDDDIRAITFKAKFQKS APSFVKISDLATHLEDKCSGVVLIK AQISELAFPITASQKIALNAHSSLKSI FSSLPNIVYTGCAKCGLELETDENRI YKQCFSCLPFTMKKIYYPALMTAI DGRHDVCIRVESKLIKILLNISADC LNRVIVPSSEITYGMVVADLFHSL AVSAEPCVLKIQSLFVLDENSYPLQ QDFSLDFYPDIVKHGANARL |
| 5399 | 10896 | A | 5722 | 122 | 390 | TFCVRSGLLDFAPPEPWRWGEKWK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | NWPESLEVWVLVLA VPLTHCDLGI LCCEDISQVLHVSQQI*PTRPGKR*L LGCAEVVLSSSASPG |
| 5400 | 10897 | A | 5723 | 605 | 902 | |
| 5401 | 10898 | A | 5724 | 116 | 470 | |
| 5402 | 10899 | A | 5725 | 1 | 9786 | |
| 5403 | 10900 | A | 5726 | 10996 | 13825 | MLTLRTRRS DGKMKSGFILGLSRAR SSFPMTKKRATPGHCRDPLEGHLRF LKNILPVYDKSLWDFLKL DVTTSIG RRQHRLRVSTAFVYTKNPNGYSFSIP VKVLADKFITPGLKLNDLNSVLVM PTFHVPFTDLQVPSCKLDFREIQIYK KLRTSSFALNLP TLPEVKFPEVDVLT KYSQPEDSLIPFFEITVPESQLTVSQF TLPKSVSDGIAALDLNAVANKIADF ELPTIIVPEQTIEIPSIKFSVPAGIVIPS FQALTARFEVDSPVYNATWSASLK NKADYVETSLDSTCSSTVQFLEYEL NVLGTHKIEDGTLASKTKGTLAHR DFSAEYEEDGKFEG LQEWEGKAHL NIKSPAFTDLHLRYQKDKKGISTA ASPAVGTVGMDMDEDDDFSKWNF YYSPQSSPDKKLTIFKTEL RVRESDE ETQIKVNWEEEAASGLL TSLKDNVP KATGVLYDYVNKYHWEHTGLTLR EVSSKLRRNLQNNAEWVYQGAIRQ IDDIDVRFQKAASGTTGT YQEWKD KAQNL YQELLTQEGQASFQGLKDN VFDGLVRVTQKFHMKVKVHLIDSLID FLNFRPFQFPGKPGIYTREELCTMFI REVGTVLSQVYSKVHNGSEILFSYF QDLVITLPFELRKHKLIDVISM YREL LKDLSKEAQEVFKAIQSLKTTEVLR NLQDLLQFIFQLIEDNIKQLKEMKFT YLINYIQDEINTIFNDYIPYVFKLLKE NLCLNLHKFNEFIQNELQEASQELQ QIHQYIMALREEYFDP SIVGWTVKY YELEEKIVSLIKNLL VALKDFHSEYI VSASNFTSQLSSQVEQFLHRNIQEY LSILTDPDGKGKEKIAELSATAQEII KSQAIATKKIISDYHQQFRYKLQDF SDQLSDYYEKFIAESKRLIDLSIQNY HTFLIYITELLKKLQSTTVMNPYMK LAPGELTIIL |
| 5404 | 10901 | A | 5727 | 3 | 182 | |
| 5405 | 10902 | A | 5728 | 2 | 221 | |
| 5406 | 10903 | A | 5729 | 577 | 722 | |
| 5407 | 10904 | A | 5730 | 3 | 176 | |
| 5408 | 10905 | A | 5731 | 1 | 496 | LLGVAPSRAFQEEILR/DRASFHE/RP NLFALKHPTSKAECTAEKCYRVTK GRGIFPSGSPFKSVTLEDGKTFIPGQ GNNA YVFPGV ALGV IAGGIRHIPDEI FLLTAEQIAQEVFEQHLSQGRLYPP LSTIRDVSLRIA IKVLDYAYKHNLD S YTWPKEAMNVQTV |
| 5409 | 10906 | A | 5732 | 228 | 448 | |
| 5410 | 10907 | A | 5733 | 3 | 1877 | EGEDRGLPRTMGAALGTGTRLAPW |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|---|
| | | | | | | PGRACGALPRWTPTAPAQGCHSKP GPARPVPLKKRGYDVTRNPHLNKG MAFTLEERLQLGIHGLIPPCFLSQDV QLLRIMRYYERQQSDLDKYIILMTL QDRNEKLFYRVLTSDEVKFMPIVYT PTVGLACQHYGLTFRPRGLFITIHD KGHLATMLNSWPEDNIKAVVVDG ERILGLGDLGCYGMGIPVGKLALYT ACGGVNPQQCLPVLLDVGTNNEEL LRDPLYIGLKHQRVHGKAYDDLDD EFMQAVTDKFGINCLIQFEDFANAN AFRLLNKYRNKYCMFNDDIQGTAS VAVAGILAAALRITNNKLSNHVVFVQ GAGEAAMGIAHLLVMALEKEGVPK AEATRKIWMVDSKGLIVKGRSHLN HEKEMFAQDHPESNSLDEVVRLVK PTAIIGVAAIAEA\FTEQILRNMAF RRAPIIFALSNPPRKAECTA\EKCYR VTEGPRGFFASGSPF*GVLIWEMGK TFIPGGRGNNAIYVFPGVATG\IA GGIRHIP\DEIFLLDSRAKLPQEVSEQ HL\SQGRLYPPLSTIRDVSLRIAIVL DYAYKHNLV\SYYPEPKDKEAFCKI PGSYTPDYDSFYT/VDSYIWAQGKA MNVQTV |
| 5411 | 10908 | A | 5734 | 14 | 304 | |
| 5412 | 10909 | A | 5735 | 3 | 413 | |
| 5413 | 10910 | A | 5736 | 2 | 328 | |
| 5414 | 10911 | A | 5737 | 3 | 472 | VTEFAKTCVADESAENCDSKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPRLVRP EVDVMCTAFHDNEETFLKKYLYEI ARRHPYFYAPELLFFAK/RLDELRD EGKASSAKQRLKCASLQKFGERAF KA\VARLSQRFP |
| 5415 | 10912 | A | 5738 | 1 | 2975 | MKWVTFISLLFLFSSAYSRGVFRRT PLGPASSLPQSFLKCLEQVRKIQGD GAALQEKLCA TYKLCHPEELVLLG HSLGIPWAPLSSCPSQALQLAGCLS QLHSGFLYQGLLQALEGISPELGPT LDTLQLDVADFATTIWQQMEELGM APALQPTQGAMPAFASAFQRRAGG VLVASHLQSFLEVSYRVLRLHAQPG GGGDAHKSEVAHRFKDLGEENFKA LVLIAFAQYLQCCPFEDHVKL VNEV TEFAKTCVADESA*/ENCDSKSLHTLF GDKLCTVATLRETYGEMADCCAK QEPERNECFLOHKDDNPRLVRP EVDVMCTAFHDNEETFLKKYLYEI AR\RHPTCIA\ELLFFAK\RYKAAFT ECCQAADKAACL\LPKLDEL\RDEG KASSAKQRLKCASLQKFGKRSFSK HGAVARL\SQEVFPKLEFCQEVSVQV *WTGL*PKFPHGNC\CHGRSCFECC WMDR/RRDLWPKYILWKIQDFDLP S*TGRDCC\EKPLVWGKIPTCICRK WEN*WRLPGLDFAFH*ACLIFVWK VKGCFGQNYCLRAKDVFPGACFLY |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | \DYARRAS*FTLFVPAEEDLPRTYET TLEECCAAADPHECYAKVFDEFKPL VEEPQNLIKQNCLEFEQLGEYKFQN A\LLVRYT\KKVPQVSTPTLVEVSRN LGKVGSKCKHPEAKRMPCAEDYL SVVLNHL CVLHEKTPVSDTVTKCC TESFVNTPPCFSALEVDETYVPKHF NAETFTFHAHISTLSQKERQIKKQT ALVDLVKHKPKATKEQLKAVMDD FAAFVEKCKADDKETCFEEGKK LVAASQAALGLTLPGLPASSLPQSFL LKCLEQVRKIQQDGAALQEKLCAT YKLCHPEELVLLGHSLGIPWAPLSS CPSQALQLAGCLSQLHSGFLYQGL LQALEGISPELGPTLDTLQLDVADF ATTIWQQMEELGMAPALQPTQGA MPAFASAFQRRAGGVLVASHLQSF LEVSYRVLRLHAQP |
| 5416 | 10913 | A | 5739 | 132 | 918 | |
| 5417 | 10914 | A | 5740 | 59 | 335 | |
| 5418 | 10915 | A | 5741 | 219 | 642 | KGWFLGAFHKLKTMKHL LLLTGMG C/VF*VKSQGVNDN\EEGFFSARGHR PLDDKKREEAP\SLRPAPPISGRWAI RASSQPKQLATSKGK*ERKSPWIAG KVVFSRLDPDLG\VVCCSLQGCSVC QGGFFLTTRGKGPFFQELVV |
| 5419 | 10916 | A | 5742 | 1 | 359 | |
| 5420 | 10917 | A | 5743 | 1 | 322 | |
| 5421 | 10918 | A | 5744 | 2 | 862 | FVDGKLHGRGSTDDKGPVAGWINA LEAYQKTGQEIPVNV\RFCLEGME SGSEGLDELIFARKDTFFKDVDYVC ISDNYWLGKKKPCITYGLRGICYFFI EVECSNKDLHSGVYGGSVHEAMTD LILLMEEHKL YDDIDFDIEEFAKDV GAQILLHSHKSHLHLLDPVVVRL GQALFHTAHFPDNIPSSSKDILMHR WRYP\SLH\GIEGAFSGGAKTVIP RKVVVGKFSIRLVNMTPEVVGEQA CGAGTRESMSSLGYP\RAEDDSGLS ALPSQPQPFILYAT |
| 5422 | 10919 | A | 5745 | 455 | 601 | SLAICGSCPFLKTFTITGVFLSSL*YD PSKPALTGRMILSQFVLLNKK |
| 5423 | 10920 | A | 5746 | 25 | 458 | |
| 5424 | 10921 | A | 5747 | 3 | 396 | |
| 5425 | 10922 | A | 5748 | 2 | 797 | AGPAALGGAGLCRAADAGLCSAGC GFVKVVKNKAYFKRYQVKFRRR\R KGKTDYYARKRLVIQDKNKYNTP KYRMIV\RV\TNRDIICQIAY\RIEGD MIVCAA*CTPNLPKYGV\KVGLTNY AAAY\CT\GLLL\ARRL\LNRF\MDN \YEGQV\EVTG\DEYNVESIDWSAQ GAF\TCY\LDAGLAR\TT\TG\NKVFG\ ALKGM\LMGG\LSIPHSSKRFLGLSI PHSTK*ILGYDSENKEFN\AEVRRKHI MGQKFADDLHCLIEEDENASKK |
| 5426 | 10923 | A | 5749 | 172 | 333 | |
| 5427 | 10924 | A | 5750 | 2 | 282 | SLSREVQRQMHLVFFSKNKLKAGY |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | LMSVESSE/CFLEEVG/SQALVAGSY MPPSTVLQQIDS/VANADIINAARKF VS/GQKSMAAGGNLGHHTPLVDEL |
| 5428 | 10925 | A | 5751 | 813 | 998 | |
| 5429 | 10926 | A | 5752 | 1 | 1418 | MKLLTRAGSFSRFYSLKVAPKVKA TAAPAGAPPQPDLEFTKLPNGLVI ASLENYSPVSRIGLFIKAGSRYEDFS NLGTTHLLRLTSSLTTKGASSFKITR GIEAVGGKLSVTATRENMAYTVEC LRGDVDILMEFLNVTTAPEFRRWE VADLQPQLKIDKAVAFQNPQTHVIE NLHAAAYQNALANPLYCPDYRIGK VTSEELHYFVQNHFTSARMALIGLG VSHPVLKQVAEQFLNMRGGLGLSG AKANYRGGEIREQNGDSLVAHAFV AESAVAGSAEANAFAVSLQHGPRLV GHHVKSQGGQPPAHLHQAVAKA/T QQP\FDVSAFNASYSDS\GLFG\YTIS QGHQLAGDCIK\AA\YNQVKTI\QG NLSNTDV\QAAQEPS*KAGIP*WSV ESSE\CFLEEVVRPRALVAGSYMPP VHSSFQQI/DSPKRGWGGAKMPDII NGGKRSFVSGPEVQWAASLENLGT LHLFV |
| 5430 | 10927 | A | 5753 | 150 | 355 | |
| 5431 | 10928 | A | 5754 | 2 | 388 | FLFFFFEMESRSVAQAGVQWCDLG SLQPPPP\GLSDSPALASSVSWITDV RHHLWLIFVFLVETGFRHVGQASLK LPTSGDLPTLASQSAGITGVSHYAW LIFVFLVETEFHHVGGQAGLELLAPS DPPA |
| 5432 | 10929 | C | 5755 | 197 | 415 | MLLYVGLEPHHHTHMLSLWPPRLMF PSVFFFFFFFFFLRQGLALLPRLECS GAILAHCNLHLLGSGDSLASF* |
| 5433 | 10930 | A | 5756 | 764 | 1079 | KGVLFFFFFFKTES\HSVAQAGV\QW CTLGSLQPP/PSRGSSDSPASASRVA GIRGVHHHARLIFVFLVETGFHYVG QAGLELPTSGDSPASASQSAGVTGV SHQCPA |
| 5434 | 10931 | A | 5757 | 213 | 383 | |
| 5435 | 10932 | A | 5758 | 1 | 981 | |
| 5436 | 10933 | A | 5759 | 124 | 354 | |
| 5437 | 10934 | A | 5760 | 2 | 646 | CGGIHGNHTFKMALNQFSDMSFAEI KHKYLWSEPQNCSATKSNYLRGTG PYPPSVDWRKKGNFVSPVKNQGAC GSCWTFSTTGALESAIAIATGKMLS LAEQQLVDCAQDFNNHGCQGGPLPS QAFEYILYNKGIMGEDTYPY\QGKD GYCK\FQPGKAIGFVKDV\ANITIYD EEAMVEAVALYNPVSAFEVTQDF MMYRTGIYSSTSCHKTPDK |
| 5438 | 10935 | A | 5761 | 1 | 218 | |
| 5439 | 10936 | A | 5762 | 272 | 364 | |
| 5440 | 10937 | A | 5763 | 1 | 1956 | |
| 5441 | 10938 | A | 5764 | 105 | 533 | |
| 5442 | 10939 | A | 5765 | 292 | 568 | |
| 5443 | 10940 | A | 5766 | 1 | 279 | |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5444 | 10941 | A | 5767 | 3 | 352 | |
| 5445 | 10942 | A | 5768 | 375 | 485 | TPGLK*FSHDLLNCWDYRCETVH LAEIAQVSEKQI |
| 5446 | 10943 | A | 5769 | 3 | 221 | |
| 5447 | 10944 | A | 5770 | 793 | 1039 | SFSFTFKMLSGRRETTFFGGRFFWF VVVFFFLAGRGSFALVAQAGVQ WRDLRSLQPPPRGFRRFCLSLPGA CGPRYLGG |
| 5448 | 10945 | C | 5771 | 33 | 334 | MSDSGKSSPVAHSILWIWGRDSDA YRDKQHILWPKRADCTESYPRVPA GGELPTYFLPPENKGLRIHELNSDD YSTEEEAQTPDCSITDFTRRHTLSYL V* |
| 5449 | 10946 | A | 5772 | 194 | 593 | |
| 5450 | 10947 | A | 5773 | 1 | 877 | |
| 5451 | 10948 | A | 5774 | 2 | 352 | |
| 5452 | 10949 | A | 5775 | 3 | 726 | EQEVDPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD EMPADLPSLAADFVESKDVCCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKHPEA KRMPCAEDYLS\VVNLNQLCVLH/EK TPVSDRVTKCCTESLVNRRPCFSAL EVDETYVPKEFNAETFTFHADICTL SEKERQIKKQTALVELVKHKPKAT KEQLKAVMDDFAAFVEKCKADD EMPADLPSLAADFVESKDVCCKNYA EAKDVFLGMFLYEYARRHPDYSVV LLLRLAKTYETTLEKCCAAADPHEC YAKVFDEFKPLVEEPQNLIKQNCCEL FEQLGEYKFQNALLVRYTKKVPQV STPTLVEVSRNLKVGSKCKHPEA KRMPCAEDYLSRGPEPVMCVA |
| 5453 | 10950 | A | 5776 | 4274 | 5255 | HTLFGDKLCTVATLRETYGEMADC CAKQEPERNECFLOHKDDNPNLPR LVRPEVDMCTAFHDNGETFLKK* VIRCL*FKIKKHGVTP*ANTL*KLP* QKYFQH*DLEVLL**FFKEVVFDTT KFYTAKNMIKDILKFJETGYNLSQK FKIDKFFNVFRYVYVMVVIDFVLV SNIILPKFNHLCCTHTHTHTLTLFST YLKNDRDKTIMCKLSLIG*LAESEF GGSGENVVDYNYFCNIVCYRK/ADCF SFLKFRYLYEIARRHPYFYAPELFF AKRYKAAFTECCQAADKAACLLPK VLCTRIEKKSLLSNLILSILWDLGT LSV |
| 5454 | 10951 | A | 5777 | 15 | 218 | |
| 5455 | 10952 | A | 5778 | 141 | 318 | |
| 5456 | 10953 | A | 5779 | 1 | 290 | TMSLNRLQEFGTSLVTLDAIPHILPE GDELLEENQEGCFS*SFLFATNATL GPRLWSPWLASGLSLPEACASPKH AAQGPHQKPPRLQPPQHSVCQ |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| 5457 | 10954 | A | 5780 | 2 | 643 | GTRLFEQLGEYKFNALLIRYTKKV PQVSTPTLVEVSRNLGKVGSKCK HPESKKECPVQEDYLSRGSWNQLL CVCIEKTPVKLTESPKC\CTESLG*T GRPLLFSALGKFDWKHYGFPRSF NCLKTFHLSMAGFMAHFFEEGRRT NSRKTNWHLFELVETQGPRQQRQ LKA\VMGGFAAFVEKCKKADDKET CFAEEGKKLVAASQAALGL |
| 5458 | 10955 | A | 5781 | 1 | 135 | |
| 5459 | 10956 | A | 5782 | 1 | 330 | |
| 5460 | 10957 | A | 5783 | 247 | 434 | |
| 5461 | 10958 | A | 5784 | 140 | 2569 | SGSPVLDPSEPQPLAAMHVIKRDGR QERVMFDKITSRIQKLCYGLNMDF VDPAQITMKVIQGLYSGVTTVELDT LAAETAATLTTHKPDYAILAARIAV SNLHKETKKVFSVDMEDLYNYINP HNGKHSPMVAKSTLDIVLANKDRL NSAIIYDRDFSINYFGFKTLERSYLL KINGKVAERPQHMLMRVSVGIHKE DIDAAIETYNLLSERWFTHASPTLFN AGTNRPQLSSCFLLSMKDDSIIEGY DTLKQCALISKSAGGIGVAVSCIRA TGSYIAGTNGNSNGLVPMLRVYNN TARYVDQGGNKRPGAFIYLEPWH LDIFEFLDLKNTGKEEQRRDLFF ALWIPDLFMKRVETNQDWSLMCPN ECPGLDEVWGEEFEKLYASYEKQG RVRKVVKAAQQLWYAIIESQTETGTP YMLYKDSCNRKSNQNLGTIKCSN LCTEIVEYTSKDEVAVCNLAALN MYVTSEHTYDFKKLAEVTKVVVRN LNKIIDINYYPVPEACLSNKRHRPIGI GVQGLADAFILMRYPFESAQAQLLN KQIFETIYYGALEASCDLAKEQGPY ETYEGSPVSKGILQYDMWNVTPTD LWDWKVLKEKIAKYGIRNSLLIAP MPTASTAQILGNNESEPYTSNIYTR RVLSGEFQIVNPHLLKDLTERGLWH EEMKNQIIACNGSIQSIPEIPDDLKQL YKTVWEISQKTVLKMAAERGAFIG QSQSLNIHIAEPNYGKLTSMHFYGW KQGLKTGMYYLRTRPAANPIQFTL NKEKLDKEKVSKEEEKERNTAA MVCSLENRDECLMCGS |
| 5462 | 10959 | A | 5785 | 1 | 161 | |
| 5463 | 10960 | A | 5786 | 2 | 170 | |
| 5464 | 10961 | C | 5787 | 219 | 398 | MSQESVILFYSVGMSLFLFLFRVVT NFTFFPLAVICIRASHLLACPLPSLS LPHQPTH* |
| 5465 | 10962 | A | 5788 | 2 | 472 | |
| 5466 | 10963 | A | 5789 | 3720 | 5308 | PLLPLSPPHLTEVEGQGRMVGTEE TWSNCSGAFKPKCSPQPICLV LAP TRELAQQVQQVADDYGKCSRLKST CIYGGAPKGPQIRDLERGVEICISTP GRIDFLESCKTNLSRCTYLVLDL DKMLDMGSEPQIL*IGDPIRPDRQTL |

| SEQ ID NO: of nucleo-tide sequence | SEQ ID NO: of peptide sequence | Me tho d | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|---|---|----------------|-------------------------------------|---|--|--|
| | | | | | | MWSATWPKEVRQLAEDFLRDYTOI NVGNLELSANHNILQIVDVCMESEK DHKLIQLMEEIMAEKENKTIIFVETK RRCDDLTRRMRRDGWPAMCIHGD KSQPERDWVLNEFRSGKAPILIATD VASRGLDVEDVKFVINYDYPNSSD YVHRIGRTARSTNKGTA YTFPTGN LKQARELIKVLEEANQAINPKLMQL VDHRGGGGGGGGKGGRSRYRTTSSA NNPNLMYQDECRRRLRGVKDGG RDSASYRDRSETDRAGYANGSGYG SPNSAFGAQAGQYTYGQGTYGAAA YGTSSYTAQEY GAGTYGASSTTSTG RSSQSSSQQFSGIGRSGQPQPLMS QQFAQPPGATNMIGYMGQTAYQYP PPPPPPPSRK |
| 5467 | 10964 | A | 5790 | 1 | 307 | |
| 5468 | 10965 | A | 5791 | 2821 | 5781 | |
| 5469 | 10966 | A | 5792 | 1 | 981 | |
| 5470 | 10967 | A | 5793 | 99 | 1023 | NHKDGEKTEQKNGKL*KSECLSKN KAGGITLPDFKLYYKATVTKTAWY WYQNRDIDQWNRTEPSEIMPHIYN HLIFDKPDKNKKWGNDSLFNKWC WENWLAICRKLKLDLPFLTPYTKINS RWIQDLNIRPKNIKTLEEILGNTIQDI GMGKDFKSKTPKAMAIAKIDKW DLIKLKSFCTEKETTIRVNRQPTWE KIFAIYSSEKGLISRIYNELQQIYKKK TNNPIQKRVKDMNRHFSKEDIYAA KKT*KNAHHMKKCSSSPAIREIQI KTTMRYHLIPRMVVIKKSGNKGCV RGCGEIGTVLH |
| 5471 | 10968 | A | 5794 | 3 | 1218 | |
| 5472 | 10969 | B | 5795 | 1 | 1098 | MIDKGDITDPSEIQTIREYYNYLY TNKLENLEEMDKFLDTYTLPRLNQ EEVESLNRPTTGSEIEAIMNSLPTKK VQDQMDSQPNSTRVLEVLARAIQ EKEIKGIQLGKEEVKLSLFADDMIV YLENPIVSARNLLKLIGNFSKVS KINVQKSQAFLYTNNRQTESQIMSE LPFTIASKRIKYLGIQLKRDVKDLFK ENYKPLLKEIKEDTNKWSIPCSWV GRINIMKMAILPKVIYRFNAIPNKLP MPFFTELEKTTLKFIWNQKRAHIAK SILSQKNKAGGITLPDFKLYYKATV TKTAWYWYQNRDIDQWNRTEPSEI MPHIYNHLIFDKPDKNKKWGKDSL FNKWCWENWQPYVES* |
| 5473 | 10970 | A | 5796 | 1 | 1245 | |
| 5474 | 10971 | A | 5797 | 1 | 969 | MIVYLENPIVSAQNLLKLIGNFSRVS GYKINVQKSQAFLYTNNRQTENQII SELPFTIASKRIKYLGIQLTRDVKDL FKENYKTLLKEIKEDTKKWKNIPCS WVGRINIVKIAILPKVIYRFSAIPIKL PMTFFTELEKTTLKFIWNQKRARIA KSILSQKNKAGGIMLPDFKLYYKAT VTKTAWYWYQNRDIDQWNRTEPS EIMLHIYKHLIFDKPDKNKQWGKDS |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|--|
| | | | | | | LFNKWCWENWLAICRKLKLDPFLT PYTKINSRWIKDLNVRPKTIKLEEN LGNTIQDIGTGKDFMSKTPKAMAT KAKIDKWDL/LRFCTAK*TTIRV |
| 5475 | 10972 | B | 5798 | 1 | 1383 | MGDFNTPLSTLDRSKRQKVKKDIQ ELNSALHQVDLIDIYRTPYPKSTEYT FFSAQHHTYSKTDHIVGSKELLSKC KRTEIITNCLSDHSAIKLELRICKLTQ NRSTTWKLNLLNLDYWVHNEMK AEIKMFFETNENKDTTYQNLRTLK AVCRGKFVALNAHQKQKISKIDTL TSQLEKEKQEQTTHSKASRRQEITKI RAELKEIETQKTLOKINDSRSWAIR QEKEIKGIQLGKEEVQLSLFADDMI VHLENPIVSAQNLLKLIGNFSKVS YKINVKKSQAFLYTNNRQTESQIMS EFPFTIASKRIKYLGIQLTRDVKDLF KENYKTLLNEIKEDTNKWKNIPCS WVGRINIVKMAILPKVIYRFNAISIK LPMFTFFTELGKPTLKLWVNQKRVRI AKSILSQKNKAGGIMLPDFKLYYKA TVTKTAWYWYQNRDIDQWNRTEP SEIMPHITTI* |
| 5476 | 10973 | A | 5799 | 1 | 1272 | MIISMDAEKAFDKIQQCFMLKTLNK LGIDGTYLKKIRAIYDKPTVNIILNG QKLEALPLKTGTRQGCPLSPLLFNIV LQALARAIRQEKEIKGIQLGKEEVK LSLFADDMIVYLENPIVKAQNLLKL ISNFSKVSGYKISMQKSQAFLYTNN RQIESQIMSELPFTIASKRIKYLGIQL TRDVKDLFKENYKPLLNEIKEDKN KWKNIPCSWVGRINIVKMAILPKFI WRQKRAHIAKSILSQKNKAGGIKLP DFKLYYKATVTKTAWYWYQNRDI DQWNRTEPSEIMLHIHNYLIFDKPD KNKKWRKDSL FNKWCWENWLAK CRKLKLHPFLTPTTKINSRWIKDLH VRPKTIKLEENLGITIQDKGMGKD FMSKTPEALATKANIDKSDLIKLS SCK\ETTIRVNRQPTWEKIFAIYSS |
| 5477 | 10974 | A | 5800 | 1 | 1398 | |
| 5478 | 10975 | A | 5801 | 564 | 2444 | LTNQKKSRTRWIHSRILPEVQGGAV LEVLARAIRQEKEVKGIGLKEEV KLSLFADDMIVYLENPIISAQNLLKL IGNFSKVSGYKINVQKSQAFLYTNN RETESQIMSELPFTTASRIKYLGIQ LTRDVKELFKETYNPLLNEIKEDTT KWKNIPCSWVGRINIVKIAILPKVICI FNAIPIKLPMTFFTELEKTTLKFIRNQ KRARIAKSILSQKNKAGDVTLPDFK LYYKATVTKTVWYWYQNRDIDQW NRTEPSEIILHIYHNLIFDTPDKNKK WGKDSL FNKLCWENWLAICRKLKL DPFFTPYTKINSRWIKDLHVRPKTIK TLEENLGNTIQDIGIGKDFMTKTQK AMATNAEIHKWDLIKLKHFTAKE TTIRVNRQPTKWENIFAIYSSDKRLI SRIYKELKHIIYKRKTNNPINKWAKD |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MNRHFSKEDIYAANRHMKKCSSSL AIREMQIKTTMRYHLTPVRMAIHK SGNNRCWRGCGENHSQQTITRTKIQ TLHVLNHRWELNNENTWTQEGEH HTLGPVVGWGRGEGQQCISPYSMG KASIPHAVLVVFFGLCQONAPNLDW SLVSLWWCLLGFTNFFCKEPDCKY VRLFRPLGIVFATPPLPPPPSSSTS S |
| 5479 | 10976 | A | 5802 | 1 | 2430 | |
| 5480 | 10977 | A | 5803 | 2022 | 4573 | |
| 5481 | 10978 | A | 5804 | 1169 | 3077 | VHCRFWILALCQMSRLQKSPLLFNI VLEVLAKAIKQEKEIKGIQLGKEEV KLSLFADDMIVYLENPIVSAQNLLIL QLISNFSKVSQYKINVQKSQAFLYT NNRQTESQMRSELPFTVATKRIKYL GIQLTRDVKDLFKENYKLLLNEIKE DTNKWKNIPRSWVGGRINLVKMAI LPKVIYRFNAIPIKLPMTFFTELEKTT LKFIWNQKRALIAKSSLSQKNKTGG ITLPDFKLYYKATVTKTSWYWYQN RDIDQWNRTEPSEIMPHIYNLIFDK PDKNKK\WGKDSL FNK WFWENCL AICRKLKLDPFL\TNYTKINSRWIKD LNFRPKTIKTLEDNLGNTIQDIGMG KDFMSLP/KTPEAMATKAKIDKWD LIKALKSFCTAKETTIRVNRQPTKWE KIFAIYSSDKGLISRIYNELKQIYKK K\TNNPIKKWAKD\TNRHFSKEDIYA ANRHMRCSSSLVIREMQIKTTMR YHLTPVRTAIKKSGDNRCWRGCGE IGTLLHCWWDCCLVQPLWKS VWR FLRDLELEIPFDPAIPLLG IYPKDYKS CCYKDTCTCMFIAALFTIAKTWNQP KCPTMIDWIKKMWHIYTM EYYAAI KNDEFVSFVG TWMKLEIILSKLSQE QKTKHCIFSLIGGN |
| 5482 | 10979 | A | 5806 | 133 | 358 | |
| 5483 | 10980 | A | 5807 | 3 | 164 | |
| 5484 | 10981 | A | 5808 | 1573 | 1720 | |
| 5485 | 10982 | A | 5809 | 1573 | 1720 | |
| 5486 | 10983 | A | 5810 | 1 | 4860 | |
| 5487 | 10984 | A | 5811 | 2 | 2887 | VRVIKSEDDVLVVCPTILTEDGMQA QHLGATLALYRLVKGQSVHQLLPP TYRDVWLEWSDAEKKREELNKME TNKPRDLFIKLLNKLKQQQQQQQ QHSENKRENSDPEESWENLVSDE DFSALSLESANVEDLEPVRNLFRL QSTPKYQKLLKERQQLPVFKHRDSI VETLKRHRVVVVAGETGSGKSTQV PHFLLLEDLLLNEWEASKCNIVCTQP RRISAVSLANRVCELGCENGPGG RNSLCGYQ\RMESRACESTRLLYCT TGVFA*GKLQEDGLSK*CVSMFIVD EV\HER\SVQSDFLIILKEILQKRSD LHLILMSATVDSEKFSTYFTHCPILR ISGRSYPVEVFHLEDIIETGTFVLEK |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | DSEYCQKFLEEEEEVTINVTSKAGGI KKYQEYIPVQTGAHADLNPFYQKY SSRTOHAILYMNPHKINLDLILELLA YLDKSPQFRNIEGAVLIFLPLGLAHQ QLYDLLSNDRRFYSERYKVIALHSI LSTQDQAAAF TLPPPGVRKIVLATNI AETGITIPDVVFVIDTGRTKENKYHE SSQMSSLVETVFSKASALQRQGRA GRVRDGF CFRMYTRERFEGFMDYS VPEILRVPLEELCLHIMKCNLGSPED FLSKALDPPQLQVISNAMNLLRKIG ACELNEPKLTPLGQHLAALPVNVKI GKMLIFGAIFGCLDPVATLAAVMTE KSPFTTPIGRKDEADLAKSALAMAD SDHLTIYNAYLGWKKARQEGGYRS EITYCRRNFLNRTSLLTLEDVKQELI KLVKAAGFSSSTTSTSWEGNRASQT LSFQEIALLKAVLVAGLYDNVGVKII YTKSVDVTEKLACIVETAQGKAQV HPSSVNRDLQTHGWLLYQEKIRYA RVYLRETTLITPPFVLLFGGDIEVQH RERLLSIDGWYFQAPVKIAVIFKQL RVLIDSVLRKKLENPKMSLENDKIL QITELIKTENN |
| 5488 | 10985 | A | 5812 | 1 | 132 | |
| 5489 | 10986 | A | 5813 | 383 | 667 | |
| 5490 | 10987 | A | 5814 | 2444 | 2755 | DYYYYFEMESCSVAQAGVQWRDL GSLQPPPP\SSRDSSASASRVAGTTG MHH/HNQLSFVFLVKMGFHHVQGQA DFELLTSSDLPVSASQSAGITGVSHR ARPLSS |
| 5491 | 10988 | A | 5815 | 1724 | 1941 | AHLLYEWIFFFFFFFFEMESHVAQA GVLWRDLSSLQAPPPGSQSDSPAS ASWVAGITGACHHARHEWNFKC |
| 5492 | 10989 | A | 5817 | 37 | 2496 | |
| 5493 | 10990 | A | 5818 | 2 | 1814 | |
| 5494 | 10991 | A | 5819 | 1 | 394 | |
| 5495 | 10992 | A | 5820 | 2 | 1785 | QLFACVPKTSPPATVISSVTSTCSSL PSVSSAPITSGQAPTTFLPASTSQAQ LSSQKMESFSAVPPTKEKVSTQDQP MANLCTPSSTANSCSSASNTPGAP ETHPSSPTPTSSNTQEEAQSSVSD LSPMSMPFASNSEPAPLTLSPRMV AADNQDTSNLPQLAVPAPRVSHRM QPRGSFYSMVPNATIHQDPQSIFVT NPVTLTPPQGPAAVQLSSAVNIMN GSQMHNIPANKSLPPTFGPATLFNH FSSLFDSSQVPANQGWGDGPLSSRV ATDASFTVQSAFLGNSVLGHLENM HPDNSKAPGFRPPSQR\VSTSPVGLP SIDPSC\SSPSSSSAPL\ASFSGIPGNQ GFFLQGP\APVGGLLSFNQRHF/SFP HPW\TSASNCDSPISVSSGSSSPLS ATS\APPTLG\QPKGSQCQSRIKGY LPPIGTERLARILQGGSVAAQAPAG\T SFVAPVGHSGVWSFGVNAV\EGLAS GWSQSVMG\NHPMAFN NFSGPKAH FSQHQP MERDDSGMVAPSNIFHQP |

| SEQ ID NO: of nucleotide sequence | SEQ ID NO: of peptide sequence | Method | SEQ ID NO: in USSN 09/770,160 | Nucleotide location of first codon for peptide sequence | Nucleotide location of last codon for last amino acid of peptide sequence | Amino acid sequence (X=Unknown; *=Stop codon; /=possible nucleotide deletion; \=possible nucleotide insertion) |
|-----------------------------------|--------------------------------|--------|-------------------------------|---|---|---|
| | | | | | | MASGFVDFSKGLPISMYGGTIIPSHP QLADVPGGPLFNGLHNPDPAWNPM IKVIQNSTECTDAQQVKWA |
| 5496 | 10993 | A | 5821 | 3 | 125 | |
| 5497 | 10994 | A | 5822 | 3448 | 3831 | KNRFCSGVSSNSKSNNSCVYVYIDR DIDTHTYIHIHTNICIHILFFFFETES HALSPRLECNGVISAHCNLHPPGASS DSPASAARVAGVTGTCHHAQLIFFF FVFLVETGFHHAAQAGSQTPDLR* S TPLGFPKC*DYRR/AAIVPGIFLLH*I R*\KVPTLLTDMRNASEYDCDFSTN KIDKEETFS*NASLNLCLLST*PYEM VTHFKGY*ILPLFFFFFLRQSL/SSVT QAGVQWHNLGSLQPLPPGFKQFSC LSLPSSWDYRYQLPRLA/NF/FVFLV ETGFHHAAQAGSQTPDLR |

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, and complementary sequences thereof.
- 5 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 10 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 15 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
- 20 7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively
25 associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - 30 (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-5497.
11. A composition comprising the polypeptide of claim 10 and a carrier.
- 35 12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- 5 b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

- a) contacting the sample under stringent hybridization conditions with
- 10 nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the
- 15 sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

20 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

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17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- 30 b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-5497, a mature protein coding portion of SEQ ID NO: 1-5497, an active domain of SEQ ID NO: 1-5497, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-5497, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 5498-10994, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprises the sequence information of at least one of SEQ ID NO: 1-5497.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 5 28 A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08656

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70; C07K 14/00

US CL : 536/23.1; 435/320.1, 455, 468; 530/300

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B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

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Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| X | Database EST, ID No. AW570442, SHOEMAKER et al. 'Public soybeen EST project', March 2000. See sequence alignment. | 1-9, 19, and 22-26 |
| X | Database EST, ID No. BE609432, SHOEMAKER et al. 'Public soybeen EST project', August 2000. See sequence alignment. | 1-9, 19, and 22-26 |
| Y | WATSON et al. Recombinant DNA. New York: Scientific American Books. 1994, especially pages 72-76. | 19, and 22-26 |



Further documents are listed in the continuation of Box C.



See patent family annex.

| | |
|---|--|
| Special categories of cited documents: | |
| *A* document defining the general state of the art which is not considered to be of particular relevance | *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
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| *O* document referring to an oral disclosure, use, exhibition or other means | * & * document member of the same patent family |
| *P* document published prior to the international filing date but later than the priority date claimed | |

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08656

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
see continuation of Box II

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-9, 19, 22-26 and SEQ ID NO:1

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/08656

Continuation of Box II

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional search fees must be paid.

Groups 1-5497 (claim(s) 1-9, 19, and 22-26), all in part, drawn to an isolated nucleic acid molecule of SEQ ID NO X, vectors, host cells containing same, and the first method of using the nucleic acid molecule to make a polypeptide, wherein X is any one of SEQ ID NOs: 1-5497. For example,

If Group 1 is elected, this correlates to SEQ ID NO:1.

Groups 5498-10994 (claim(s) 10-11, and 20-21), all in part, drawn to a polypeptide of SEQ ID NO Y, wherein Y is any one of SEQ ID NOs: 5498-10994. For example,

If Group 5498 is elected, this correlates SEQ ID NO:5498.

Groups 10995-16491 (claim(s) 12), drawn to an antibody which binds to a protein with SEQ ID NO Y encoded by a nucleic acid with SEQ ID NO X. For example,

If Group 10995 is elected, this correlates to SEQ ID NO:1, and SEQ ID NO:5498.

Groups 16492-21988 (claim(s) 13-16), drawn to methods of detecting the polynucleotide of SEQ ID NO X. For example,

If Group 16492 is elected, this correlates to SEQ ID NO:1

Groups 21989-27485 (claim(s) 17-18), drawn to methods of identifying a binding partner to a polypeptide of SEQ ID NO Y. For example,

If Group 21989 is elected, this correlates to SEQ ID NO:5498.

Groups 27486-32982 (claim(s) 27), drawn to a method for treatment by administering a polypeptide of SEQ ID NO Y. For example,

If Group 27486 is elected, this correlates to SEQ ID NO:5498.

Groups 32983-38479 (claim(s) 28), drawn to a method for treatment by administering an antibody against a protein with SEQ ID NO Y encoded by a nucleic acid with SEQ ID NO X. For example,

If Group 32983 is elected, this correlates to SEQ ID NO:1, and SEQ ID NO:5498.

The inventions listed as Groups 1-38479 do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reason:

The polynucleotides and polypeptides of each invention are unrelated, each to each other. GIBCO BRL discloses random priming nucleic acids comprising sequences that are complements of, and can hybridize to the claimed polynucleotides in claim 1 (GIBCO BRL Catalogue and Reference Guide, 1990). Such nucleic acid renders claims 1 and 2, among the others, not novel. Thus, the technical feature of the polynucleotide sequence is not special and the groups are not so linked under PCT Rule 13.1. Additionally the claimed methods produce different products and/or different results which are not coextensive and which do not share the same technical feature.

Furthermore, the claims are directed to different genes corresponding to SEQ ID NOs: 1-5497. Each of these genes are separate entities which encode different proteins with different activities, binding reactions, antibody recognition, etc. and thus each has its own special technical feature.

Thus, in summary, the inventions listed as Groups 1-38479 are not so linked under PCT Rule 13.1.